Package 'wiqid'

January 2, 2019

Type Package

Title Quick and Dirty Estimates for Wildlife Populations

Version 0.2.1

Date 2019-01-01

Depends HDInterval

Imports stats, truncnorm, MASS, coda

Suggests secr (>= 3.0), shiny, rjags

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Description Provides simple, fast functions for maximum likelihood and Bayesian estimates of wildlife population parameters, suitable for use with simulated data or bootstraps. Early versions were indeed quick and dirty, but optional error-checking routines and meaningful error messages have been added. Includes single and multi-season occupancy, closed capture population estimation, survival, species richness and distance measures.

License GPL-3

NeedsCompilation no

Repository CRAN

Date/Publication 2019-01-02 13:20:03 UTC

R topics documented:

wiqid-package *Fast, simple estimation functions for wildlife population models*

Description

Quick and dirty functions to estimate occupancy, survival, abundance, species richness and diversity, etc. for wildlife populations.

Details

There are a number of sophisticated programs for the analysis of wildlife data, producing estimates of occupancy, survival, abundance, or density. **wiqid** began as a collection of fast, bare-bones functions which can be run from R suitable for use when you are generating hundreds of simulated data sets. The package takes its name from the quick-and-dirty nature of the original functions.

We now use **wiqid** in basic wildlife study design and data analysis workshops, and most functions now have options to check the input data and give informative error messages. Workshop participants have used `lm`, `glm` and functions in the `secr` and `BEST` packages. So **wiqid** tries to match the look and feel of these functions.

All functions use standard data frames or matrices for data input. ML estimation functions return objects of class `wiqid` with parameter estimates on the transformed scale (usually logit functions), variance-covariance matrix, and back-transformed 'real' values; there are `print`, `logLik` and `predict` methods. Bayesian functions (distinguished by an initial "B") return class `Bwiqid` objects, a data frame with a column of MCMC observations for each parameter, plus attributes for MCMC diagnostics; there are `print`, `summary` and `plot` methods.

Simulations and bootstraps often generate weird data sets, eg. capture histories with no captures. These functions do not throw errors or give warnings if the data are weird, but return NAs if estimates cannot be calculated. Errors may still occur if the data are impossible, eg. 6 detections in 5 occasions.

Note that in version 0.2.0 the scaling of continuous covariates has changed to SD=1 (previously SD=0.5). This means that beta coefficients will now be exactly half the size, matching the output from other software.

The functions are listed by topic below.

SIMPLE BAYESIAN POSTERIORS

`Bbinomial`	generate draws from a conjugate beta posterior distribution
`Bpoisson`	generate draws from a conjugate gamma posterior distribution
`Bnormal`	fit a basic normal model to data

OCCUPANCY

Single-season occupancy

occSS	general-purpose ML function; allows site- and survey-specific covariates
BoccSS	general-purpose Bayesian implementation of the above
occSS0	a basic psi(.) p(.) model, faster if this is all you need
BoccSS0	a Bayesian implementation of the psi(.) p(.) model
occSSrn	Royle-Nichols method
occSStime	faster if you have only time effects, also does a plot
occSScovSite	faster if you only have site-specific covariates
occ2sps	single-season two-species models

Multi-season occupancy

occMS	general-purpose function; parameters depend on covariates; slow
occMScovSite	smaller range of covariate options
occMS0	a simple multi-season model with four parameters; faster
occMStime	parameters vary by season; faster

DENSITY from spatial capture-recapture data

We use the **secr** package for ML estimation of density. For Bayesian estimation, **wiqid** offers:

Bsecr0	a Bayesian implementation of the intercept-only model

ABUNDANCE from closed-population capture-recapture data

Although data for genuinely closed populations are rare, this is an important conceptual stepping-stone from CJS models to robust models for survival.

closedCapM0	simple model with constant capture probability
closedCapMb	permanent behavioural response to first capture
closedCapMt	capture probability varies with time
closedCapMtcov	allows for time-varying covariates
closedCapMh2	heterogeneity with 2-mixture model
closedCapMhJK	jackknife estimator for heterogeneity

SURVIVAL from capture-recapture data

Cormack-Jolly-Seber models

survCJS	model with time-varying covariates
BsurvCJS	a Bayesian implementation of the above
survCJSaj	allows for different survival for adults and juveniles

Pollock's robust design

survRDah	2-stage estimation of survival and recruitment
survRD	single stage maximum likelihood estimation

Note that the RD functions are preliminary attempts at coding these models and have not been fully

tested or benchmarked.

SPECIES RICHNESS from species x sample matrices

Rarefaction

richRarefy	Mao's tau estimator for rarefaction
richCurve	a shell for plug-in estimators, for example...
richSobs	the number of species observed
richSingle	the number of singletons observed
richDouble	the number of doubletons observed
richUnique	the number of uniques observed
richDuplicate	the number of duplicates observed

Coverage estimators

richACE	Chao's Abundance-based Coverage Estimator
richICE	Chao's Incidence-based Coverage Estimator
richChao1	Chao1 estimator
richChao2	Chao2 estimator
richJack1	first-order jackknife estimator
richJack2	second-order jackknife estimator
richJackA1	abundance-based first-order jackknife estimator
richJackA2	abundance-based second-order jackknife estimator
richBoot	bootstrap estimator
richMM	Michaelis-Menten estimator
richRenLau	Rennolls and Laumonier's estimator

BIODIVERSITY INDICES

Alpha diversity

All of these functions express diversity as the number of common species in the assemblage.

biodSimpson	inverse of Simpson's index of dominance
biodShannon	exponential form of Shannon's entropy
biodBerger	inverse of Berger and Parker's index of dominance
biodBrillouin	exponential form of Brillouin's index

Beta diversity / distance

All of these functions produce distance measures (not similarity) on a scale of 0 to 1. The function distShell provides a wrapper to produce a matrix of distance measures across a number of sites.

distBrayCurtis	complement of Bray-Curtis index, aka 'quantitative Sorensen'
distChaoJaccCorr	complement of Chao's Jaccard corrected index
distChaoJaccNaive	complement of Chao's Jaccard naive index
distChaoSorCorr	complement of Chao's Sorensen corrected index
distChaoSorNaive	complement of Chao's Sorensen naive index
distChord	distance between points on a normalised sphere

distJaccard	complement of Jaccard's index of similarity
distMorisitaHorn	complement of the Morisita-Horn index of similarity
distOchiai	complement of the Ochiai coefficient of similarity
distPreston	Preston's coefficient of faunal dissimilarity
distRogersTanimoto	complement of the Rogers and Tanimoto's coefficient of similarity
distSimRatio	complement of the similarity ratio
distSorensen	complement of the Sorensen or Dice index of similarity
distWhittaker	Whittaker's index of association

DATA SETS

dippers	Capture-recapture data for European dippers
distTestData	artificial data set for distance measures
GrandSkinks	multi-season occupancy data
KanhaTigers	camera-trap data for tigers
KillarneyBirds	abundance of birds in Irish woodlands
MeadowVoles	mark-recapture data from a robust design study
railSims	simulated detection/non-detection data for two species of rails
salamanders	detection/non-detection data for salamanders
seedbank	number of seeds germinating from samples of soil
Temburong	counts of tree species in a 1ha plot in Brunei
TemburongBA	basal area of tree species in a 1ha plot in Brunei
weta	detection/non-detection data and covariates for weta

DISTRIBUTIONS

These are convenience wrappers for the related d/p/q/r functions in the `stats` package which allow for parameterisation with mean and sd or (for Beta) mode and concentration.

dbeta2 etc	Beta distribution with mean and sd
dbeta3 etc	Beta distribution with mode and concentration
dgamma2 etc	Gamma distribution with mean and sd
dt2 etc	t-distribution with mean, sd and df parameters

UTILITY FUNCTIONS

AICc	AIC with small-sample correction
AICtable	tabulate AIC for several models
allCombinations	model formulae for combinations of covariates
plotPost	graphic display of a posterior distribution
postPriorOverlap	calculation and display of posterior/prior overlap
as.Bwiqid	converts a range of classes of MCMC output to class `Bwiqid` so that `wiqid`'s print and plot functions ca
diagnostic plots	trace, density, and auto-correlation plots for MCMC output.
simpleRhat	a fast alternative to `gelman.diag`.
standardize	a simple alternative to `scale`.

Author(s)

Mike Meredith

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`AICc` *Akaike's Information Criterion with small-sample correction - AICc*

Description

Akaike's Information Criterion with small-sample correction - AICc

Usage

```
AICc(object, ..., nobs, df)
```

Arguments

`object`	a fitted model object for which there exists a logLik method to extract the corresponding log-likelihood, number of parameters, and number of observations.
`...`	optionally more fitted model objects.
`nobs`	scalar; the value to use for the effective sample size; overrides the value contained in the model object(s).
`df`	the value to use for the number of parameters; usually a vector of length = number of models; non-NA elements override the value contained in the corresponding model object.

Details

AICc is Akaike's information Criterion (AIC) with a small sample correction. It is

$$AICc = AIC + 2K(K+1)/(n-K-1)$$

where *K* is the number of parameters and *n* is the number of observations.

This is an S3 generic, with a default method which calls `logLik`, and should work with any class that has a `logLik` method.

Value

If just one object is provided, the corresponding AICc.

If multiple objects are provided, a data frame with rows corresponding to the objects and columns representing the number of parameters in the model (df) and the AICc.

The result will be `Inf` for over-parameterised models, ie. when `df >= nobs - 1`.

Note

For some data types, including occupancy data, there is debate on the appropriate effective sample size to use.

Author(s)

Essentially the same as AIC in package stats. Modified to return AICc by Mike Meredith.

References

Burnham, K P; D R Anderson 2002. *Model selection and multimodel inference: a practical information-theoretic approach*. Springer-Verlag.

See Also

AIC.

Examples

```
# Occupancy models
data(salamanders)
mt <- occSStime(salamanders, p ~ .time, plot=FALSE)
mT <- occSStime(salamanders, p ~ .Time, plot=FALSE)
AIC(mt, mT)
AICc(mt, mT)
# The default sample size = the number of sites
nobs(mt) == nrow(salamanders)
# It is sometimes taken to be the total number of surveys...
AICc(mt, mT, nobs=length(salamanders))
# ... or the minimum of ...
n <- min(sum(rowSums(salamanders) > 0), # sites where species was detected
         sum(rowSums(salamanders) == 0)) # sites where species was not detected
AICc(mt, mT, nobs=n)

# Survival models
data(dippers)
DH <- dippers[1:7]  # Extract the detection histories
null <- survCJS(DH)  # the phi(.) p(.) model
phit <- survCJS(DH, phi ~ .time)  # the phi(t) p(.) model
full <- survCJS(DH, list(phi ~ .time, p ~ .time))  # the phi(t) p(t) model
AICc(null, phit, full)
# for the full model, all 12 parameters cannot be estimated;
#   we can manually set df=11 for this model:
AICc(null, phit, full, df=c(NA, NA, 11))
```

`AICtable` *Make a table for AIC or other criterion*

Description

Takes the output from a call to AIC or AICc returns a data frame with model likelihoods and model weights.

Usage

```
AICtable(x, digits=3, sort)
```

Arguments

`x`	A data frame with the second column being AIC-type values, as returned by `AIC` or `AICc`.
`digits`	integer indicating the number of decimal places to retain.
`sort`	logical indicating whether the table should be sorted by AIC; if missing, the rows are sorted if the table has row names.

Value

Returns the original data frame with the following extra columns

`Delta`	The difference between each value in x and min(x)
`ModelLik`	The model likelihood
`ModelWt`	The model weight

If sort = TRUE, the rows will be sorted by increasing values of AIC/AICc.

Author(s)

Mike Meredith

References

Burnham and Anderson (2002) *Model selection and multimodel inference: a practical information-theoretic approach*, 2 edn. Springer-Verlag.

Examples

```
data(KanhaTigers)
mods <- NULL
mods$M0 <- closedCapM0(KanhaTigers)
mods$Mh2 <- closedCapMh2(KanhaTigers)
mods$MhJK <- closedCapMhJK(KanhaTigers)
mods$Mt <- closedCapMt(KanhaTigers)
AICc <- sapply(mods, AICc)
```

```
AICtable(AICc)
# MhJK does not use likelihood maximisation
```

`allCombinations` *Create formulae for all combinations of covariates*

Description

Create formulae for all combinations of covariates, currently main effects only.

Usage

```
allCombinations(response = "", covars, formulae = TRUE)
```

Arguments

`response`	a character vector of length 1 specifying the response variable.
`covars`	a character vector specifying the covariates/predictors.
`formulae`	if TRUE, only the formulae are returned; otherwise a TRUE/FALSE matrix is returned, with the formulae as row names.

Value

If `formulae = TRUE`, returns a character vector with elements corresponding to the formulae for all possible combinations of main effects.

Otherwise, returns a TRUE/FALSE matrix indicating which covariates are included in each model with the model formulae as the row names.

Author(s)

Mike Meredith

Examples

```
longNames <- colnames(swiss)
# these would produce formulae too long for the console.
names(swiss) <- abbreviate(longNames)
vars <- colnames(swiss)
vars

# Get the formulae for all combinations of covars:
formulae <- allCombinations(vars[1], vars[-1])
formulae[1:10]

# Run all the models with 'lm', put results into a list:
# lms <- lapply(formulae, lm, data=swiss) # This works, but the call is a mess!
lms <- vector('list', 32)
for(i in 1:32)
```

```
  lms[[i]] <- lm(formulae[i], data=swiss)
names(lms) <- formulae

# Extract AICs and look at top model:
AICs <- sapply(lms, AIC)
head(sort(AICs))
lms[[which.min(AICs)]]

# Do a nice table of results:
DeltaAIC <- AICs - min(AICs)
AICllh <- exp(-DeltaAIC/2)
AICwt <- AICllh / sum(AICllh)
order <- order(AICs)
head(round(cbind(AIC=AICs, DeltaAIC, AICllh, AICwt)[order, ], 3))

# Get AIC weights for each of the covars:
is.in <- allCombinations(vars[1], vars[-1], form=FALSE)
head(is.in)   # shows which covars are in each model
covarWts <- AICwt %*% is.in
round(sort(covarWts[1, ], dec=TRUE), 3)
  # the [1, ] is needed because %*% returns a 1-row matrix; 'sort' will coerce
  #   that to a vector but strips out the names in the process.
```

`Bayesian binomial simulation`

Bayesian analysis of binomial data

Description

Simulates a sample from the posterior for a binomial likelihood and beta prior.

Usage

```
Bbinom(y, n, priors=NULL, sample=10000)
Bbinomial(y, n, priors=NULL, sample=100000)
```

Arguments

`y`	the number of successes
`n`	the number of trials
`priors`	an optional list with elements specifying the priors for the mode and concentration of the beta prior distribution; see Details.
`sample`	the number of MCMC observations to be returned.

Details

The function generates a vector of random draws from the posterior distribution of the probability of success. It uses conjugacy to determine the parameters of the posterior beta distribution, and draws independent samples from this.

A prior can be specified with the `priors` argument. A beta prior is used, specified by mode, `mode`, and concentration, `conc`.

When `priors = NULL` (the default), a uniform prior corresponding to beta(1, 1) is used.

Value

Returns an object of class `Bwiqid`, which is a data frame with a column for each parameter in the model.

There are `print` and `plot` methods for class `Bwiqid`, as well as diagnostic plots.

Author(s)

Mike Meredith.

Examples

```
# Generate a sample from a binomial distribution, maybe the number of sites
#   where a species was detected:
n <- 10  # number of trials (sites visited)
( y <- rbinom(1, n, 0.75) ) # number of successes (sites where species detected)
Bbinomial(y, n)  # with uniform prior
Bbinomial(y, n, priors=list(mode=0.4, conc=5))  # with informative prior
```

Bayesian normal estimation

Bayesian modelling of a normal (Gaussian) distribution

Description

Bayesian estimation of centre (μ) and scale (σ) of a normal distribution based on a sample. `Bnormal` uses a gamma prior on the precision, $\tau = 1/\sigma^2$, while `Bnormal2` applies a gamma prior to σ.

Usage

```
Bnormal(y, priors=NULL,
            chains=3, sample=10000, burnin=100)

Bnormal2(y, priors=NULL,
            chains=3, sample=3e4, burnin=0, thin=1, adapt=1000,
            doPriorsOnly=FALSE, parallel=NULL, seed=NULL)
```

Arguments

`y`	a vector (length > 1) with observed sample values; missing values not allowed.
`priors`	an optional list with elements specifying the priors for the centre and scale; see Details.
`doPriorsOnly`	if TRUE, `Bnormal2` returns MCMC chains representing the prior distributions, *not* the posterior distributions for your data set.
`chains`	the number of MCMC chains to run.
`sample`	the number of MCMC observations per chain to be returned.
`thin`	thinning rate. If set to n > 1, n steps of the MCMC chain are calculated for each one returned. This is useful if autocorrelation is high.
`burnin`	number of steps to discard as burn-in at the beginning of each chain.
`adapt`	number of steps for adaptation.
`seed`	a positive integer (or NULL): the seed for the random number generator, used to obtain reproducible samples if required.
`parallel`	if NULL or TRUE and > 3 cores are available, the MCMC chains are run in parallel. (If TRUE and < 4 cores are available, a warning is given.)

Details

The function generates vectors of random draws from the posterior distributions of the population centre (μ) and scale (σ). `Bnormal` uses a Gibbs sampler implemented in R, while `Bnormal2` uses JAGS (Plummer 2003).

Priors for all parameters can be specified by including elements in the `priors` list. For both functions, μ has a normal prior, with mean `muMean` and standard deviation `muSD`. For `Bnormal`, a gamma prior is used for the precision, $\tau = 1$
$sigma^2$, with parameters specified by `tauShape` and `tauRate`. For `Bnormal2`, a gamma prior is placed on σ, with parameters specified by mode, `sigmaMode`, and SD, `sigmaSD`.

When `priors = NULL` (the default), `Bnormal` uses improper flat priors for both μ and τ, while `Bnormal2` uses a broad normal prior (muMean = mean(y), muSD = sd(y)*5) for μ and a uniform prior on (sd(y) / 1000, sd(y) * 1000) for σ.

Value

Returns an object of class `Bwiqid`, which is a data frame with a column for each parameter in the model.

There are `print` and `plot` methods for class `Bwiqid`, as well as diagnostic plots.

Author(s)

Mike Meredith, `Bnormal` based on code by Brian Neelon, `Bnormal2` adapted from code by John Kruschke.

References

Kruschke, J K. 2013. Bayesian estimation supersedes the *t* test. *Journal of Experimental Psychology: General* 142(2):573-603. doi: 10.1037/a0029146

Plummer, Martyn (2003). JAGS: A Program for Analysis of Bayesian Graphical Models Using Gibbs Sampling, *Proceedings of the 3rd International Workshop on Distributed Statistical Computing (DSC 2003)*, March 20-22, Vienna, Austria. ISSN 1609-395X

Examples

```
# Generate a sample from a normal distribution, maybe the head-body length of a
#   carnivore in mm:
HB <- rnorm(10, 900, 15)
Bnormal(HB)  # with improper flat priors for mu and tau
Bnormal(HB, priors=list(muMean=1000, muSD=200))
Bnormal(HB, priors=list(muMean=1, muSD=0.2)) # a silly prior produces a warning.

Bnormal2(HB)  # with broad normal prior for mu, uniform for sigma
Bnormal2(HB, priors=list(muMean=1000, muSD=200, sigmaMode=20, sigmaSD=10))
```

Bayesian Occupancy Single Season

Bayesian single-season occupancy modelling

Description

Functions to estimate occupancy from detection/non-detection data for a single season using a Gibbs sampler coded in R or JAGS.

`BoccSS0` runs a model in R without covariates, and allows priors to be specified as beta distributions for probability of occupancy and probability of detection.

`BoccSS` runs a model in R allowing for covariates, using a probit link and conjugate normal priors, which can be specified as mean and covariance.

Usage

```
BoccSS0(y, n, psiPrior=c(1,1), pPrior=c(1,1),
                    chains=3, sample=30000, burnin=100)

BoccSS(DH, model=NULL, data=NULL, priors=list(),
                    chains=3, sample=30000, burnin=1000, thin=1, parallel,
                    seed=NULL, doWAIC=FALSE)
```

Arguments

`y`	a vector with the number of detections at each site; or a 1/0/NA matrix (or data frame) of detection histories, sites x occasions.
`n`	a scalar or vector with the number of visits (survey occasions) at each site; ignored if `y` is a matrix or data frame.
`psiPrior, pPrior`	parameters for beta distributions to be used as priors for psi and p.
`DH`	a 1/0/NA matrix (or data frame) of detection histories, sites x occasions.
`model`	a list of formulae symbolically defining a linear predictor for each parameter in terms of covariates. If NULL, an intercept-only model is used, ie, psi(.) p(.).
`data`	a data frame containing the variables in the model. For `occSStime`, a data frame with a row for each survey occasion; otherwise, a row for each site. Each site covariate has one column. Each survey covariate has one column for each occasion, and the column name must end with the occasion number (without leading zeros); eg, `Cov1, Cov2, ..., Cov15`. All covariates should be included in `data`, otherwise they will be sought in enclosing environments, which may not produce what you want – and they won't be standardised.
`priors`	a list with elements for prior mean and variance for coefficients; see Details. If NULL, improper flat priors are used.
`chains`	number of MCMC chains to run.
`sample`	minimum number of values to return. The actual number will be a multiple of the number of chains.
`burnin`	number of iterations per chain to discard as burn-in.
`thin`	the thinning interval between consecutive values in the sample
`parallel`	logical; if TRUE *and* `n.chains` > 1 *and* available cores (as returned by `parallel::detectCores`) > 2, chains will be run in parallel. If missing, chains will be run in parallel if `n.chains` < available cores.
`doWAIC`	logical; if TRUE, the Watanabe-Akaike Information Criterion is calculated. NOTE: THIS FEATURE IS STILL EXPERIMENTAL.
`seed`	for reproducible results; note that parallel and sequential methods use different random number generators, so will give different results with the same seed.

Details

`BoccSS0` implements a simple model with one parameter for probability of occupancy and one for probability of detection, ie. a `psi(.) p(.)` model, using a Gibbs sampler implemented in R.

Independent beta distributions are used as priors for `BoccSS0`, as specified by `psiPrior` and `pPrior`. The defaults, `c(1, 1)`, correspond to uniform priors on the probabilities of occupancy and detection.

`BoccSS` uses a probit link to model occupancy and detection as a function of covariates (Dorazio and Rodriguez 2011); most software uses a logistic (logit) link. See Links. Coefficients on the probit scale are about half the size of the equivalent on the logit scale.

Priors for `BoccSS` are listed in the `priors` argument, which may contain elements:

`muPsi` and `muP` : the means for occupancy and detection coefficients respectively. This may be a vector with one value for each coefficient, including the intercept, or a scalar, which will be used for all. The default is 0.

`sigmaPsi` and `sigmaP` : the (co)variance for occupancy and detection coefficients respectively. This may be (1) a vector with one value for each coefficient, including the intercept, which represents the variance, assuming independence, or (2) a scalar, which will be used for all, or (3) a variance-covariance matrix. The default is 1, which for a probit link and standardized covariates is only mildly informative.

When specifying priors, note that numerical covariates are standardized internally before fitting the model. For an intercept-only model, a prior of Normal(0, 1) on the probit scale implies a Uniform(0, 1) or Beta(1, 1) prior on the probability scale.

If you are unsure of the order of predictors, do a short run and check the output, or pass unusable values (eg, `muPsi=numeric(100)`) and check the error message.

Value

Returns an object of class `Bwiqid`, which is a data frame with a column for each parameter in the model.

There are `print` and `plot` methods for class `Bwiqid`, as well as diagnostic plots.

Author(s)

Mike Meredith. `BoccSS` uses the Gibbs sampler described by Dorazio and Rodriguez (2012).

References

MacKenzie, D I; J D Nichols; A J Royle; K H Pollock; L L Bailey; J E Hines 2006. *Occupancy estimation and modeling : inferring patterns and dynamics of species occurrence*. Elsevier Publishing.

Dorazio and Rodriguez. 2012. A Gibbs sampler for Bayesian analysis of site-occupancy data. *Methods in Ecology and Evolution*, 3, 1093-1098

See Also

See the examples for the `weta` data set.

Examples

```
# The blue ridge salamanders data from MacKenzie et al (2006) p99:
data(salamanders)
y <- rowSums(salamanders)
n <- rowSums(!is.na(salamanders))

tmp <- BoccSS0(y, n)
tmp
occSS0(y, n)  # for comparison
plot(tmp)
```

`Bayesian Poisson simulation`
Bayesian analysis of count data

Description

Simulates a sample from the posterior for a Poisson likelihood and gamma prior.

Usage

```
Bpoisson(y, n, priors=NULL, sample=10000)
```

Arguments

`y`	the count
`n`	the sample size
`priors`	an optional list with elements specifying the priors for the mode and SD of the gamma prior distribution; see Details.
`sample`	the number of MCMC observations to be returned.

Details

The function generates a vector of random draws from the posterior distribution of the probability of the observed count. It uses conjugacy to determine the parameters of the posterior gamma distribution, and draws independent samples from this.

A prior can be specified with the `priors` argument. A gamma prior is used, specified by mode, `mode`, and SD, `sd`.

When `priors = NULL` (the default), a uniform prior corresponding to gamma(1, 0) is used.

Value

Returns an object of class `Bwiqid`, which is a data frame with a column for each parameter in the model.

There are `print` and `plot` methods for class `Bwiqid`, as well as diagnostic plots.

Author(s)

Mike Meredith.

Examples

```
# Generate a sample from a gamma distribution, maybe the number of ticks
#   observed on a sample of rodents:
n <- 10  # number of trials (rodents examined)
( y <- rpois(n, 1.2) ) # number of ticks on each rodent
Bpoisson(sum(y), n)  # with uniform prior
```

```
plot(Bpoisson(sum(y), n))
Bpoisson(sum(y), n, priors=list(mode=1, sd=3))  # with informative prior
plot(Bpoisson(sum(y), n, priors=list(mode=1, sd=3)))
```

Bayesian SCR *Spatially explicit capture-recapture (secr) density estimation using MCMC*

Description

Functions to estimate density from mark-recapture data using MCMC methods and JAGS.

Usage

```
Bsecr0(capthist, buffer = 100, start = NULL, nAug = NA, maxSig = 2*buffer,
                    chains=3, sample=1e4, burnin=0, thin=1, adapt=1000,
                    priorOnly=FALSE, parallel=NULL, seed=NULL)
```

Arguments

capthist	a capthist object as defined in package secr including capture data and detector (trap) layout
buffer	scalar mask buffer radius (default 100 m)
start	an optional object of class secr, ie, output from the secr.fit function in package secr; objects of other classes are silently ignored.
nAug	number of individuals in the augmented population; if NA, a suitable default is chosen based on the object passed to start or a preliminary run of secr.fit.
maxSig	maximum value for the scale parameter of the detection function: the prior is *Uniform(0, maxSig)*.
chains	the number of Markov chains to run.
sample	the total number of values to return. The number of values calculated per chain is adapt + burnin + ceiling(sample / chains) * thin.
burnin	the number of values to discard at the beginning of each chain.
thin	the thinning rate. If set to n > 1, n values are calculated for each value returned.
adapt	the number of iterations to run in the JAGS adaptive phase.
priorOnly	if TRUE, the function produces random draws from the appropriate *prior* distributions, with a warning.
seed	set a seed for the random number generators.
parallel	if TRUE or NULL and sufficient cores are available, the MCMC chains are run in parallel; if TRUE and insufficient cores are available, a warning is given.

Details

Bsecr0 implements an intercept-only model (D ~ 1, g0 ~ 1, sigma ~ 1).

Value

Returns an object of class `Bwiqid`, data frame with one column for each parameter, ie. D, lam0 and sigma.

There are print, plot, and window methods for `Bwiqid`.

Author(s)

Mike Meredith

References

Borchers & Efford (2008) Spatially explicit maximum likelihood methods for capture-recapture studies *Biometrics* 64, 377-385

Royle & Dorazio (2008) *Hierarchical modeling and inference in ecology*. Academic Press

See Also

The function `secr.fit` in package `secr`.

Examples

```
# The stoats data set in 'secr'
require(secr)
data(stoatDNA)
# This takes ca 10 mins on a multicore machine:
Bout <- Bsecr0(stoatCH, buffer=1000)
Bout
plot(Bout)
# look at diagnostic plots to see if D is constrained by nAug:
tracePlot(Bout)
densityPlot(Bout)  # Upper values of D doesn't look constrained.
```

`BetaDist` *The Beta Distribution*

Description

Density, distribution function, quantile function and random generation for the Beta distribution with parameters `mean` and `sd` OR `mode` and `concentration`. These are wrappers for `stats::dbeta`, etc. `getBeta*Par` returns the shape parameters.

Usage

```
dbeta2(x, mean, sd)
pbeta2(q, mean, sd, lower.tail=TRUE, log.p=FALSE)
qbeta2(p, mean, sd, lower.tail=TRUE, log.p=FALSE)
rbeta2(n, mean, sd)
getBeta2Par(mean, sd)

dbeta3(x, mode, concentration)
pbeta3(q, mode, concentration, lower.tail=TRUE, log.p=FALSE)
qbeta3(p, mode, concentration, lower.tail=TRUE, log.p=FALSE)
rbeta3(n, mode, concentration)
getBeta3Par(mode, concentration)
```

Arguments

x	vector of parameter values
q	vector of quantiles
p	vector of probabilities
n	number of random draws required.
mean	mean of the beta distribution; cannot be 0 or 1.
sd	standard deviation of the beta distribution; this must be less than `sqrt(mean * (1-mean))`, larger values will return NA, with a warning.
mode	mode of the beta distribution; may be 0 or 1.
concentration	concentration of the beta distribution; concentration = 2 is uniform, and the distribution becomes narrower as concentration increases. It is sometimes referred to as 'sample size', but best thought of as sample size + 2.
lower.tail	logical; if TRUE (default), cumulative probabilities up to x, otherwise, above x.
log.p	logical; if TRUE, probabilities p are given as log(p).

Value

`dbeta*` gives the density, `pbeta*` gives the distribution function, `qbeta*` gives the quantile function, and `rbeta*` generates random deviates.

`getBeta*Par` returns a 2-column matrix with the shape parameters corresponding to `mean` and `sd` OR `mode` and `concentration`.

Author(s)

Mike Meredith

See Also

See the **stats** functions `dbeta`, `pbeta`, `qbeta`, `rbeta`.

Examples

```
# Plot some curves with dbeta2
xx <- seq(0, 1, length.out=101)
plot(xx, dbeta2(xx, 0.4, 0.12), xlab="x", ylab="Probability density",
  main="Beta curves with mean = 0.4", type='l', lwd=2)
lines(xx, dbeta2(xx, 0.4, 0.24), col='darkgreen', lwd=2)
lines(xx, dbeta2(xx, 0.4, 0.28), col='red', lwd=2)
lines(xx, dbeta2(xx, 0.4, 0.36), col='blue', lwd=2)
abline(v=0.4, lty=3, lwd=2)
legend('topright', paste("sd =", c(0.12,0.24, 0.28, 0.36)), lwd=2,
  col=c('black', 'darkgreen', 'red', 'blue'), bty='n')

# Get shape and rate parameters for mean = 0.4 and sd = c(0.12,0.24, 0.28, 0.36, 0.49)
# The last value for sd is too big and will produce NAs and a warning
getBeta2Par(mean = 0.4, sd = c(0.12,0.24, 0.28, 0.36, 0.49))

# The parameterisation with mean and sd doesn't seem intuitive,
#   let's try mode and concentration.
# This does not allow 'bathtub' curves, which are bimodal.
plot(xx, dbeta3(xx, 0.4, 16), xlab="x", ylab="Probability density",
  main="Beta curves with mode = 0.4", type='l', lwd=2)
lines(xx, dbeta3(xx, 0.4, 8), col='darkgreen', lwd=2)
lines(xx, dbeta3(xx, 0.4, 4), col='red', lwd=2)
lines(xx, dbeta3(xx, 0.4, 2), col='blue', lwd=2)
abline(v=0.4, lty=3, lwd=2)
legend('topright', , lwd=2, paste("concentration =", c(16, 8, 4, 2)),
  col=c('black', 'darkgreen', 'red', 'blue'), bty='n')

# The mode can be at 0 or 1:
plot(xx, dbeta3(xx, 1, 16), xlab="x", ylab="Probability density",
  main="Beta curves with mode = 1", type='l', lwd=2)
lines(xx, dbeta3(xx, 1, 8), col='darkgreen', lwd=2)
lines(xx, dbeta3(xx, 1, 4), col='red', lwd=2)
lines(xx, dbeta3(xx, 1, 2), col='blue', lwd=2)
legend('topleft', paste("concentration =", c(16, 8, 4, 2)), lwd=2,
  col=c('black', 'darkgreen', 'red', 'blue'), bty='n')

# Cumulative plots with pbeta3
plot(xx, pbeta3(xx, 0.4, 16), xlab="x", ylab="Cumulative probability",
  main="Beta curves with mode = 0.4", type='l', lwd=2)
lines(xx, pbeta3(xx, 0.4, 8), col='darkgreen', lwd=2)
lines(xx, pbeta3(xx, 0.4, 4), col='red', lwd=2)
lines(xx, pbeta3(xx, 0.4, 2), col='blue', lwd=2)
abline(v=0.4, lty=3, lwd=2)
legend('topleft', paste("concentration =", c(16, 8, 4, 2)), lwd=2,
  col=c('black', 'darkgreen', 'red', 'blue'), bty='n')

# Generate random draws and plot a histogram
rnd <- rbeta3(1e5, 0.4, 8)
hist(rnd, freq=FALSE)
# Add the curve:
lines(xx, dbeta3(xx, 0.4, 8), col='darkgreen', lwd=2)
```

```
# Get shape and rate parameters for mode = 0.4 and concentration = c(2, 4, 8, 16)
getBeta3Par(mode = 0.4, concentration = c(2, 4, 8, 16))
```

`Bwiqid-class` *Conversion to class Bwiqid*

Description

Convert output containing MCMC chains to the class `Bwiqid`. The function is generic, with methods for a range of input objects.

Usage

```
as.Bwiqid(object, ...)

## Default S3 method:
as.Bwiqid(object, ...)

## S3 method for class 'data.frame'
as.Bwiqid(object, header, defaultPlot,
  n.chains=1, Rhat=TRUE, n.eff=TRUE, ...)

## S3 method for class 'mcmc.list'
as.Bwiqid(object, header, defaultPlot, ...)

## S3 method for class 'bugs'
as.Bwiqid(object, header, defaultPlot, ...)

## S3 method for class 'rjags'
as.Bwiqid(object, header, defaultPlot, ...)

## S3 method for class 'runjags'
as.Bwiqid(object, header, defaultPlot, ...)
```

Arguments

`object`	an object containing the MCMC chains; see Details.
`header`	an optional character object with the text to be displayed by `print.Bwiqid`
`defaultPlot`	an optional character object specifying which column should be plotted by default.
`n.chains`	integer, the number of chains included in the object.
`Rhat`	either logical or a vector of Rhat values of length equal to the number of columns in `object`; if `Rhat=TRUE`, `simpleRhat` will be called to provide values.

`n.eff`	either logical or a vector of effective sample sizes of length equal to the number of columns in `object`; if `n.eff=TRUE`, `effectiveSize` will be called to provide values.
`...`	named parameters to be passed to other methods.

Details

Several R packages provide interfaces with WinBUGS, OpenBUGS or JAGS, and have their own classes and methods for printing, plotting, etc. `as.Bwiqid` allows all of these to be converted to a common class.

Value

An object of class `Bwiqid`. This is a data frame with a column for the MCMC chain for each parameter. Column names are stripped of square brackets, and commas are replaced with dots, so (eg) `p[1, 1]` becomes `p1.1`.

Any of the following attributes may be present:

`header`	text to be displayed as the first line when the object is printed.
`call`	the original function call.
`n.chains`	the number of chains.
`n.eff`	a vector of effective sample sizes for the parameters.
`MCerror`	a vector with Monte Carlo errors for the parameters.
`Rhat`	a vector with potential scale reduction factors for the parameters.
`defaultPlot`	the name of the parameter to be plotted as the default by `plot.Bwiqid`.
`timetaken`	an object of class `difftime` with the time taken for the MCMC run.

Author(s)

Mike Meredith.

`Closed Captures` *Analysis of mark-recapture data for closed populations*

Description

Functions to analyse the classical models for closed populations without individual covariates, ie. full likelihood models.

Usage

```
closedCapM0(CH, ci = 0.95, ciType=c("normal", "MARK"), ...)

closedCapMb(CH, ci = 0.95, ciType=c("normal", "MARK"), ...)

closedCapMt(CH, ci = 0.95, ciType=c("normal", "MARK"), ...)
```

```
closedCapMtcov(CH, model=list(p~1), data=NULL, ci = 0.95,
    ciType=c("normal", "MARK"), ...)

closedCapMh2(CH, ci = 0.95, ciType=c("normal", "MARK"), ...)

closedCapMhJK(CH, ci = 0.95)
```

Arguments

`CH`	a 0/1 capture history matrix, animals x occasions; NAs not permitted. For functions `closedCapM0`, `closedCapMh2` and `closedCapMhJK`, `CH` can be a vector of capture frequencies of length equal to the number of occasions - trailing zeros are required.
`model`	a list of formulae symbolically defining a linear predictor for p in terms of covariates.
`data`	a data frame containing the variables in the model, with one row for each occasion.
`ci`	the required confidence interval.
`ciType`	the method used to calculate the confidence interval for population size (N); see Details.
`...`	other arguments passed to `nlm`.

Details

Model M0 assumes all animals have the same capture probability.

Model Mb allows for a permanent behavioural response: capture probability is different for animals that have already been captured at least once.

Model Mh2 and the jackknife estimator allow for heterogeneity in capture probability.

The likelihood maximization routine produces an estimate and standard error for beta = log(*f0*), where *f0* is the number of animals never captured. If `ciType == "normal"`, a confidence interval for beta is calculated as beta +/- crit * SE.beta, where crit is the appropriate multiplier for the confidence interval required, 1.96 for a 95% CI. This confidence interval is then back-transformed to the real scale and added to the number of animals captured (M[t+1]) to give estimates of N.

If `ciType == "MARK"`, the method used by MARK to calculate confidence intervals is used (see MARK help page for Closed Capture Models and Burnham et al (1987, p212)). The beta values are back-transformed with f0.hat = exp(beta) and SE.f0 = SE.beta * f0.hat, and hence CV = SE.f0 / f0.hat. The confidence limits are then

Lower = f0.hat / C + M[t+1]

Upper = f0.hat * C + M[t+1]

where C = exp(crit * sqrt(log(1 + CV^2))).

Confidence intervals for capture probabilities are always calculated on the logit scale and back-transformed to real values.

Value

Returns an object of class `wiqid`, which is a list with the following elements:

`call`	The call used to produce the results
`beta`	Values of the coefficients of the terms in the linear predictors, with standard errors and confidence intervals.
`beta.vcv`	The variance-covariance matrix for the beta estimates.
`real`	Estimates of population size (N) and probability of detection on the real scale, with confidence intervals.
`logLik`	a vector with elements for log(likelihood), number of parameters, and effective sample size. If the variance-covariance matrix cannot be calculated, the second element should be `NA`.

The jackknife estimator does not use likelihood maximisation, so elements `beta` and `beta.vcv` are NULL and `logLik = NA`.

There are `print`, `logLik`, and `nobs` methods for class `wiqid`.

Author(s)

Mike Meredith

References

Basic work on mark-recapture for closed populations is in:

Otis, D L; K P Burnham; G C White; D R Anderson. 1978. Statistical inference from capture data on closed animal populations. *Wildlife Monographs* 62:1-135.

White, G C; D R Anderson; K P Burnham; D L Otis. 1982. *Capture-recapture and removal methods for sampling closed populations*. Los Alamos National Laboratory, Los Alamos NM.

Calculation of the confidence interval for N is in:

Burnham, K.P., Anderson, D.R., White, G.C., Brownie, C., & Pollock, K.H. 1987. *Design and analysis methods for fish survival experiments based on release-recapture*. American Fisheries Society, Bethesda MD.

The jackknife estimator is described in:

Burnham, K P; W S Overton. 1979. Robust estimation of population size when capture probabilities vary among animals. *Ecology* 60:927-936.

Rexstad, E; K Burnham 1992. *User's guide for interactive program CAPTURE*. USGS Patuxent.

Data sets in the examples are from:

White et al, op. cit.

Karanth, Nichols, Kumar, Link, Hines (2004) Tigers and their prey: Predicting carnivore densities from prey abundance. PNAS 101:4854-4858

Examples

```
# Data from White et al (1982):
freq1 <- c(50, 46, 35, 24, 14, 5, 0) # there were 7 capture occasions
closedCapM0(freq1)
closedCapM0(freq1, ci=0.8)
closedCapMh2(freq1)
closedCapMhJK(freq1)

# Kanha tiger data from Karanth et al (2004)
data(KanhaTigers)
closedCapM0(KanhaTigers)
closedCapMb(KanhaTigers)
closedCapMh2(KanhaTigers)
closedCapMhJK(KanhaTigers)
closedCapMt(KanhaTigers)
closedCapMtcov(KanhaTigers, p~.Time)
# Generate some mythical covariates:
covars <- data.frame(Temp = runif(ncol(KanhaTigers), 15, 25),
  Cloud = sample(0:8, ncol(KanhaTigers), replace=TRUE))
closedCapMtcov(KanhaTigers, p~Cloud, data=covars)

# Compare the normal (default) and MARK confidence intervals for N:
rbind(closedCapMt(KanhaTigers)$real[1, ],
      closedCapMt(KanhaTigers, ciType="MARK")$real[1, ])
```

`densityFolded` *Folded kernel density estimation*

Description

Parameters are often constrained to be greater than zero (eg, standard deviation) or within the range (0, 1) (eg, probabilities), but the function `density` often returns non-zero densities outside these ranges. Simple truncation does not work, as the area under the curve is < 1. The function `densityFolded` attempts to identify these constraints and gives an appropriate density.

Usage

```
densityFolded(x, bw = "nrd0", adjust = 1, from, to, ...)
```

Arguments

`x`	a numeric vector from which the estimate is to be computed; missing values not allowed.
`bw`	the smoothing bandwidth to be used; see `link{density}` for details.
`adjust`	the bandwidth used is actually `adjust*bw`.
`from, to`	the lower and upper ends of the grid at which the density is to be estimated; ignored and replaced with 0 or 1 if a constraint is detected.
`...`	other arguments passed to `density`.

Value

Returns an object of class density.

Author(s)

Mike Meredith

Examples

```
require(graphics)
par(mfrow=2:1)

x1 <- rnorm(1e4)            # no constraint on x1
plot(density(x1))
plot(densityFolded(x1))     # no difference

x2 <- abs(rnorm(1e4))       # x2 >= 0, with mode at 0
plot(density(x2))           # density > 0 when x2 < 0, mode around 0.2
abline(v=0, col='grey')
plot(densityFolded(x2))     # mode plotted correctly
abline(v=0, col='grey')

x3 <- rbeta(1e4, 1.5, 1.5)  # 0 <= x3 <= 1
plot(density(x3))           # density > 0 when x2 < 0 and x2 > 1
abline(v=0:1, col='grey')
plot(densityFolded(x3))
abline(v=0:1, col='grey')

x4 <- rbeta(1e4, 1.5, 0.9)  # 0 <= x4 <= 1, with mode at 1
plot(density(x4))           # mode appears to be around 0.95
abline(v=0:1, col='grey')
plot(densityFolded(x4))     # mode plotted correctly
abline(v=0:1, col='grey')

par(mfrow=c(1,1))
```

---

diagnostic plots *Diagnostic graphics for MCMC output*

Description

Display trace plots, density plots or autocorrelation plots for the chains in the MCMC output. Each chain is plotted with a different colour.

Usage

```
diagPlot(object, which, howMany, ask=TRUE, maxRow=4, RhatBad=1.05, ...)
```

```
tracePlot(object, ask=TRUE, ...)

densityPlot(object, ask=TRUE, ...)

acfPlot(object, lag.max=NULL, ask=TRUE, ...)
```

Arguments

object	An object of class Bwiqid.
which	An optional vector of parameter names or numbers.
howMany	How many iterations to plot; if negative, the iterations at the end of the chains will be plotted.
ask	If TRUE, the user will be prompted before the next page of output is displayed.
maxRow	Maximum number of rows to display in one window; each row consists of a trace plot and a density plot for one parameter.
RhatBad	Threshold for Rhat; parameters with Rhat > RhatBad are highlighted in red.
lag.max	Maximum lag at which to calculate the acf; see acf.
...	Additional graphical parameters.

Value

Return NULL invisibly. Used for their plotting side-effects.

Author(s)

Mike Meredith

See Also

plotPost for a histogram and summary statistics.

Examples

```
# Create a fake Bwiqid object:
fake <- data.frame(
  mu0 = rnorm(3000),        # normal, mean zero
  mu10 = rnorm(3000, 10),   # normal, mean 10
  sigma=rlnorm(3000),       # non-negative, skewed
  prob = rbeta(3000, 2,2),  # probability, central mode
  prob0 = rbeta(3000, 1,2), # probability, mode = 0
  N = rpois(3000, 20),      # large integers (no zeros)
  n = rpois(3000, 2),       # small integers (some zeros)
  const1 = rep(1, 3000),    # all values = 1
  const3.2 = rep(3.2, 3000))# all values the same but not integer
class(fake) <- c("Bwiqid", "data.frame")
attr(fake, "n.chains") <- 3
attr(fake, "Rhat") <- c(1, 1.01, 1.05, 1.1, 1.2, 1, NA, 1, NA)
```

```
attr(fake, "n.eff") <- c(2345, NA, 457, 63, 1234, 324, 543, 1, 1)

fake
diagPlot(fake)
diagPlot(fake, which=3:6)
diagPlot(fake, which="prob0")

par(mfrow=c(3,3))
tracePlot(fake, ask=FALSE)
densityPlot(fake, col=1:5, lwd=2, ask=FALSE)
acfPlot(fake, lag.max=10, ask=FALSE)
par(mfrow=c(1,1))
```

`dippers` *Capture-recapture data for European dippers*

Description

A data set that accompanies Program MARK and is included in the `RMark` package in a different format under the name `dipper`.

Usage

```
data(dippers)
```

Format

A data frame with 294 observations on the following 8 variables.

Y1, Y2, Y3, Y4, Y5, Y6, Y7 detection histories for 294 dippers over 7 years: '1' if captured, '0' if not captured.

sex sex of each bird captured.

Source

Lebreton, J-D; K P Burnham; J Clobert; D R Anderson. 1992. Modeling survival and testing biological hypotheses using marked animals: a unified approach with case studies. *Ecological Monographs*, 62, 67-118.

References

Analysis given in many books and papers, notably:

Cooch, E; G White 2014 (13th edition, but constantly updated). *Program MARK: a gentle introduction*. Available online in PDF format at: http://www.phidot.org/software/mark/docs/book/

Examples

```
data(dippers)

DH <- dippers[1:7]  # Extract the detection histories
survCJS(DH)  # the phi(.) p(.) model
survCJS(DH, phi ~ .time)  # the phi(t) p(.) model

# Floods affected the 2nd and 3rd intervals
df <- data.frame(flood = c(FALSE, TRUE, TRUE, FALSE, FALSE, FALSE))
survCJS(DH, phi ~ flood, data=df)

# Including a grouping factor:
survCJS(DH, phi ~ flood * group, data=df, group=dippers$sex)

# Bayesian estimation:


Bdip <- BsurvCJS(DH, parallel=FALSE)
plot(Bdip)
BdipFlood <- BsurvCJS(DH, list(phi ~ flood, p ~ .time), data=df)
BdipFlood
op <- par(mfrow=2:1)
plot(BdipFlood, "phi1", xlim=c(0.3, 0.75), main="No flood")
plot(BdipFlood, "phi2", xlim=c(0.3, 0.75), main="Flood")
par(op)
ratio <- BdipFlood$phi2 / BdipFlood$phi1
plotPost(ratio, compVal=1)
```

`Distance Measures` *Plug-in distance-measure functions for* `distShell`.

Description

Each function takes two (interchangeable) vectors of data and returns a measure of distance between them. Vectors may be just 1/0 values (presence-absence data) or non-negative integers (count data).

Usage

```
distBrayCurtis(d1, d2)
distChaoJaccCorr(d1, d2)
distChaoJaccNaive(d1, d2)
distChaoSorCorr(d1, d2)
distChaoSorNaive(d1, d2)
distChord(d1, d2)
distJaccard(d1, d2)
distMatching(d1, d2)
distMorisitaHorn(d1, d2)
distOchiai(d1, d2)
```

```
distPreston(d1, d2)
distRogersTanimoto(d1, d2)
distSimRatio(d1, d2)
distSorensen(d1, d2)
distWhittaker(d1, d2)
```

Arguments

`d1, d2`	vectors of equal length, specifying the two cases to be compared.

Details

distBrayCurtis Complement of the Bray-Curtis index, see Magurran p.246, where it is referred to as the 'quantitative Sorensen' index. Based on count data.

distChaoJaccCorr, distChaoJaccNaive, distChaoSorCorr, distChaoSorNaive Each is the complement of one of a series of similarity indices which allow for (1) relative abundance of shared species and (2) estimation of number of shared species not detected. Based on count data. See Chao et al. 2005.

distChord Both vectors are normalized so that the sum of squares = 1, ie. they lie on the surface of a sphere of unit radius. The distance measure is the length of the cord joining the two points through the sphere, which is in [0, sqrt(2)], ie. it is sqrt(2) for sites with no species in common. Based on count data. See Zuur et al 2007:166, Legendre & Legendre 1998:279.

distJaccard Complement of the Jaccard index of similarity; also known as "Marczewski-Steinhaus distance". Based on presence-absence data. No. of shared species / Overall number of species.

distMatching A simple matching index: the proportion of elements which match in two presence-absence vectors (ie. present in both or absent in both). Zuur et al 2007:165.

distMorisitaHorn The complement of the Morisita-Horn index of similarity. Based on count data. See Magurran 2004:246 The Morisita-Horn index is also known as "simplified Morisita". The "Morisita" and "Horn" indices are different again! See Krebs 1999:470-471.

distOchiai Complement of the Ochiai coefficient of similarity. Based on count data. See Zuur et al 2007:167, Legendre & Legendre 1998:276.

distPreston Preston's coefficient of faunal dissimilarity (z). Based on presence-absence data. See Preston 1962:418.

distRogersTanimoto Complement of Rogers and Tanimoto's coefficient of similarity. Based on presence-absence data. See Zuur et al 2007:165.

distSimRatio Complement of the Similarity Ratio. Based on count data. See Zuur et al 2007:167.

distSorensen Complement of Sorensen (or Dice) index of similarity. Based on presence-absence data. No. of shared species / Average number of species. Same as Whittaker's distance measure for Incidence (presence-absence) data minus one (Magurran 2004:244).

distWhittaker Whittaker's index of association for Abundance (count) data. See Zuur et al 2007:170.

Value

a scalar, the distance between the two vectors.

Author(s)

Mike Meredith

References

- Chao, A; R L Chazdon; R K Colwell; T-J Shen. 2005. A new statistical approach for assessing similarity of species composition with incidence and abundance data. *Ecology Letters* 8:148-159.
- Krebs, C J 1999. Ecological Methodology. Addison Wesley Longman.
- Magurran, A E 2004. *Measuring biological diversity*. Blackwell.
- Preston, F W. 1962. The canonical distribution of commonness and rarity: Part II. *Ecology* 43:410-432.
- Zuur, A F; E N Ieno; G M Smith 2007. *Analysing ecological data*. Springer.
- Legendre, P; L Legendre 1998. *Numerical ecology*. Elsevier, Amsterdam NL.

See Also

The basic distance computation function is `dist` in package stats. Other functions are `vegan::vegdist` and `labdsv::dsvdis`.

These functions provide the following distance measures:

- binary (in dist) = asymmetric binary = Steinhaus
- binomial (in vegdist)
- bray/curtis (in dsvdis) = bray (in vegdist)
- canberra (in dist and vegdist)
- chao (in vegdist)
- chisq (in dsvdis)
- euclidean (in dist and vegdist)
- gower (in vegdist)
- horn (in vegdist) = Morisita-Horn or simplified Morisita
- jaccard (in vegdist)
- kulczynski (in vegdist)
- manhattan (in dist and vegdist)
- maximum (in dist)
- minkowski (in dist)
- morisita (not simplified!) (in vegdist)
- mountford (in vegdist)
- ochiai (in dsvdis)
- raup (in vegdist) = Raup-Crick
- roberts (in dsvdis)
- ruzicka (in dsvdis)
- sorensen (in dsvdis)
- steinhaus (in dsvdis)= binary

Examples

```
data(distTestData)

distShell(distTestData, distJaccard)

distShell(distTestData, distMorisitaHorn)
```

`distShell` *Distance Matrix Computation*

Description

Produces a 'dist' object using a user-defined distance measure.

Usage

```
distShell(DATA, FUNC, diag = FALSE, upper = FALSE, ...)
```

Arguments

`DATA`	a matrix-like object with variables in COLUMNS, cases in ROWS.
`FUNC`	the distance function; takes two vector arguments and returns a single scalar distance measure. See Details.
`diag`	logical value indicating whether the diagonal of the distance matrix should be printed by print.dist.
`upper`	logical value indicating whether the upper triangle of the distance matrix should be printed by print.dist.
`...`	further arguments, passed to FUNC.

Details

FUNC must be a function of the form foo(x1, x2, ...). The first two arguments must be vectors of equal length, specifying the two cases to be compared. It must return a single scalar distance measure. Similarity measures will work, but for consistency stick to distance measures.

A number of example functions are provided in the package; see `Distance Measures`.

Value

`distShell` returns an object of class `"dist"`, including the attribute `call`.

See `dist` for details of this class.

Author(s)

Mike Meredith, 10 Dec 2006, updated 1 Sept 2012.

See Also

dist in package stats. Also vegan::vegdist and labdsv::dsvdis. See Distance Measures for details of plug-in functions.

Examples

```
# Use the artificial data set, see ?distTestData
data(distTestData)

# Using distance measure functions in this package:
distShell(distTestData, distSorensen)
distShell(distTestData, distMorisitaHorn)

# Write a customised distance function:
K <- function(a1, a2)  {
  shared <- sum(a1 > 0 & a2 > 0)
  notshared <- sum(xor(a1 > 0, a2 > 0))
  shared / notshared
}
distShell(distTestData, K)
# This returns Inf if the number of species not shared is zero. May not be a good measure!
```

---

distTestData *An artificial data set to test distance/dissimilarity measures*

Description

Artificial data for counts of 32 species at 5 sites.

Usage

```
data(distTestData)
```

Format

A matrix with 5 rows (sites), labelled A-B, and 32 columns (species).

Details

Sites A, B and C each have 16 species and 158 individuals.
Sites A and B have the same species, but the numbers of each are different.
Site C has a completely different set of 16 species, but the same number of individuals.
Site D has the same species in the same proportions as A, but twice the number of individuals.
Site E has 32 species and 316 individuals.

Source

Artificial data.

Examples

```
data(distTestData)
# Display the data:
print(t(distTestData))

distShell(distTestData, distJaccard)
#     A   B   C   D
# B 0.0
# C 1.0 1.0
# D 0.0 0.0 1.0
# E 0.5 0.5 0.5 0.5
# Jaccard index ignores counts, so sees AB, AD and BD as identical (zero distance).

round(distShell(distTestData, distMorisitaHorn), 2)
#      A    B    C    D
# B 0.89
# C 1.00 1.00
# D 0.00 0.89 1.00
# E 0.33 0.93 0.33 0.33
# Morisita-Horn index considers proportions, so AD are identical but not AB or BD.

round(distShell(distTestData, distBrayCurtis), 2)
#      A    B    C    D
# B 0.84
# C 1.00 1.00
# D 0.33 0.84 1.00
# E 0.33 0.89 0.33 0.50
# Bray-Curtis index is affected by abundance as well as proportions, so AD are no longer identical.
# Site C only overlaps with D, so AC, BC and CD are 1.00 for all indices.
# Site E overlaps with all the others, so AE, BE, CE and DE all lie between 0 and 1 for all indices.
```

`Diversity indices` *Biodiversity indices*

Description

Common indices of biodiversity, expressed as the number of common species.

Usage

```
biodSimpson(abVec, correct = TRUE)
biodShannon(abVec)
biodBerger(abVec)
biodBrillouin(cntVec)
```

Arguments

`abVec`	a vector of measures of abundance, eg. counts of individuals or biomass, one element per species; or a corresponding matrix or data frame, which will be converted to a vector with `rowSums`.

`cntVec` a vector (or matrix or data frame) of counts of individuals, one element per species. Non-integers will be rounded without warning.

`correct` if TRUE, a small sample correction is applied, and in that case `abVec` should have count data (non-integers will be silently rounded).

Details

biodSimpson Inverse of Simpson's (1949) index of dominance. If `correct = TRUE`, a small-sample correction is applied, giving Hurlbert's (1971) diversity index. Otherwise, the result is equivalent to Hill's (1973) N_2.

biodShannon Exponential form of Shannon's (1948) entropy measure, equivalent to Hill's (1973) N_1.

biodBerger Inverse of Berger & Parker's (1970) index of dominance, equivalent to Hill's (1973) N_Inf.

biodBrillouin Exponential form of Brillouin's index: for small, completely censused populations, Brillouin's index is a more appropriate measure of entropy than Shannon's measure (Maurer & McGill 2011:61).

Value

The relevant index.

Warning

It is important that the proportions of each species in the *sample* represent those in the *population* from which it is drawn. This will not be the case if probability of inclusion varies among species, as often occurs when samples are collected in the field.

Author(s)

Mike Meredith

References

Berger, W H; F L Parker. 1970. Diversity of planktonic Foramenifera in deep sea sediments. *Science* 168:1345-1347.

Hill, M O. 1973. Diversity and evenness: a unifying notation and its consequences. *Ecology* 54:427-431.

Hurlbert, S H. 1971. The nonconcept of species diversity: A critique and alternative parameters. *Ecology* 52:577-586.

Maurer, B A; B J McGill. 2011. Measurement of species diversity. 55-64 in Magurran, A E, and B J McGill, editors. *Biological diversity: frontiers in measurement and assessment.* Oxford University Press, Oxford, New York NY

Shannon, C E. 1948. A mathematical theory of communication. *Bell System Technical Journal* 27:379-423

Simpson, E H. 1949. Measurement of diversity. *Nature* 163:688.

See Also

richSobs and Species richness estimators for alternatives to indices.

Examples

```
data(KillarneyBirds)
apply(KillarneyBirds, 2, biodSimpson)
```

GammaDist *The Gamma Distribution*

Description

Density, distribution function, quantile function and random generation for the Gamma distribution with parameters mean and sd. These are wrappers for stats::dgamma, etc. getGammaPar returns the shape and rate parameters.

Usage

```
dgamma2(x, mean, sd)
pgamma2(q, mean, sd, lower.tail=TRUE, log.p=FALSE)
qgamma2(p, mean, sd, lower.tail=TRUE, log.p=FALSE)
rgamma2(n, mean, sd)
getGammaPar(mean, sd)
```

Arguments

x	vector of parameter values
q	vector of quantiles
p	vector of probabilities
n	number of random draws required.
mean	mean of the gamma distribution
sd	standard deviation of the gamma distribution
lower.tail	logical; if TRUE (default), cumulative probabilities up to x, otherwise, above x.
log.p	logical; if TRUE, probabilities p are given as log(p).

Value

dgamma2 gives the density, pgamma2 gives the distribution function, qgamma2 gives the quantile function, and rgamma2 generates random deviates.

codegetGammaPar returns a 2-ccolumn matrix with the shape and rate parameters corresponding to mean and sd.

Author(s)

Mike Meredith

See Also

See the **stats** functions dgamma, pgamma, qgamma, rgamma.

Examples

```
# Plot some curves with dgamma2
xx <- seq(0, 20, length.out=101)
plot(xx, dgamma2(xx, 5, 1), xlab="x", ylab="Probability density",
  main="Gamma curves with mean = 5", type='l', lwd=2)
lines(xx, dgamma2(xx, 5, 2), col='darkgreen', lwd=2)
lines(xx, dgamma2(xx, 5, 4), col='red', lwd=2)
lines(xx, dgamma2(xx, 5, 8), col='blue', lwd=2)
abline(v=5, lty=3, lwd=2)
legend('topright', paste("sd =", c(1,2,4,8)), lwd=2,
  col=c('black', 'darkgreen', 'red', 'blue'), bty='n')

# Cumulative plots with pgamma2
plot(xx, pgamma2(xx, 5, 1), xlab="x", ylab="Cumulative probability",
  main="Gamma curves with mean = 5", type='l', lwd=2)
lines(xx, pgamma2(xx, 5, 2), col='darkgreen', lwd=2)
lines(xx, pgamma2(xx, 5, 4), col='red', lwd=2)
lines(xx, pgamma2(xx, 5, 8), col='blue', lwd=2)
abline(v=5, lty=3, lwd=2)
legend('bottomright', paste("sd =", c(1,2,4,8)), lwd=2,
  col=c('black', 'darkgreen', 'red', 'blue'), bty='n')

# Generate random draws and plot a histogram
rnd <- rgamma2(1e5, 5, 2)
hist(rnd, freq=FALSE)
# Add the curve:
lines(xx, dgamma2(xx, 5, 2), col='darkgreen', lwd=2)

# Get shape and rate parameters for mean = 5 and sd = c(1,2,4,8)
getGammaPar(mean = 5, sd = c(1,2,4,8))
```

---

getMCerror *MCMC error using the batch method*

Description

The Monte Carlo error is a result of using (pseudo-)random numbers to generate the MCMC chain: multiple runs with different random number sequences produce different chains with slightly different summary statistics. A simple way to estimate MC error is to divide values into batches and calculate the variance of the batch means. See Lunn et al (2013, p77) for details. There is a trade-off

between number of batches and batch size, and we make these approximately equal (only approximately as the number of batches must be a multiple of the number of chains). The function gives the same values as `coda::batchSE` with an appropriate `batchSize`.

Usage

```
getMCerror(object, n.chains, SDpc=FALSE)
```

Arguments

`object`	a vector, matrix or data frame with MCMC output in columns
`n.chains`	scalar integer, the number of chains concatenated to form the columns of `x`.
`SDpc`	logical, if TRUE the MC error is expressed as a percentage of the standard deviation of the corresponding posterior.

Value

If SDpc is FALSE (the default), a named vector with the estimates of MC error. If TRUE, the MC error as a percentage of the standard deviation of the posterior chain. A value <5% of SD is adequate for most purposes, but <1.5% is needed to properly estimate tail probabilities (Lunn et al 2013, p78-79).

Author(s)

Mike Meredith

References

Lunn, D., Jackson, C., Best, N., Thomas, A., & Spiegelhalter, D. (2013) *The BUGS book: a practical introduction to Bayesian analysis*, Chapman and Hall.

Roberts, G.O. (1996). Markov chain concepts related to sampling algorithms. In *Markov Chain Monte Carlo in practice* (eds W.R. Gilks, D.J. Spiegelhalter & S. Richardson). Chapman & Hall, London.

Examples

```
# Get some output to use
data(salamanders)
y <- rowSums(salamanders)
( out <- BoccSS0(y, 5) )

getMCerror(out)
getMCerror(out, SDpc=TRUE)
```

GrandSkinks *Multi-season detection data for grand skinks*

Description

Results of an occupancy survey of 352 rocky outcrops ("tors") looking for grand skinks. Tors were surveyed up to 3 times per year for 5 years. The surrounding terrain was characterised as natural grassland or pasture.

Usage

```
data(GrandSkinks)
```

Format

A data frame with 352 observations on the following 16 variables.

A1, A2, A3, B1, B2, B3, C1, C2, C3, D1, D2, D3, E1, E2, E3 an array of observations of detection (1) or nondetection (0) of skinks for each of 3 occasions in 5 years. NA indicates occasions when a tor was not visited.

habitat a factor indicating the type of grassland surrounding the tor.

Details

The data are provided as a data frame, such as would result from reading in data from a text file. Further formatting is needed before using these for analysis: see the examples.

Source

Data distributed with PRESENCE.

References

MacKenzie, D I; J D Nichols; A J Royle; K H Pollock; L L Bailey; J E Hines 2006. *Occupancy estimation and modeling : inferring patterns and dynamics of species occurrence*. Elsevier Publishing.

Examples

```
data(GrandSkinks)

# Extract detection histories:
DH <- GrandSkinks[, 1:15]
occMS0(DH, 3)
```

KanhaTigers *Capture history matrix for camera-trapped tigers*

Description

Capture history matrix for camera-trapped tigers

Usage

```
data(KanhaTigers)
```

Format

A matrix with 26 rows for animals trapped and 10 columns for the trapping occasions. KanhaTigers[i, j] = 1 if animal i was trapped on occasion j, zero otherwise.

Source

Karanth, Nichols, Kumar, Link, Hines (2004) Tigers and their prey: Predicting carnivore densities from prey abundance. PNAS 101:4854-4858

Examples

```
data(KanhaTigers)
dim(KanhaTigers)
closedCapMt(KanhaTigers)
```

KillarneyBirds *Abundance of woodland birds*

Description

The number of territories held by breeding males in 9 blocks of woodland habitat in County Killarney, Ireland.

Usage

```
data(KillarneyBirds)
```

Format

A data frame with counts for 31 species in 9 blocks of habitat. Row names are the English species names.

`Oak1` first of 3 oak wood sites

`Oak2` second of 3 oak wood sites

`Oak3` third of 3 oak wood sites

`Yew` a mature yew wood

`Sitka` a Sitka spruce plantation

`Norway` a Norway spruce plantation

`Mixed` a mixed broadleaf wood

`Patchy` a wood with patches of broadleaf and conifer trees

`Swampy` a swampy seasonally-flooded woodland

Source

Batten L. A. (1976) Bird communities of some Killarney woodlands. *Proceedings of the Royal Irish Academy* 76:285-313.

References

Magurran (2004) *Measuring Biological Diversity*, p237

Solow (1993) A simple test for change in community structure. *J Animal Ecology* 62:191-193.

Examples

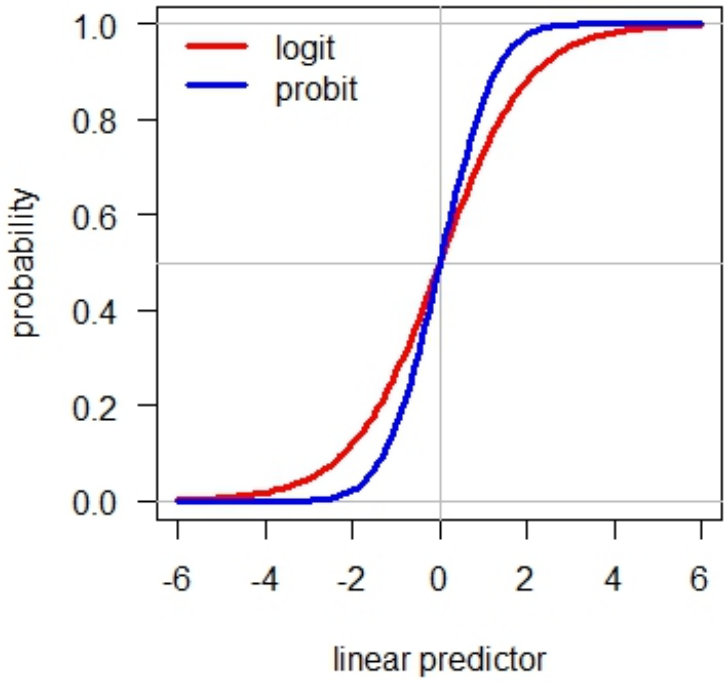
```
data(KillarneyBirds)
## number of species in each block of habitat:
colSums(KillarneyBirds > 0)
```

`Links` *Logit and probit links for generalised linear modelling*

Description

Generalised linear models with binomial resonse variables ("logistic regression") use a link function to link the response on a (0,1) scale to a linear predictor on (-Inf, Inf). The canonical link is the logistic ("logit") function, which has some nice theoretical properties and can be interpreted as the log of the odds of success. Other links are available, notably the cumulative standard normal ("probit") link, which allows for Gibbs sampling with truncated normal distributions. For that reason, several of the Bayesian estimation functions in **wiqid** use the probit link.

The form of the logit and probit links are shown in the figure below.



Both curves are symmetric, with probability = 0.5 when the linear predictor = 0. The probit curve is steeper, so coefficients in a probit regression will be smaller than those in a logit regression (by a factor of about 1.7).

`MeadowVoles` *Robust design mark-recapture data for meadow voles*

Description

Data for adult male meadow voles *Microtus pennsylvanicus* from a live-trapping study at Patuxent Wildlife Research Center (Nichols et al 1984). Trapping was carried out for 5 consecutive nights each month for 6 months (June to December 1981).

Usage

```
data(MeadowVoles)
```

Format

A data frame with 171 observations on the following 31 variables.

A1, A2, A3, A4, A5, B1, B2, B3, B4, B5, C1, C2, C3, C4, C5, D1, D2, D3, D4, D5, E1, E2, E3, E4, E5, F1, F2, F3, F4, F
: a 1/0 array of capture data for voles for each of 5 occasions per month for 6 months.

freq a column with -1/1, where -1 indicates that the animal was not released after the last recorded capture.

Details

The data are provided as a data frame, such as would result from reading in data from a text file. Further formatting is needed before using these for analysis: see the examples.

Source

Williams, Nichols, Conroy (2002) *Analysis and management of animal populations: modeling, estimation, and decision making* Academic Press, San Diego CA

References

Nichols, Pollock, Hines (1984) The use of a robust capture-recapture design in small mammal population studies: A field example with *Microtus pennsylvanicus. Acta Theriologica* 29:357-365.

Examples

```
data(MeadowVoles)

# Extract detection histories:
DH <- MeadowVoles[, 1:30]
freq <- MeadowVoles$freq

survRD(DH, freq=freq, occsPerSeason=5)
```

---

occ2sps *Single-season two-species occupancy estimation*

Description

Estimates occupancy and probability of detection for two species, where one (dominant) species affects the occupancy or detection of the other (subordinate) species (see Richmond et al, 2010). The model has the following parameters:

psiA	probability of occupancy of species A
psiBa	probability of occupancy of B if A is absent
psiBA	probability of occupancy of B if A is present
pA	probability of detection of species A if B is absent
rA	probability of detection of species A if both are present
pB	probability of detection of species B if A is absent
rBa	probability of detection of species B if both are present but A was not detected
rBA	probability of detection of species B if both are present and A was detected

Usage

```
occ2sps(DHA, DHB, model=NULL, data=NULL, ci = 0.95, verify=TRUE)
```

Arguments

DHA	a 1/0/NA matrix (or data frame) of detection histories, sites x occasions, for the dominant species.
DHB	detection histories for the subordinate species in the same format as DHA.
model	a list of formulae symbolically defining a linear predictor for any of the parameters in the model. The default, NULL, is equivalent to `list(psiA~1, psiBa~1, pA~1, pB~1)`; parameters not included in the list are given the following values: `psiBA <- psiBa, rA <- pA, rBa <- p`
data	a data frame containing the variables in the model. If `data = NULL`, a faster algorithm is used, and any covariates in the model will be ignored.
ci	the confidence interval to use.
verify	if TRUE, the data provided will be checked.

Value

Returns an object of class `wiqid`, see wiqid-class for details.

Benchmarks

Output has been checked against output from PRESENCE (Hines 2006) v.5.5 for the `railSims` data set. Real values are the same to 4 decimal places, and AICs are the same.

Author(s)

Mike Meredith

References

Richmond, Hines, Beissinger (2010) Two-species occupancy models: a new parameterization applied to co-occurrence of secretive rails. *Ecological Applications* 20(7):2036-2046

MacKenzie, D I; J D Nichols; A J Royle; K H Pollock; L L Bailey; J E Hines 2006. *Occupancy estimation and modeling : inferring patterns and dynamics of species occurrence*. Elsevier Publishing.

See Also

See the example data set `railSims`. See `occSS` for single-season single-species occupancy estimation.

Examples

```
data(railSims)
# Extract the two detection histories
DHA <- railSims[, 1:3]
DHB <- railSims[, 4:6]

# Default model (no interaction)
occ2sps(DHA, DHB)


# Add a submodel for psiBA, so that psiBA and psiBa are separated:
occ2sps(DHA, DHB, model = psiBA ~ 1)

# Add covariates for psiA and psiBA; only display beta coefficients:
occ2sps(DHA, DHB, model = list(psiA ~ logArea, psiBA ~ reeds), data=railSims)$beta

# Model corresponding to the data generation model
occ2sps(DHA, DHB, list(psiA ~ logArea, psiBA ~ reeds, rBA ~ 1), data=railSims)$beta
```

Occupancy Multi-Season

Multi-season occupancy estimation

Description

Functions to estimate occupancy from detection/non-detection data for multiple seasons. `occMS` is the general purpose function; it allows for site-, season- and survey-level covariates, but it is slow. `occMScovSite` excludes survey-level covariates, but is fast. `occMStime` and `occMS0` are simpler and faster.

Usage

```
occMS0(DH, occsPerSeason, ci=0.95, verify=TRUE, ...)

occMStime(DH, occsPerSeason, model=NULL, data=NULL, ci=0.95, verify=TRUE, ...)

occMS(DH, occsPerSeason, model=NULL, data=NULL, ci=0.95, verify=TRUE, ...)

occMScovSite(DH, occsPerSeason, model=NULL, data=NULL, ci=0.95, verify=TRUE, ...)
```

Arguments

`DH`	a 1/0/NA matrix (or data frame) of detection histories, sites x occasions. Rows with all NAs are silently removed.
`occsPerSeason`	the number of survey occasions per season; either a scalar if the number of surveys is constant, or a vector with one element for each season.

`model`	a list of formulae symbolically defining a linear predictor for each parameter in terms of covariates. The default corresponds to an intercept-only model.
`data`	a data frame containing the variables in the model: one row for each season or between-season period for `occMStime` and one for each site for `occMScovSite`. Each survey covariate has one column for each occasion, and the column name must end with the occasion number (without leading zeros); eg, `Cov1, Cov2, ..., Cov15`.
`ci`	the confidence interval to use.
`verify`	if TRUE, the data provided will be checked.
`...`	other arguments passed to `nlm`.

Details

`occMS0` implements a simple multi-season model with one parameter each for initial occupancy, colonisation, local extinction, and probability of detection, ie. a `psi1(.) gamma(.) epsilon(.) p(.)` model.

`occMStime` allows for between-season differences in colonisation, local extinction, and probability of detection, either with covariates given in `data` or the in-built covariates `.interval` (for colonisation or extinction, or `.season` (for detection).

`occMScovSite` allows for between-season differences in colonisation, local extinction, and probability of detection with the in-built covariate `.season` and for between-site differences with covariates defined in `data`.

`occMS` allows for survey-level covariates in addition to the above, and separate covariates for between-season colonisation and local extinction.

Value

Returns an object of class `wiqid`, see wiqid-class for details.

Benchmarks

Output has been checked against output from PRESENCE (Hines 2006) v.5.5 for the `GrandSkinks` data set. Real values are mostly the same to 4 decimal places, though there is occasionally a discrepancy of 0.0001. AICs are the same.

Author(s)

Mike Meredith

References

MacKenzie, D I; J D Nichols; G B Lachman; S Droege; J A Royle; C A Langtimm. 2002. Estimating site occupancy rates when detection probabilities are less than one. *Ecology* 83:2248-2255.

MacKenzie, D I; J D Nichols; A J Royle; K H Pollock; L L Bailey; J E Hines 2006. *Occupancy estimation and modeling : inferring patterns and dynamics of species occurrence*. Elsevier Publishing.

Hines, J. E. (2006). PRESENCE - Software to estimate patch occupancy and related parameters. SGS-PWRC. http://www.mbr-pwrc.usgs.gov/software/presence.html.

MacKenzie, D I; J D Nichols; J E Hines; et al 2003. Estimating site occupancy, colonization, and local extinction when a species is imperfectly detected. *Ecology* 84, 2200-2207.

Examples

```
data(GrandSkinks)
DH <- GrandSkinks[, 1:15]

occMS0(DH, 3)

occMStime(DH, 3, model=list(gamma ~ .interval, epsilon~1, p~.season))
occMScovSite(DH, 3,
   model=list(psi1~habitat, gamma ~ .interval, epsilon~habitat, p~.season),
   data=GrandSkinks)
```

Occupancy Single Season

Single-season occupancy estimation

Description

Functions to estimate occupancy from detection/non-detection data for a single season. `occSS` is the general-purpose function, and `occSStime` provides plots of detection probability against time. `occSS0` and `occSScovSite` are faster functions for simpler models with summarized data. See `occSSrn` for the Royle-Nichols model for abundance-induced heterogeneity in detection probability.

Usage

```
occSS(DH, model=NULL, data = NULL, ci=0.95, link=c("logit", "probit"), verify=TRUE, ...)

occSStime(DH, model=p~1, data=NULL, ci=0.95, plot=TRUE, link=c("logit", "probit"),
  verify=TRUE, ...)

occSS0(y, n, ci=0.95, link=c("logit", "probit"), ...)

occSScovSite(y, n, model=NULL, data = NULL, ci=0.95, link=c("logit", "probit"), ...)
```

Arguments

`DH`	a 1/0/NA matrix (or data frame) of detection histories, sites x occasions.
`model`	a list of formulae symbolically defining a linear predictor for each parameter in terms of covariates. If NULL, an intercept-only model is used, ie, psi(.) p(.).
`ci`	the confidence interval to use.

`data`	a data frame containing the variables in the model. For `occSStime`, a data frame with a row for each survey occasion; otherwise, a row for each site. Each site covariate has one column. Each survey covariate has one column for each occasion, and the column name must end with the occasion number (without leading zeros); eg, `Cov1, Cov2, ..., Cov15`. All covariates should be included in `data`, otherwise they will be sought in enclosing environments, which may not produce what you want – and they won't be standardised.
`link`	the link function to use, either logit or probit; see Links.
`verify`	if TRUE, the data provided will be checked.
`plot`	if TRUE (default), draws a plot of probability of detection vs time.
`y`	a vector with the number of detections at each site.
`n`	a scalar or vector with the number of visits (survey occasions) at each site.
`...`	other arguments passed to `nlm`.

Details

`occSS` allows for psi or p to be modelled as a logistic or probit function of site covariates or survey covariates, as specified by `model`. It includes a built in `.time` covariate which can be used for modelling p with time as a fixed effect, and `.Time` for a linear or quadratic trend. A built-in `.b` covariate corresponds to a behavioural effect, where detection depends on whether the species was detected on the previous occasion or not.

`occSStime` allows for time-varying covariates that are the same across all sites, eg, moon-phase. A categorical time variable `.time` and a time trend `.Time` are built-in. A plot of detection probability vs time is produced if `plot=TRUE`.

`occSS0` implements a simple model with one parameter for probability of occupancy and one for probability of detection, ie. a `psi(.) p(.)` model.

`occSScovSite` allows for site covariates but not for occasion or survey covariates.

Numeric covariates in `data` are standardised to facilitate convergence. This applies to binary covariates coded as 1/0; if this is not what you want, code these as TRUE/FALSE or as factors.

For speed, use the simplest function which will cope with your model. For example, you can run psi(.) p(.) models in `occSScovSite` or `occSS`, but `occSS0` is much faster.

Value

Returns an object of class `wiqid`, see wiqid-class for details.

Benchmarks

Output has been checked against output from PRESENCE (Hines 2006) v.5.5 for the `salamanders` and `weta` data sets. Real values are mostly the same to 4 decimal places, though there is occasionally a discrepancy of 0.0001. AICs are the same.

Author(s)

Mike Meredith

References

MacKenzie, D I; J D Nichols; G B Lachman; S Droege; J A Royle; C A Langtimm. 2002. Estimating site occupancy rates when detection probabilities are less than one. *Ecology* 83:2248-2255.

MacKenzie, D I; J D Nichols; A J Royle; K H Pollock; L L Bailey; J E Hines 2006. *Occupancy estimation and modeling : inferring patterns and dynamics of species occurrence*. Elsevier Publishing.

Hines, J. E. (2006). PRESENCE - Software to estimate patch occupancy and related parameters. SGS-PWRC. http://www.mbr-pwrc.usgs.gov/software/presence.html.

See Also

See the examples for the `weta` data set. See `occ2sps` for single-season two-species models and `occMS` for multi-season models.

Examples

```
# The blue ridge salamanders data from MacKenzie et al (2006) p99:
data(salamanders)
occSS(salamanders)
occSStime(salamanders, p ~ .time)  # time as a fixed effect
occSStime(salamanders, p ~ .Time + I(.Time^2))  # a quadratic time effect
occSS(salamanders, p ~ .b)

# or use the fast functions with y, n format:
y <- rowSums(salamanders)
n <- rowSums(!is.na(salamanders))
occSS0(y, n)
occSScovSite(y, n)
```

`plot.Bwiqid` *Plot method for objects of class 'Bwiqid'*

Description

Method to display a plot showing the posterior probability distribution of one of the parameters of interest.

Usage

```
## S3 method for class 'Bwiqid'
plot(x, which=NULL, credMass=0.95,
           ROPE=NULL, compVal=NULL, showCurve=FALSE,
           showMode=FALSE, shadeHDI=NULL,  ...)
```

Arguments

x	an object of class Bwiqid.
which	character: indicates which parameter to plot. If NULL and x has a defaultPlot attribute, that parameter is plotted; otherwise the parameter in column 1 is plotted.
credMass	the probability mass to include in credible intervals; NULL suppresses plotting.
ROPE	a two element vector, such as c(-1, 1), specifying the limit of the ROPE on the estimate; see Details.
compVal	a value for comparison with the parameter.
showCurve	logical: if TRUE, the posterior density will be represented by a kernel density function instead of a histogram.
showMode	logical: if TRUE, the mode of the posterior density will be shown instead of the mean.
shadeHDI	specifies a colour to shade the area under the curve corresponding to the HDI; NULL for no shading. Ignored if showCurve = FALSE. Usecolours() to see a list of possible colours.
...	other graphical parameters.

Details

The posterior distribution is shown as a histogram or density curve (if showCurve = TRUE), together with the Highest Density Interval. A ROPE and comparison value are also shown if appropriate.

The probability that a parameter precisely zero (or has any other point value) is zero. More interesting is the probability that the difference from zero may be too small to matter. We can define a region of practical equivalence (ROPE) around zero, and obtain the posterior probability that the true value lies therein.

Value

Returns an object of class histogram invisibly. Used mainly for the side effect.

Author(s)

Mike Meredith, adapted from code by John Kruschke.

References

Kruschke, J. K. 2013. Bayesian estimation supersedes the *t* test. *Journal of Experimental Psychology: General* 142(2):573-603. doi: 10.1037/a0029146

See Also

plotPost.

Examples

```
# See examples in dippers.
```

plotComb *Display a posterior probability distribution from the comb method*

Description

Plot the posterior probability distribution for a single parameter calculated using the comb method described by Kruschke (2015).

Usage

```
plotComb(x, y, credMass = 0.95, plot = TRUE, showMode = FALSE, shadeHDI = NULL, ...)
```

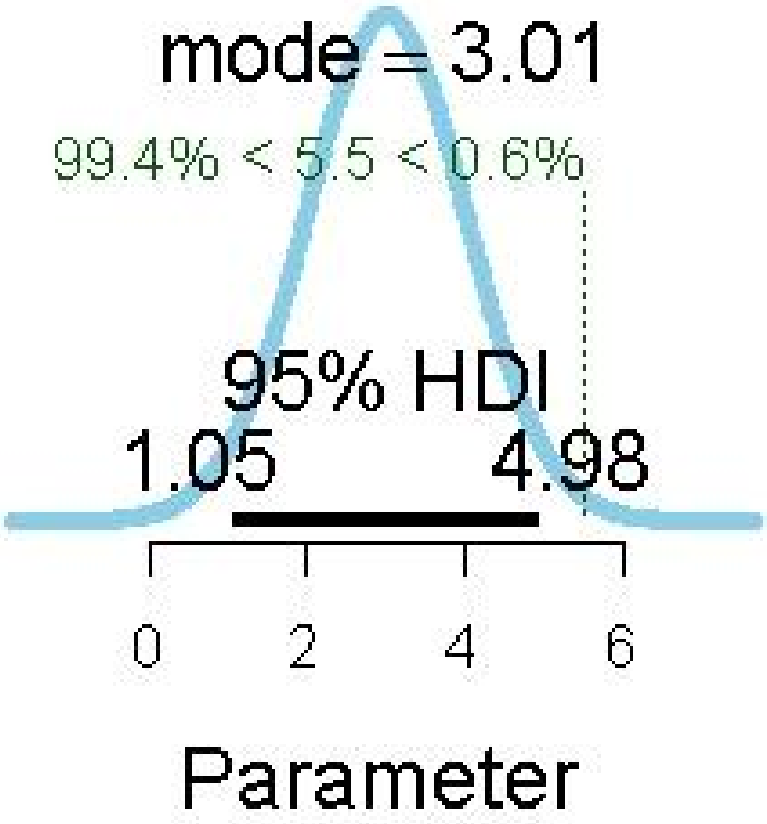
Arguments

x	A vector of equally-spaced possible values for the parameter. The range should cover all values of the parameter with non-negligible probability. (To restrict the range displayed in the plot, use xlim.)
y	A vector of probabilities corresponding to the values in x.
credMass	the probability mass to include in credible intervals; set to NULL to suppress plotting of credible intervals.
plot	logical: if TRUE, the posterior is plotted.
showMode	logical: if TRUE, the mode is displayed instead of the mean.
shadeHDI	specifies a colour to shade the area under the curve corresponding to the HDI; NULL for no shading. Use colours() to see a list of possible colours.
...	additional graphical parameters.

Details

The function calculates the Highest Density Interval (HDI). A multi-modal distribution may have a disjoint HDI, in which case the ends of each segment are calculated. No interpolation is done, and the end points correspond to values of the parameter in x; precision will be determined by the resolution of x.

If plot = TRUE, the probability density is plotted together with either the mean or the mode and the HDI.



Value

Returns a matrix with the upper and lower limits of the HDI. If the HDI is disjoint, this matrix will have more than 1 row. It has attributes `credMass` and `height`, giving the height of the probability curve corresponding to the ends of the HDI.

Author(s)

Mike Meredith

See Also

For details of the HDI calculation, see `hdi`.

Examples

```
# Generate some data:
N <- 0:100
post <- dpois(N, 25)
# Do the plots:
plotComb(N, post)
plotComb(N, post, showMode=TRUE, shadeHDI='pink', xlim=c(10, 50))
```

```
# A bimodal distribution:
post2 <- (dnorm(N, 28, 8) + dnorm(N, 70, 11)) / 2
plotComb(N, post2, credMass=0.99, shade='pink')
plotComb(N, post2, credMass=0.80, shade='grey')
```

---

plotPost *Graphic display of a posterior probability distribution*

Description

Plot the posterior probability distribution for a single parameter from a vector of samples, typically from an MCMC process, with appropriate summary statistics.

Usage

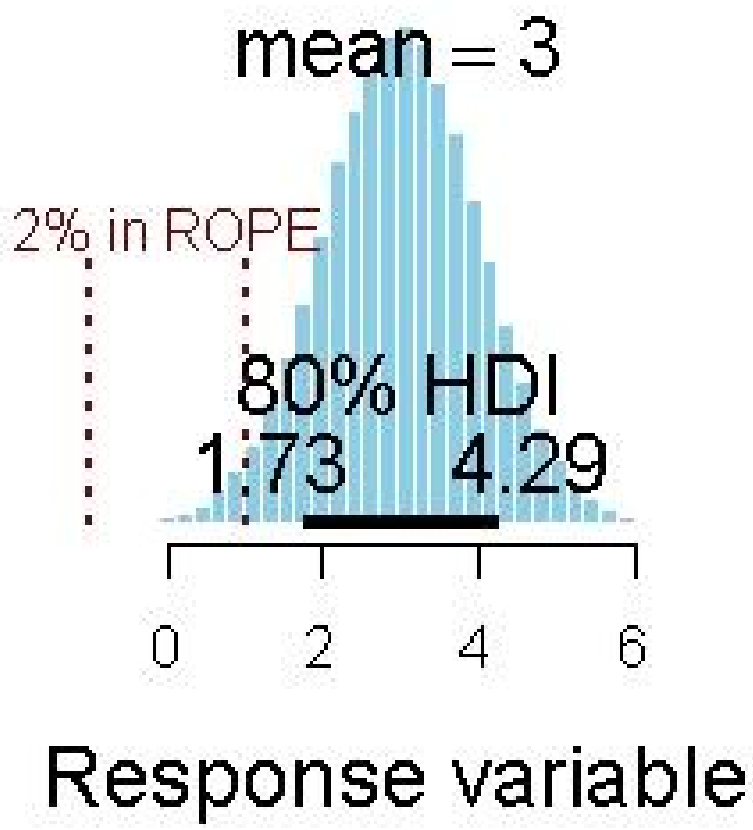
```
plotPost(paramSampleVec, credMass = 0.95, compVal = NULL, ROPE = NULL,
  HDItextPlace = 0.7, showMode = FALSE, showCurve = FALSE, shadeHDI = NULL, ...)
```

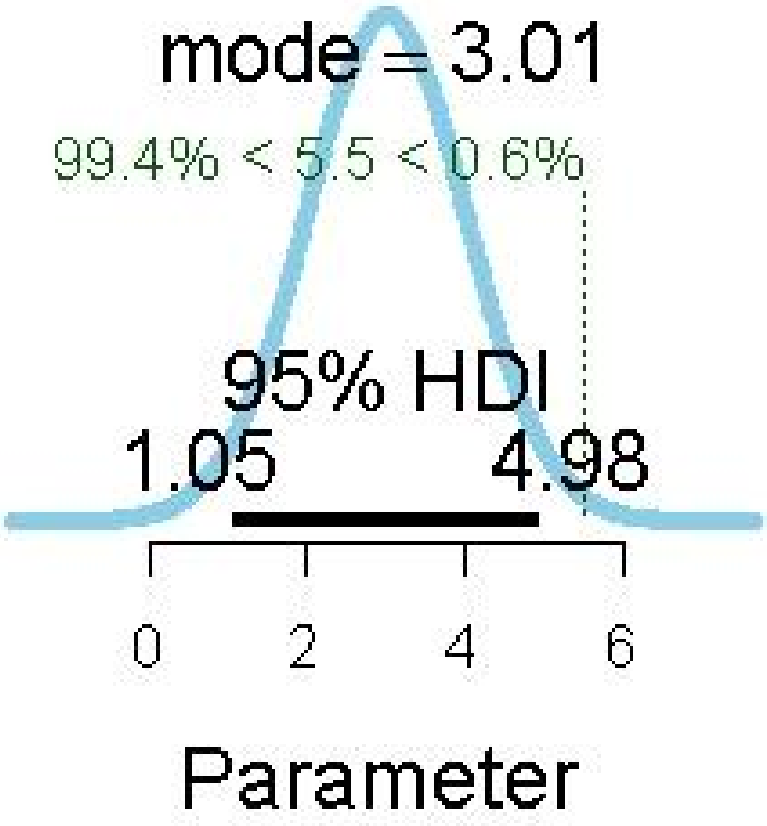
Arguments

paramSampleVec	A vector of samples drawn from the target distribution.
credMass	the probability mass to include in credible intervals; set to NULL to suppress plotting of credible intervals.
compVal	a value for comparison with those plotted.
ROPE	a two element vector, such as c(-1, 1), specifying the limits of the Region Of Practical Equivalence.
HDItextPlace	a value in [0,1] that controls the horizontal position of the labels at the ends of the HDI bar.
showMode	logical: if TRUE, the mode is displayed instead of the mean.
showCurve	logical: if TRUE, the posterior density will be represented by a kernel density function instead of a histogram.
shadeHDI	specifies a colour to shade the area under the curve corresponding to the HDI; NULL for no shading. Ignored if showCurve = FALSE. Usecolours() to see a list of possible colours.
...	graphical parameters and the breaks parameter for the histogram.

Details

The data are plotted either as a histogram (above) or, if showCurve = TRUE, as a fitted kernel density curve (below). Either the mean or the mode of the distribution is displayed, depending on the parameter showMode. The Highest Density Interval (HDI) is shown as a horizontal bar, with labels for the ends of the interval.


mean = 3
2% in ROPE
80% HDI
1.73
4.29
0
2
4
6
Response variable



If values for a ROPE are supplied, these are shown as dark red vertical dashed lines, together with the percentage of probability mass within the ROPE. If a comparison value (`compVal`) is supplied, this is shown as a vertical green dotted line, together with the probability mass below and above this value.

Value

Returns an object of class `histogram` invisibly. Used for its plotting side-effect.

Author(s)

John Kruschke, modified by Mike Meredith

See Also

For details of the HDI calculation, see `hdi`.

Examples

```
# Generate some data
tst <- rnorm(1e5, 3, 1)
plotPost(tst)
plotPost(tst, col='wheat', border='magenta')
```

```
plotPost(tst, credMass=0.8, ROPE=c(-1,1), xlab="Response variable")
plotPost(tst, showMode=TRUE, showCurve=TRUE, compVal=5.5)

# For integers:
tst <- rpois(1e5, 12)
plotPost(tst)

# A severely bimodal distribution:
tst2 <- c(rnorm(1e5), rnorm(5e4, 7))
plotPost(tst2)                  # A valid 95% CrI, but not HDI
plotPost(tst2, showCurve=TRUE)  # Correct 95% HDI
plotPost(tst2, showCurve=TRUE, shadeHDI='pink')
```

`postPriorOverlap` *Overlap between posterior and prior probability distributions.*

Description

Calculates and displays the overlap between a posterior distribution (as a vector of samples, typically from an MCMC process) and a prior distribution (as a vector of samples or as a function).

Usage

```
postPriorOverlap(paramSampleVec, prior, ..., yaxt="n", ylab="",
           xlab="Parameter", main="", cex.lab=1.5, cex=1.4,
           xlim=range(paramSampleVec), ylim=NULL,
           colors=c("skyblue", "yellow", "green", "white"), breaks=NULL)
```

Arguments

`paramSampleVec`	a vector of samples drawn from the target distribution.
`prior`	*either* a vector of samples drawn from the prior distribution *or* the name for the density function of the distribution; standard R functions for this have a `d-` prefix, eg. `dbeta`. Arguments required by the function must be specified by their (abbreviated) names in the `...` argument; see the examples.
`...`	named parameters to be passed to `prior` when it is a function.
`yaxt`	a character which specifies the y axis type; the default, "n", suppresses plotting, "s" allows plotting.
`ylab`	text to use as the label of the y axis.
`xlab`	text to use as the label of the x axis.
`cex.lab`	the magnification to be used for x and y labels relative to the current setting of `cex`
`cex`	a numerical value giving the amount by which plotting text and symbols should be magnified relative to the default
`xlim`	a vector of length 2 giving the limits for the x axis.

ylim	a vector of length 2 giving the limits for the y axis, or NULL to adjust for the actual range of density.
colors	A vector of four colours for the posterior, prior, overlap, and borders. See the Color Specification section of par
main	text to use as the main title of the plot
breaks	controls the histogram break points or the number of bars; see hist.

Value

Returns the overlap, the area lying under the lower of the two density curves.

Author(s)

Mike Meredith

Examples

```
# Generate some data
tst <- rbeta(1e6, 5, 7)

# check overlap with a Beta(0.2, 0.2) prior:
postPriorOverlap(tst, dbeta, shape1=0.2, shape2=0.2)

# check overlap with a Uniform(0, 1) prior:
postPriorOverlap(tst, runif(1e6))
```

---

predict.wiqid *Predict method for objects of class 'wiqid'*

Description

Obtains predictions, with estimates, standard errors and confidence intervals, from a fitted model object of class wiqid, as produced by frequentist estimation functions in the **wiqid** package. Not all functions produce objects that enable predictions to be made; see Details. Please treat this as a 'beta' version and check output carefully.

Usage

```
## S3 method for class 'wiqid'
predict(object, newdata, parameter, ci, type=c("link", "response"), ...)
```

Arguments

object	an object of class wiqid.
newdata	a data frame with columns for each of the covariates in the model. Unused columns are ignored. Missing values are not allowed. See Details.
parameter	character; the name of the parameter to predict; this will appear on the left hand side of one of the formulae in the model.
ci	the confidence interval to use; the default is to use object$ci or, if that is NULL, 0.95.
type	the type of prediction required. The default is on the scale of the linear predictors; the alternative "response" is on the scale of the response variable. Thus if the parameter is a probability, the default predictions are on the logit or probit scale and type = "response" gives the predicted probabilities. May be abbreviated.
...	further arguments for other methods.

Details

Most **wiqid** functions have models with multiple submodels, corresponding to the formulae in the model argument. Check object$formulae for a list of the available submodels.

The argument newdata is required (even for intercept-only models), and must be a data frame with named columns for each of the covariates in the submodel. For factors, the levels must be (a subset of) the levels in the original data; check object$xlev for possible levels.

predict is not yet implemented for the following functions:

occSStime and occSScovSite	: use occSS instead.
occMStime and occMScovSite	: use occMS instead.
closedCap* functions	: these models have no covariates.
surv* functions	: these have no covariates.

Value

Returns a matrix with four columns (estimate, SE, lower and upper confidence limits) and a row for each row in newdata. If newdata has row names, these will be used for the output. Note that for an intercept-only submodel, all rows will have identical values. Attributes give information on the link used and the confidence level.

Author(s)

Mike Meredith.

Examples

```
# Generate some simulated occupancy data for 300 sites:
set.seed(2017)
original.data <- data.frame(
  elev = runif(300, 0, 1000),
  forType = factor(sample(c("dry", "swamp", "mangrove"), size=300, replace=TRUE, prob=3:1)))
```

```
modMat <- model.matrix( ~ elev + forType, data = original.data)
psiCoef <- c(3, -0.003, -3, -1) # declines with 'elev'; highest for 'dry', lowest 'mangrove'
psi <- plogis(modMat %*% psiCoef)
hist(psi, breaks=20)
z <- rbinom(300, 1, psi)
mean(z)  # true realized occupancy
# detection history for 3 replicates, constant p = 0.6:
DH <- matrix(rbinom(300*3, 1, 0.6*z), nrow=300)
# fit models
m0 <- occSS(DH)
mE <- occSS(DH, psi ~ elev, data = original.data)
mEF <- occSS(DH, psi ~ elev + forType, data = original.data)

# now try predictions:
newdata <- expand.grid(elev=c(200, 500, 800), forType=c("dry", "swamp"))
predict(mEF, newdata, "psi")
cbind(newdata, predict(mEF, newdata, "psi", type='res'))
cbind(newdata, predict(mE, newdata, "psi", type='res'))
cbind(newdata, predict(m0, newdata, "psi", type='res'))

# do a nice plot
xx <- seq(0, 1000, length=51)
plotdata <- expand.grid(elev=xx, forType=c("dry", "swamp", "mangrove"))
toPlot <- predict(mEF, plotdata, "psi", type='res')
plot(xx, rep(0.5, 51), type='n', las=1, ylim=range(toPlot),
  xlab="Elevation", ylab="Occupancy probability")
ciCols <- adjustcolor(c('lightgreen', 'skyblue', 'pink'), 0.5)
estCols <- c('darkgreen', 'blue', 'red')
for(i in 1:3) {
  this1 <- toPlot[plotdata$forType == levels(plotdata$forType)[i], ]
  polygon(c(xx, rev(xx)), c(this1[, 3], rev(this1[, 4])), col=ciCols[i])
  lines(xx, this1[, 1], col=estCols[i])
}
legend('topright', levels(plotdata$forType), lty=1, col=estCols, bty='n')

# Add a survey-level covariate: observer ID with different detection probabilities
observer <- c(sample(1:2, size=300, replace=TRUE),  # A and B on first survey occasion
              sample(1:3, size=300, replace=TRUE),  # A, B and C for second
              sample(2:3, size=300, replace=TRUE))  # only B and C for third
obsID <- matrix(LETTERS[observer], nrow=300)
colnames(obsID) <- c("obs1", "obs2", "obs3")
original.data <- cbind(original.data, as.data.frame(obsID))
str(original.data)
p <- c(0.4, 0.6, 0.8)[observer]
DH <- matrix(rbinom(300*3, 1, p*z), nrow=300)
mEFO <- occSS(DH, list(psi ~ elev + forType, p ~ obs), data = original.data)
# Check the categorical covariate names and levels:
mEFO$xlev
predict(mEFO, data.frame(obs=c("A", "B", "C")), "p")
predict(mEFO, data.frame(obs=c("A", "B", "C")), "p", type="resp")
```

print.Bwiqid *Print and summary methods for objects of class 'Bwiqid'*

Description

Both functions print details of the MCMC process to the Console. `print` also prints a table of summary statistics for the parameters and several MCMC diagnostic measures to the Console, while `summary` returns invisibly a corresponding data frame, which can be passed to `View`.

Usage

```
## S3 method for class 'Bwiqid'
print(x, digits=4, ...)

## S3 method for class 'Bwiqid'
summary(object, digits=3, ...)
```

Arguments

`x, object`	an object of class `Bwiqid`.
`digits`	the number of digits to print or include in the output.
`...`	further arguments for the print or summary function.

Details

The `print` function prints a table with a row for each parameter *after* removing duplicated rows. Duplication usually arises because a covariate has only a few unique values.

There are columns for each of the following summary statistics ...

`mean`	the mean of each MCMC chain.
`sd`	the standard deviation of each MCMC chain.
`median`	the median of each MCMC chain.
`HDIlo` and `HDIup`	the lower and upper values of a 95% Highest Density Interval CrI for each MCMC chain.

... and for some or all of the following diagnostics, depending on the MCMC engine used for fitting the model:

`n.eff`	the effective sample sizes for the parameters adjusted for autocorrelation; for stable estimates of credible intervals
`MCerror`	the Monte Carlo errors for the parameters, expressed as a percentage of the standard deviation. Values less than 5%
`Rhat`	the with potential scale reduction factors for the parameters, which is 1 on convergence and should be < 1.05 for al

Value

`print` returns `x` invisibly. `summary` returns the table of summary statistics.

Author(s)

Mike Meredith.

Examples

```
# See examples for dippers.
```

`Priors` *Standardisation and priors*

Description

This page documents the priors used in the Bayesian analysis. For logistic models, sensible priors depend on the range of values and thus on the standardisation scheme used, which is also detailed here.

At present, this represents good intentions! It has not been implemented in all the functions in **wiqid**.

Standardisation

Continuous variables are standardised to facilitate writing models, and optimisation. Standardisation also means that the size of regression coefficients directly reflect the importance of the corresponding variables.

Binary variables coded as TRUE/FALSE and dummy variables are not changed. To make continuous variables comparable with these, they are centred by subtracting the mean, and then divided by their standard deviation.

Update: In versions prior to 0.2.x, continuous variables were centred by subtracting the mean, and then divided by *two times* their standard deviation (Gelman, 2008). With the new default, beta coefficients will be exactly have the size. There many some rounding errors in the fourth decimal place for other estimates.

Note that all numerical inputs (ie, `is.numeric == TRUE`) that appear in the `data` argument will be standardised, including binary variables coded as 0/1. Variables coded as TRUE/FALSE or as factors are not affected.

The same standardisation strategy is used for both Bayesian and maximum likelihood functions.

Priors for logistic regression coefficients

Following Gelman et al (2008), we use independent Cauchy priors with centre 0 and scale 10 for the intercept and scale 2.5 for all other coefficients.

Priors for probabilities

We use independent Uniform(0, 1) priors for probabilities.

References

Gelman, A. (2008) Scaling regression inputs by dividing by two standard deviations. *Statistics in Medicine*, 27, 2865-2873

Gelman, Jakulin, Pittau and Su (2008) A weakly informative default prior distribution for logistic and other regression models. *Annals of Applied Statistics* 2, 1360-1383.

`railSims` *Simulated detection/non-detection data for two species of rails*

Description

A data set for single-season two-species occupancy modeling. See `occ2sps` for details of these kinds of models.

Usage

```
data("railSims")
```

Format

A data frame with detection (1) vs non-detection data for 2 species at 160 sites on three occasions.

A1, A2, A3 detection histories for the dominant species on 3 occasions

B1, B2, B3 detection histories for the subordinate species on 3 occasions

logArea a continuous site covariate, standardised to mean 0, sd 1

reeds a logical site covariate.

Details

The data come from a simulated scenario with the following parameters:

psiA	= plogis(0 + 2*logArea)	= probability of occupancy of species A
psiBa	= 0.77	= probability of occupancy of B if A is absent
psiBA	= plogis(-1 + 2*reeds)	= probability of occupancy of B if A is present
pA	= 0.75	= probability of detection of species A if B is absent
rA	= pA	= probability of detection of species A if both are present
pB	= 0.80	= probability of detection of species B if A is absent
rBa	= pB	= probability of detection of species B if both are present but A was not detected
rBA	= 0.40	= probability of detection of species B if both are present and A was detected

Source

Simulated data

References

Richmond, O.M.W., Hines, J.E., & Beissinger, S.R. (2010) Two-species occupancy models: a new parameterization applied to co-occurrence of secretive rails. Ecological Applications, 20, 2036-2046.

Examples

```
data(railSims)
# Separate the two detection histories
DHA <- railSims[, 1:3]
DHB <- railSims[, 4:6]

# Default model (no interaction)
occ2sps(DHA, DHB)


# Model with full interaction
occ2sps(DHA, DHB, list(psiBA ~ 1, rA ~ 1, rBa ~ 1, rBA ~ 1))

# Model corresponding to the data generation model
occ2sps(DHA, DHB, list(psiA ~ logArea, psiBA ~ reeds, rBA ~ 1), data=railSims)
```

`richCurve` *Species richness estimates based on accumulation curves*

Description

Provides a shell into which species richness estimators may be plugged to provide estimates based on species accumulation curves, as provided by EstimateS.

Usage

```
richCurve(obsMat, FUNC, runs = 10, ...)

richSobs(incVec)
richSingle(cntVec)
richDouble(cntVec)
richUnique(incMat)
richDuplicate(incMat)
```

Arguments

`incVec`	a vector of species incidences (presences) in one or more samples; a vector of counts or a species x sites matrix of incidences or counts may be supplied.
`cntVec`	a vector of species counts (abundances); a species x sites matrix of counts may be supplied and will be converted to a vector with `rowSums`.

incMat	a 1/0 matrix of species incidence (presence), species x sites. A matrix of counts may also be provided.
obsMat	a matrix of species counts, species x sites; a matrix of incidences will be sufficient if accepted by FUNC.
FUNC	a function to estimate species richness based on a matrix of observations; see Species richness estimators for examples.
runs	the number of randomisations of samples (ie. columns in the input matrix) to perform to calculate mean and standard deviation.
...	additional arguments passed to FUNC.

Details

The reliability of estimates of species richness depends on the sampling effort. To investigate this effect, and judge whether the current sampling effort is adequate, we calculate richness estimates for subsets of the data. Assuming that the columns of the data matrix are independent samples from the population, richCurve calculates estimates for 1 sample, 2 samples, and so on. This is repeated for many runs, and the mean and standard deviation calculated.

The other functions documented here are trivial, but useful for plugging into richCurve:

richSobs : the number of species observed.

richSingle : the number of singletons, ie. species represented by just 1 individual in the pooled samples.

richDouble : the number of doubletons, ie. species represented by exactly 2 individuals in the pooled samples.

richUnique : the number of uniques, ie. species represented in just one sample.

richDuplicate : the number of duplicates, ie. species represented in exactly 2 samples.

Value

richCurve returns a list with elements:

mean	A matrix (possibly 1-column) with a row for each sample and a column for each value returned by FUNC.
SD	The corresponding matrix with the standard deviations of the estimates from the runs.

The other functions return scalars.

Author(s)

Mike Meredith

Examples

```
data(seedbank)
plot(richCurve(seedbank, richSobs)$mean, type='l', ylim=c(0, 35))
lines(richCurve(seedbank, richSingle)$mean, col='blue')
lines(richCurve(seedbank, richDouble)$mean, col='blue', lty=2)
```

richRarefy *Sample-based rarefaction curves*

Description

Uses Mao's tau estimator (Colwell et al, 2004) to obtain a rarefaction curve indicating the expected number of species observed if fewer samples were collected.

Usage

```
richRarefy(incmat)
```

Arguments

incmat	a 1/0 matrix of species incidence (presence), species x sites. A matrix of counts may also be provided.

Value

A matrix with columns for the estimate and its standard deviation and rows for the number of samples pooled. Confidence limits may be obtained with estimate +/- 1.96 * SD.

Author(s)

Mike Meredith

References

Colwell, R. K., C. X. Mao, & J. Chang. 2004. Interpolating, extrapolating, and comparing incidence-based species accumulation curves. Ecology 85, 2717-2727.

Examples

```
data(seedbank)
plot(richRarefy(seedbank)[, 1], type='l')
```

Royle-Nichols occupancy model *Royle-Nichols model for single-season occupancy estimation*

Description

These functions implement the Royle-Nichols method (Royle & Nichols 2003) for estimation of site occupancy allowing for abundance-induced heterogeneity in detection probability. Probability of detection is modelled as a function of the number of animals available for detection, n, and the probability of detection of an individual animal, r. Probability of occupancy is derived as the probability that $n > 0$.

Function `occSSrn` allows for site-specific covariates to be included in the model. `occSSrnSite` and `occSSrn0` are fast alternatives that do not require a full detection history matrix.

Usage

```
occSSrn(DH, model=NULL, data = NULL, ci=0.95, link=c("logit", "probit"),
    verify=TRUE, ...)

occSSrn0(y, n, ci=0.95, link=c("logit", "probit"), ...)

occSSrnSite(y, n, model=NULL, data = NULL, ci=0.95, link=c("logit", "probit"), ...)
```

Arguments

`DH`	a 1/0/NA matrix (or data frame) of detection histories, sites x occasions.
`model`	a list of formulae symbolically defining a linear predictor for each parameter in terms of covariates. If NULL, an intercept-only model is used, ie, lambda(.) r(.).
`data`	a data frame containing the variables in the model, with a row for each site. Each site covariate has one column. Each survey covariate has one column for each occasion, and the column name must end with the occasion number (without leading zeros); eg, `Cov1, Cov2, ..., Cov15`. All covariates should be included in `data`, otherwise they will be sought in enclosing environments, which may not produce what you want – and they won't be standardised. Note: currently only site covariates can be handled.
`ci`	the confidence interval to use.
`link`	the link function to use, either logit or probit; see Links.
`verify`	if TRUE, the data provided will be checked.
`y`	a vector with the number of detections at each site.
`n`	a scalar or vector with the number of visits (survey occasions) at each site.
`...`	other arguments passed to `nlm`.

Details

Numeric covariates in `data` are standardised to facilitate convergence. This applies to binary covariates coded as 1/0; if this is not what you want, code these as TRUE/FALSE or as factors.

Value

Returns an object of class `wiqid`, see wiqid-class for details.

Benchmarks

Output has been checked against output from PRESENCE (Hines 2006) v.6.9 for the weta data set. Real values are mostly the same to 4 decimal places, though there is occasionally a discrepancy of 0.001. AICs are the same.

Author(s)

Mike Meredith

References

MacKenzie, D I; J D Nichols; A J Royle; K H Pollock; L L Bailey; J E Hines 2006. *Occupancy estimation and modeling : inferring patterns and dynamics of species occurrence*. Elsevier Publishing.

Hines, J. E. (2006). PRESENCE - Software to estimate patch occupancy and related parameters. SGS-PWRC. http://www.mbr-pwrc.usgs.gov/software/presence.html.

Royle, J. A., Nichols, J. D. (2003) Estimating abundance from repeated presence-absence data or point counts. *Ecology* 84(3) 777-790.

See Also

See the examples for the weta data set. See occ2sps for single-season two-species models and occMS for multi-season models.

Examples

```
# The weta data from MacKenzie et al (2006) p116:
data(weta)
DH <- weta[, 1:5]
occSS(DH) # for comparison
occSSrn(DH)
y <- rowSums(DH, na.rm=TRUE)
n <- rowSums(!is.na(DH))
occSSrnSite(y, n, lambda ~ Browsed, data=weta)
```

---

salamanders *Occupancy data for blue ridge salamanders*

Description

Detection/non-detection data for blue ridge salamanders (Eurycea wilderae) in Great Smoky Mountains National Park.

Usage

```
data(salamanders)
```

Format

A matrix with 39 rows corresponding to sites and 5 columns corresponding to survey occasions. 1 means that one or more salamanders were observed at the site/survey, 0 means none were seen.

Source

Described in MacKenzie et al (2006) p99. The data are distributed with the software package PRESENCE.

References

MacKenzie, D I; J D Nichols; A J Royle; K H Pollock; L L Bailey; J E Hines 2006. *Occupancy estimation and modeling : inferring patterns and dynamics of species occurrence*. Elsevier Publishing.

Examples

```
data(salamanders)

occSStime(salamanders, p ~ .time)
```

---

seedbank *Seed abundances in soil samples*

Description

Number of seeds of different species germinating from 121 soil samples collected in a tropical secondary forest.

Usage

```
data(seedbank)
```

Format

A matrix with 34 rows for species and 121 columns corresponding to different soil samples.

Source

Butler & Chazdon 1998. Example data distributed with the EstimateS program (Colwell 2005).

References

Butler, B. J., & R. L. Chazdon. 1998. Species richness, spatial variation, and abundance of the soil seed bank of a secondary tropical rain forest. *Biotropica* 30:214-222.

Colwell, R K; J A Coddington. 1994. Estimating terrestrial biodiversity through extrapolation. *Philosophical Transactions of the Royal Society of London B* 345:101-118.

Colwell, R. K. 2005. EstimateS: Statistical estimation of species richness and shared species from samples. Version 7.5. User's Guide and application published at: http://purl.oclc.org/estimates.

Examples

```
data(seedbank)
##
```

---

showShinyApp *Display a 'shiny' application*

Description

Displays one of the built-in interactive 'shiny' applications in the browser. See Details for the apps available.

Usage

```
showShinyApp(topic)
```

Arguments

topic	The name of the shiny app to display. If missing, a list of available apps will be returned. Partial matching can be used.

Details

Three apps are currently included in the **wiqid** package:

"Beta" displays a beta distribution and sliders which allow you to change the parameters. You can also input binomial data and obtain the conjugate beta posterior distribution.

"Gamma" displays a gamma distribution with variable parameters, and can produce the conjugate gamma posterior for Poisson-distributed count data.

"Quadratic" plots a quadratic relationship with variable parameters, showing how the quadratic term can add a hump or hollow to a relationship.

Value

If `topic` is missing, a list of available apps. Otherwise, nothing useful; the function is run for its side effect.

Author(s)

A much simplified version of code by Jason Bryer on Github at https://github.com/jbryer/IS606, adapted by Mike Meredith.

Examples

```
showShinyApp() # Shows a list of available apps

# The following command will cause R to freeze until you press Esc:
# showShinyApp("Be")
```

`simpleRhat` *The Brooks-Gelman-Rubin (BGR) convergence diagnostic*

Description

An 'interval' estimator of the 'potential scale reduction factor' (Rhat) for MCMC output. Similar to the function `gelman.diag` in **coda**, but much faster when thousands of parameters are involved and will not cause R to crash.

Usage

```
simpleRhat(object, n.chains, burnin=0)
```

Arguments

`object`	a vector, matrix or data frame with MCMC output in columns
`n.chains`	scalar integer, the number of chains concatenated to form the columns of `x`; multiple chains are required to calculate Rhat; if `n.chains` is missing and `object` has an attribute `n.chains`, that value will be used.
`burnin`	scalar, between 0 and 0.9; the proportion of values at the start of each chain to discard as burn-in.

Details

Calculates the Gelman-Rubin convergence statistic, as modified by Brooks and Gelman (1998). Following the WinBUGS User Manual (Spiegelhalter et al, 2003), we use the width of the central 80% interval as the measure of width. Rhat is the ratio of the width of the pooled chains to the mean width of the individual chains. At convergence, this should be 1; values less than 1.1 or 1.05 are considered satisfactory.

Value

A named vector with the Rhat values.

Author(s)

Mike Meredith

References

Brooks, S.P. & Gelman, A. (1998) General methods for monitoring convergence of iterative simulations. *Journal of Computational and Graphical Statistics*, 7, 434-455.

Spiegelhalter, Thomas, Best & Lunn (2003) WinBUGS User Manual Version 1.4, on line here.

Examples

```
# Get some output to use
data(salamanders)
y <- rowSums(salamanders)
( out <- BoccSS0(y, 5) )

simpleRhat(out)
```

Species richness estimators

Species richness estimators

Description

Functions to estimate species richness, based on samples from one or more surveys (quadrats, sites, occasions, ...) as included in EstimateS. See Details for individual estimators.

Usage

```
richACE(cntVec, threshold = 10)
richICE(incMat, threshold = 10)
richChao1(cntVec, correct = FALSE, ci = 0.95)
richChao2(incMat, correct = FALSE, ci = 0.95)
richJack1(incMat)
richJack2(incMat)
richJackA1(cntVec)
richJackA2(cntVec)
richBoot(incMat)
richMM(incMat)
richRenLau(cntVec)
```

Arguments

`cntVec`	a vector of species counts (abundances) with one element for each species. A matrix of counts, species x sites, may also be provided and will be converted to a vector with `rowSums`. Zeros are allowed, but not missing values; non-integers are rounded.
`incMat`	a 1/0 matrix of species incidence (presence), species x sites. A matrix of counts may also be provided and will be converted to 1/0 after rounding.
`threshold`	the definition of rare or infrequent species: species with `threshold` or smaller counts (ACE) or incidences (ICE) are rare or infrequent.
`correct`	if TRUE, bias-corrected estimates are calculated.
`ci`	the required confidence interval.

Details

`richACE` and `richICE` calculate Anne Chao's Abundance-based and Incidence-based Coverage Estimators of species richness respectively (Chao et al, 2000).

`richChao1` and `richChao2` calculate Anne Chao's Chao 1 (abundance-based) and Chao 2 (incidence-based) estimators (Chao 1984, 1987).

`richJack1` and `richJack2` calculate first and second order incidence-based jackknife estimators of species richness (Smith & van Belle, 1984).

`richBoot` calculates a bootstrap estimator of species richness (Smith & van Belle, 1984).

`richMM` calculates the asymptotic species richness from a Michaelis-Menten curve fitted to the species rarefaction curve (Colwell et al. 2004).

See the EstimateS Users Guide at `http://viceroy.eeb.uconn.edu/estimates/` for the equations for the functions above.

The following are not included in EstimateS v.8.2:

`richJackA1` and `richJackA2` calculate first and second order abundance-based jackknife estimators of species richness (Gotelli & Colwell 2011).

`richRenLau` calculates Rennolls & Laumonier's (2006) 'shadow species' abundance-based estimator of richness.

Value

`richChao1` and `richChao2` return a vector with a point estimate, upper and lower confidence limits, and standard deviation.

The other functions return a scalar.

Benchmarks

Output for estimators included in EstimateS 8.2 has been checked against EstimateS for the `seedbank` and `killarneyBirds` data sets. EstimateS results are often 0.01 lower, as EstimateS appears to truncate rather than rounding.

Author(s)

Mike Meredith

References

Chao, A. 1984. Non-parametric estimation of the number of classes in a population. *Scandinavian Journal of Statistics* 11, 265-270.

Chao, A. 1987. Estimating the population size for capture-recapture data with unequal capture probabilities. *Biometrics* 43:783-791.

Chao, A., W.-H. Hwang, Y.-C. Chen, and C.-Y. Kuo. 2000. Estimating the number of shared species in two communities. *Statistica Sinica* 10:227-246.

Colwell, R. K., C. X. Mao, & J. Chang. 2004. Interpolating, extrapolating, and comparing incidence-based species accumulation curves. *Ecology* 85, 2717-2727.

Gotelli, N J; R K Colwell. 2011. Estimating species richness. 39-54 in Magurran, A E, and B J McGill, editors. *Biological diversity: frontiers in measurement and assessment*. Oxford University Press, Oxford, New York NY.

Rennolls, K; Y Laumonier. 2006. A new local estimator of regional species diversity, in terms of 'shadow species', with a case study from Sumatra. *J Tropical Ecology* 22:321-329.

Smith, E.P. & van Belle, G. 1984. Nonparametric estimation of species richness. *Biometrics* 40, 119-129.

See Also

`richRarefy` for rarefaction curves, and `richCurve` for a function to give richness estimates for sub-sets of samples.

Examples

```
data(seedbank)

richACE(seedbank)
```

`standardize` *Scaling and centring of vectors, matrices and arrays*

Description

Maps a numeric variable to a new object with the same dimensions. `standardize` is typically used to standardise a covariate to mean 0 and SD 1. `standardize2match` is used to standardise one object using the mean and SD of another; it is a wrapper for `standardize(x, center=mean(y), scale=sd(y))`.

Usage

```
standardize(x, center = TRUE, scale = TRUE)
standardize2match(x, y)
```

Arguments

`x, y`	a numeric vector, matrix or multidimensional array; `NA` and `NaN` are allowed; `Inf` and `-Inf` will produce all-`NaN` output if either `center` or `scale` is `TRUE`.
`center`	either a logical or a numeric value of length 1.
`scale`	either a logical or a numeric value of length 1.

Details

`standardize` differs from `scale` by (1) accepting multidimensional arrays but not data frames; (2) *not* standardizing column-wise but using a single value to center or to scale; (3) if `x` is a vector, the output will be a vector (not a 1-column matrix). If each column in the matrix represents a different variable, use `scale` not `standardize`.

Centring is performed before scaling.

If `center` is numeric, that value will be subtracted from the whole object. If logical and TRUE, the mean of the object (after removing NAs) will be subtracted.

If `scale` is numeric, the whole object will be divided by that value. If logical and TRUE, the standard deviation of the object (after removing NAs) will be used; this may not make sense if `center = FALSE`.

Value

A numeric object of the same dimensions as `x` with the standardized values. NAs in the input will be preserved in the output.

For the default arguments, the object returned will have mean approximately zero and SD 1. (The mean is not exactly zero as scaling is performed after centring.)

Author(s)

Mike Meredith, after looking at the code of `base::scale`.

Examples

```
# Generate some fake elevation data:
elev <- runif(100, min=100, max=500)
mean(elev) ; sd(elev)
str( e <- standardize(elev) )
mean(e) ; sd(e)

# Standardize so that e=0 corresponds to exactly 300m and +/- 1 to
#   a change of 100m:
e <- standardize(elev, center=300, scale=100)
mean(e)
mean(elev) - 300
range(e)
range(elev) - 300

# Generate data matrix for survey duration for 3 surveys at 10 sites
dur <- matrix(round(runif(30, 20, 60)), nrow=10, ncol=3)
d <- standardize(dur)
mean(d) ; sd(d)

# Standardize new data to match the mean and SD of 'dur'
(new <- seq(20, 60, length.out=11))
standardize2match(new, dur)

# compare with base::scale
```

```
dx <- base::scale(dur)
colMeans(dx) ; apply(dx, 2, sd)
colMeans(d) ; apply(d, 2, sd)
# Don't use 'standardize' if the columns in the matrix are different variables!
```

Survival (CJS) *Survival from recapture data with Cormack-Jolly-Seber (CJS) model*

Description

Calculation of apparent survival (accounting for recapture probability) from mark-recapture data, with time-dependent phi or p, possibly with covariates. Function survCHSaj allows for different survival parameters for juveniles and adults; juveniles are assumed to become adults after the first interval. BsurvCJS is a Bayesian version.

Usage

```
survCJS(DH, model=list(phi~1, p~1), data=NULL, freq=1, group, interval=1,
    ci = 0.95, link=c("logit", "probit"), ...)

survCJSaj(DHj, DHa=NULL, model=list(phiJ~1, phiA~1, p~1), data=NULL,
    freqj=1, freqa=1, ci = 0.95, link=c("logit", "probit"), ...)

BsurvCJS(DH, model=list(phi~1, p~1), data = NULL, freq=1, priors=NULL,
    chains=3, sample=1e4, burnin=1000, thin=1, adapt=1000,
    parallel = NULL, seed=NULL, priorOnly=FALSE)
```

Arguments

DH	a 1/0 matrix with detection histories with a row for each animal captured and a column for each capture occasion.
model	a list of formulae symbolically defining a linear predictor for each parameter in terms of covariates.
data	a data frame with a row for each survival interval / recapture occasion and columns for each of the covariates used to estimate phi or p.
freq	a scalar or a vector of length nrows(DH) with the frequency of each detection history. Negative values indicate trap losses.
group	an optional factor of length nrows(DH); if provided, group can be included in the model definition, see Examples.
interval	the time interval between capture occasions; scalar if all intervals are equal or a vector of length ncols(DH) - 1; the units used must be the same as those for the apparent survival estimate, eg, for annual survival use years.
DHj, DHa	detection history matrices for animals marked as juveniles and adults respectively; DHa should be NULL if no animals were marked as adults.
freqj, freqa	frequencies of each detection history in DHj and DHa; freqa is ignored if DHa = NULL.

`ci`	the required confidence interval.
`link`	the link function to use, either logit or probit; see Links.
`...`	other arguments passed to `nlm`.
`priors`	a list with elements for prior mean and variance for coefficients; see Details.
`chains`	the number of Markov chains to run.
`sample`	the minimum number of values to return; the actual number returned may be slightly higher, as it will be a multiple of `chains`.
`burnin`	the number of values to discard at the beginning of each chain.
`thin`	the thinning rate. If set to n > 1, n values are calculated for each value returned.
`adapt`	the number of iterations to run in the JAGS adaptive phase.
`priorOnly`	if TRUE, the function produces random draws from the appropriate *prior* distributions, with a warning.
`parallel`	if TRUE or NULL and sufficient cores are available, the MCMC chains are run in parallel; if TRUE and insufficient cores are available, a warning is given.
`seed`	a positive integer, the seed for the random number generators.

Details

`BsurvCJS` uses a probit link to model apparent survival and detection as a function of covariates; most software uses a logistic (logit) link. See Links. Coefficients on the probit scale are about half the size of the equivalent on the logit scale.

Priors for `BsurvCJS` are listed in the `priors` argument, which may contain elements:

`muPhi` and `muP` : the means for apparent survival and detection coefficients respectively. This may be a vector with one value for each coefficient, including the intercept, or a scalar, which will be used for all. The default is 0.

`sigmaPhi` and `sigmaP` : the variance for apparent survival and detection coefficients respectively. This may be (1) a vector with one value for each coefficient, including the intercept, which represents the variance, assuming independence, or (2) a scalar, which will be used for all. The function does not currently allow a variance-covariance matrix. The default is 1, which is somewhat informative.

When specifying priors, note that numerical covariates are standardized internally before fitting the model. For an intercept-only model, a prior of Normal(0, 1) on the probit scale implies a Uniform(0, 1) or Beta(1, 1) prior on the probability scale.

Value

`survCJS` and `survCJSaj` return an object of class `wiqid`, a list with elements:

`call`	The call used to produce the results
`beta`	Estimates of the coefficients in the linear predictors for phi and p.
`beta.vcv`	The variance-covariance matrix for the beta estimates.
`real`	Back-transformed estimates of phi and p for each interval / occasion.

logLik — a vector with elements for log(likelihood), number of parameters, and effective sample size. If the variance-covariance matrix cannot be calculated, the second element should be NA.

There are print, logLik, and nobs methods for class wiqid.

BsurvCJS returns an object of class Bwiqid, a data frame with columns for each p and psi value containing the series of MCMC samples, and attributes for details of the MCMC run.

Benchmarks

Output of survCJS has been checked against program MARK with the dipper data set: coefficients are not the same as MARK uses models without an intercept, but the real values agree to 3 decimal places.

Author(s)

Mike Meredith

References

Lebreton, J-D; K P Burnham; J Clobert; D R Anderson. 1992. Modeling survival and testing biological hypotheses using marked animals: a unified approach with case studies. *Ecological Monographs* 62:67-118.

Examples

```
data(dippers)

DH <- dippers[1:7]  # Extract the detection histories
survCJS(DH)  # the phi(.) p(.) model
survCJS(DH, phi ~ .time)  # the phi(t) p(.) model
df <- data.frame(flood = c(FALSE, TRUE, TRUE, FALSE, FALSE, FALSE))
survCJS(DH, phi ~ flood, data=df)  # the phi(flood) p(.) model
# Including a grouping factor:
survCJS(DH, phi ~ flood*group, data=df, group=dippers$sex)

# With unequal intervals - suppose no data were collected in year 5:
DH1 <- DH[, -5]
survCJS(DH1, phi ~ .time, interval = c(1, 1, 1, 2, 1))

# See also the examples in the dippers help file.
```

Survival (RD) *Survival from mark-recapture data with robust design*

Description

Calculation of apparent survival and recruitment rate from data collected using Pollock's robust design, ie, with multiple capture occasions within each season, where the population is closed within each season.

Function `survRDah` implements the second stage of a two-stage analysis, where abundance and recapture probability are estimated using closed-capture function for each season.

Function `survRD` combines the two stages into a single maximum likelihood estimation step, using model M0 for the within-season data.

NOTE: These are preliminary attempts at coding these models and have not been properly tested or benchmarked.

Usage

```
survRD(DH, freq=1, occsPerSeason)

survRDah(DH, freq=1, occsPerSeason, N, pStar)
```

Arguments

`DH`	a 1/0 matrix with detection histories with a row for each animal captured and a column for each capture occasion.
`freq`	a scalar or a vector of length `nrow(DH)` with the frequency of each detection history. Negative values indicate trap losses.
`occsPerSeason`	the number of survey occasions per season; currently this must be scalar and the number of occasions must be the same for all seasons.
`N`	a vector with an element for each season giving the number of animals available for capture as estimated in the first stage of a 2-stage analysis.
`pStar`	a vector with an element for each season giving the probability of recapture as estimated in the first stage of a 2-stage analysis.

Value

A list with elements:

`phiHat`	Estimates of apparent survival for each interval between seasons.
`bHat`	Estimates of the recruitment rate for each interval.
`pStarHat`	The estimated probability of capture during each season.
`Nhat`	The estimated number of animals available for capture during each season.
`pHat`	The estimated probability of capture on one occasion for each season.

For `survRDah`, the values of `pStarHat` and `Nhat` will equal the values of `pStar` and `N` input, and `pHat` with be NULL.

Author(s)

Mike Meredith

References

Kendall, Pollock, and Brownie (1995) A likelihood-based approach to capture-recapture estimation of demographic parameters under the robust design. *Biometrics* 51:293-308

Kendall, Nichols, Hines (1997) Estimating temporary emigration using capture-recapture data with Pollock's robust design. *Ecology* 78(2):563-578

Examples

```
data(MeadowVoles)
# Extract detection histories:
DH <- MeadowVoles[, 1:30]
freq <- MeadowVoles$freq

# With single stage maximum likelihood estimation:
survRD(DH, freq=freq, occsPerSeason=5)

# The 2-stage approach:
# Stage 1 - using the jackknife estimator to estimate N and p for each season:
MhResult <- matrix(NA, 6, 2)
colnames(MhResult) <- c("N", "p")
seasonID <- rep(1:6, each=5)
for(i in 1:6) {
  dh <- DH[, seasonID==i]
  MhResult[i, ] <- closedCapMhJK(dh)$real[, 1]
}
MhResult
# Calculate the probability of being captured at least once in the season:
pStar <- 1 - (1 - MhResult[, "p"])^5

# Stage 2 - pass N and pStar to a modified CJS estimation routine:
survRDah(DH, freq=freq, occsPerSeason=5, N=MhResult[, "N"], pStar=pStar)
```

TDist *The Student t Distribution*

Description

Density, distribution function, quantile function and random generation for the t distribution with df degrees of freedom, using mean and sd instead of a t-statistic. These are wrappers for stats::dt, etc.

Usage

```
dt2(x, mean, sd, df)
pt2(x, mean, sd, df, lower.tail=TRUE, log.p=FALSE)
qt2(p, mean, sd, df, lower.tail=TRUE, log.p=FALSE)
rt2(n, mean, sd, df)
```

Arguments

x	vector of parameter values
mean	mean of the t-distribution
sd	standard deviation of the t-distribution
df	degrees of freedom
lower.tail	logical; if TRUE (default), cumulative probabilities up to x, otherwise, above x.
log.p	logical; if TRUE, probabilities p are given as log(p).
p	probability.
n	number of random draws required.

Value

dt gives the density, pt gives the cumulative probability, qt gives the quantile function, and rt generates random deviates.

Author(s)

Mike Meredith

See Also

See the **stats** functions dt, pt, qt, rt.

Examples

```
## to do
```

Temburong *Tree species count data*

Description

Basal area and number of individual trees >= 5cm dbh of each species in a 1ha plot in Ulu Temburong - Brunei. There were 1012 trees of 276 species.

Usage

```
data(Temburong)
```

Format

The data set consists of two objects:

Temburong is a vector of length 276, with the counts of each species.

TemburongBA is a similar vector with the basal area (ie. the sum of the cross-sectional area at breast height of all of trees) of each species.

Source

Small, A; T G Martin; R L Kitching; K M Wong. 2004. Contribution of tree species to the biodiversity of a 1 ha Old World rainforest in Brunei, Borneo. *Biodiversity and Conservation* 13:2067-2088.

Examples

```
data(Temburong)
richChao1(Temburong)
biodShannon(TemburongBA)
```

`WAIC` *Extract the Watanabe-Akaike Information Criterion (WAIC)*

Description

Extracts the Watanabe-Akaike Information Criterion from objects of class `Bwiqid` which have a WAIC attribute.

Usage

```
WAIC(object, ...)
```

Arguments

`object`	a fitted model object with an attribute giving the WAIC and pD for the fitted model.
`...`	optionally more fitted model objects.

Value

If just one object is provided, the corresponding WAIC.

If multiple objects are provided, a data frame with rows corresponding to the objects and columns representing the number of parameters in the model (pD) and the WAIC.

Note

The code to produce WAIC is new and not fully tested: it probably harbours bugs!

Author(s)

Mike Meredith.

References

Burnham, K P; D R Anderson 2002. *Model selection and multimodel inference: a practical information-theoretic approach*. Springer-Verlag.

Examples

```
## TODO
```

`weta` *Detection data for weta in gorse bushes*

Description

Results of an occupancy survey to see if presence/absence of weta in 72 gorse bushes is affected by browsing of the bushes by goats. Probability of detection may be different for each observer, and observer ID is also recorded.

Usage

```
data(weta)
```

Format

A data frame with 72 observations on the following 11 variables.

D1, D2, D3, D4, D5 a numeric vector for each of 5 daily surveys, showing whether weta were detected (1) or not detected (0); NA if the bush was not surveyed on the relevant day.

Browsed a logical vector indicating whether the bush was browsed (TRUE) or not browsed (FALSE)

ObsD1, ObsD2, ObsD3, ObsD4, ObsD5 a factor with levels `A B C`, indicating which observer carried out each survey.

Details

The data are provided as a data frame, such as would result from reading in data from a text file. Further formatting is needed before using these for analysis: see the examples.

Source

Discussed in MacKenzie et al (2006) p116. Data distributed with PRESENCE.

References

MacKenzie, D I; J D Nichols; A J Royle; K H Pollock; L L Bailey; J E Hines 2006. *Occupancy estimation and modeling : inferring patterns and dynamics of species occurrence*. Elsevier Publishing.

Examples

```
data(weta)

DH <- weta[, 1:5]  # extract the detection history:
occSS(DH)
occSStime(DH, p~.time)
# With covariates
occSS(DH, list(psi ~ Browsed, p ~ ObsD), data=weta)
occSS(DH, list(psi ~ Browsed, p ~ Browsed), data=weta)

# Bayesian analysis

# Model with separate intercepts for occupancy in Browsed and Unbrowsed
#  bushes, and a time trend for probability of detection; specify uniform
#  priors for probability of occupancy:
Bwet <- BoccSS(DH, model=list(psi~Browsed-1, p~.Time), data=weta,
  priors=list(sigmaPsi=c(1,1)), chains=2)
Bwet
plot(Bwet)
plot(Bwet, "p_.Time")
```

`window.Bwiqid` *Time windows for 'Bwiqid' objects*

Description

`window.Bwiqid` is a method for `Bwiqid` objects for the `window` generic function. It extracts the subset of the observations between `start` and `end`. Setting `thin = k` selects every kth observation starting from `start`.

Usage

```
## S3 method for class 'Bwiqid'
window(x, start=NULL, end=NULL, thin=1, ...)
```

Arguments

`x`	an object of class `Bwiqid`.
`start`	the first observation to retain.
`end`	the last observation to retain.
`thin`	the interval between retained observations.
`...`	further arguments for the window function.

Value

Returns an object of class `Bwiqid` with the subset of observations.

Convergence diagnostics included as attributes in `x` are not retained, as they are unlikely to be valid for the subset.

Author(s)

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Examples

```
# Create a fake Bwiqid object:
fake <- data.frame(mu = rnorm(3000), sigma=rlnorm(3000))
class(fake) <- c("Bwiqid", "data.frame")
attr(fake, "n.chains") <- 3
fake

new <- window(fake, start=501, thin=10)
dim(new)
new
```

---

wiqid-class *The 'wiqid' S3 class*

Description

All the maximum likelihood functions in the **wiqid** package should produce an object of class `wiqid`. Bayesian estimation runs produce objects of class `Bwiqid`.

Structure

A `wiqid` object is a list with the following elements:

call The call used to produce the results

link Either a named list with the link functions used, or a single value if the same link is used for all parameters. For probabilities, usually `logit` or `probit`.

beta A matrix of values of the coefficients of the terms in the linear predictors, with standard errors and confidence intervals.

beta.vcv The variance-covariance matrix for the beta estimates.

real Estimates of occupancy and probability of detection on the real scale, with confidence intervals.

logLik a vector with elements for `log(likelihood)`, number of parameters, and effective sample size. If the variance-covariance matrix cannot be calculated, the second element should be `NA`.

ci intended coverage of the confidence intervals.

formulae a named list with the formulae of each of the submodels.

index a named list indicating which rows of the `beta` and `beta.vcv` matrices correspond to each submodel.

xlev a named list of factors included in the original `data` object with their levels.

scaling a named list of numerical covariates included in the original `data` object with the values used to standardise them, `c(centre, spread)`.

Methods

The following methods are available for objects of class `wiqid`:

`print`, `logLik`, `nobs`, `coef`, `vcov`, `predict.wiqid`.

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