Package ‘glmmBUGS’

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Type Package

Title Generalised Linear Mixed Models with BUGS and JAGS

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Depends R (>= 3.0.0)

Imports abind, methods, MASS, sp, graphics, stats

Suggests spdep

Enhances nlme, diseasemapping, geoRglm, R2WinBUGS, R2OpenBUGS, BRugs,
R2jags, rjags

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Description Automates running Generalized Linear Mixed Models, including
spatial models, with WinBUGS, OpenBUGS and JAGS. Models are specified with
formulas, with the package writings model files, arranging unbalanced data
in ragged arrays, and creating starting values. The model is re-parameterized,
and functions are provided for converting model outputs to the original
parameterization.

SystemRequirements Compiling vignette requires JAGS
(http://mcmc-jags.sourceforge.net)

License GPL

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NeedsCompilation no

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addSpatial

Calculate adjacency values for WinBUGS

Description
Put an adjacency object in a ragged array

Usage
addSpatial(map, raggedArray, effect = NULL, prefix=NULL)

Arguments
map a spatialPolygonsDataFrame object, or an nb object or a list of two vectors, adj and num
raggedArray the result from winBugsRaggedArray
effect a character vector listing the effect names
prefix Character string to be appended to variable names

Details
Computes the values need by the car.normal distribution in WinBUGS. This function is called by glmmBUGS when a spatial argument is provided, addSpatial is usually not called by a user.
Value

The ragged array is returned, with the following additional elements

num a vector of the number of neighbours of each region
adj a vector containing the neighbours
weights a vector of ones, the same length as adj
NregionSpatial where ‘region’ is replaced by the name of the effect. The number of regions.

Author(s)

Patrick Brown

References

Also see the geoBUGS manual

Examples

## Not run:

# get a winbugs model and data ready, without a spatial effect
data(ontario)

forBugs = glmBUGS(formula=observed + logExpected ~ 1,
  effects="CSDUID", family="poisson",
  data=data.frame(ontario))

# now add a spatial effect.
# first, compute the adjacency matrix
# if region ID’s are stored as factors, make sure to convert
# them to characters rather than the default of converting them
# to integers
library(diseasemapping)
data(popdata)
popDataAdjMat = poly2nb(popdata,row.names=as.character(popdata[["CSDUID"]]))

data(popDataAdjMat)

# add the adjacency matrix to the ragged array
raggedWithSpatial = addSpatial(popDataAdjMat, forBugs$ragged, "CSDUID")

# write a new bugs model with a spatial effect
writeBugsModel("model.bug", "CSDUID", NULL, c("count", "expected"),
  "poisson", spatial="CSDUID")
startingValues = forBugs$startingValues
source("getInits.R")

library(R2WinBUGS)
popResult = bugs(raggedWithSpatial, getInits,
  parameters.to.save = names(getInits()), model.file="model.bug",
  inits=forBugs$startingValues,
  model.file="model.bug",
  chains=1, iterations=1000, burnin=100, thin=2,.seed=42)
Convert Bernoulli observations to Binomial

Description
Combines multiple Bernoulli observations with the same covariates into one Binomial response

Usage
binToBinom(obs, covariates)

Arguments
- obs: logical vector of observations
- covariates: Data frame or matrix of covariates

Value
A data frame with one row for each unique value for the covariates, including the covariates and the following additional columns:

- y: Number of positive observations for the corresponding covariate values
- N: Total number of observations for these covariates

Author(s)
Patrick Brown

Examples
```r
thedata = data.frame(sex = rep(c("m", "f"), 10), age=rep(c(20,30), c(10, 10))
y = rbinom(dim(thedata)[1], 1, 0.5)
bindata = binToBinom(y, thedata)
bindata$zeros = bindata$N - bindata$y
glm(as.matrix(bindata[,c("y", "zeros")]) ~ sex, data=bindata, family=binomial)
```
checkChain

Plot an MCMC run

Description

Makes time series plots of the parameters (not the random effects) of an MCMC run.

Usage

checkChain(chain, parameters=NULL, oneFigure=TRUE)

Arguments

chain
The result from restoreParams, or the sims.array component of a bugs call.

parameters
Vector of character strings giving names of parameters to plot. Default is all parameters with names starting with either "beta", "intercept", or "SD".

oneFigure
if TRUE, use par(mfrow=c(a, b)) to put all plots on the same device. Otherwise create a new device for each plot.

Value

Plots are produced, nothing is returned

Author(s)

Patrick Brown

See Also

restoreParams, summaryChain

Examples

thethechain = list(beta = array(1, c(10, 3,4)),
                   dimnames = list(NULL, NULL, paste("beta", 1:4, "", sep=""))),
                   intercept = matrix(1, 10, 3))

checkChain(thethechain)
cholInvArray  

**Precision matrices to variance matrices for Winbugs output**

**Description**
Given an array containing simulations from the posterior of a precision matrix, each individual precision matrix is converted to variances, covariances, and correlations.

**Usage**
\[ \text{cholInvArray}(x, \text{prefix} = \text{“T”}, \text{chol=FALSE}) \]

**Arguments**
- **x**: An array of winbugs output, with precision matrix entries of the form \"T[1,3]\"
- **prefix**: The name of the precision matrix in winbugs, the \"T\" in \"T[1,2]\"
- **chol**: If TRUE, the cholesky decomposition is returned instead of the inverse

**Details**
Inverts the matrices with the cholesky decomposition, but operating on all matrices simultaneously using array arithmetic.

**Value**
An array with the third dimension’s precision matrix entries changed to
- \"sdT[i,i]\" for the standard deviation of component i
- \"covT[i,j]\" for the covariance between i and j
- \"corrT[i,j]\" for the correlations between i and j

**Examples**
```r
# create a random positive definite matrix by
generating a lower triangle
N=4
lmat = diag(runif(N, 1, 10))
thetri = lower.tri(lmat)
lmat[thetri] = rnorm(sum(thetri), 0, 2)
# precmat = solve(lmat %*% t(lmat))
precmat = solve(lmat %*% t(lmat))

# put this matrix into an array
precarray = array(c(precmat), dim=c(1,1,length(precmat)))
dimnames(precarray) = list(NULL, NULL,
paste("T", rep(1:N, N), ",", rep(1:N, rep(N,N)), "\]",sep="")

# invert it with cholInvArray and the solve function
```
getDesignMatrix

cholInvArray(precarray)[1,1]
# the off diagonals of solve(precmat) should be
# the covT elements of cholInvArray(precarray)
solve(precmat)
# the standard deviations in cholInvArray(precarray) should be the
# root of the diagonals of solve(precmat)
sqrt(diag(solve(precmat)))

getDesignMatrix Computes a design matrix from factors and interactions

Description

Converts all factors and interactions to indicator variables, suitable for passing to WinBUGS.

Usage

getDesignMatrix(formula, data, effects = NULL)

Arguments

formula A formula object specifying the fixed effects for the model
data A data frame containing the covariates and factors for random effects
effects A vector of character strings containing the grouping levels, from most general to most specific

Details

The most populous level of a factor is made the baseline.

Value

A matrix containing the covariates, the response(s), and the random effect factors. Also attributes
covariates A list giving the covariates which apply at each level, suitable for passing to
winBugsRaggedArray
response A vector of character strings giving the responses

Author(s)

Patrick Brown

See Also

winBugsRaggedArray, glmmBUGS
getStartingValues

Extract starting values for an MCMC chain from glmmPQL results

Description

Parameter estimates and random effect predictions are extracted from a glmmPQL model fit, and formatted to correspond to the levels in the supplied ragged array.

Usage

getStartingValues(pql, ragged, prefix=NULL, reparam=NULL)

getRaggedSeq

Get one sequence for a ragged array

Description

This function is called by winBugsRaggedArray

Usage

getRaggedSeq(data)

Arguments

data a data frame with two columns

Value

The ragged sequence

Author(s)

Patrick Brown <patrick.brown@utoronto.ca>

See Also

winBugsRaggedArray

Examples

library(nlme)
data(Muscle)
muscleDesign = getDesignMatrix(conc ~ length, data=Muscle, effects="Strip")
attributes(muscleDesign)$covariates
attributes(muscleDesign)$response

getRaggedSeq
Arguments

- `pql`: output from the `glmmPQLstrings` function
- `ragged`: a ragged array, from `winBugsRaggedArray`
- `prefix`: string to append to object names
- `reparam`: vector of random effect names, subtract covariates at this level from the intercept.

Details

This function produces a list suitable for passing to `startingFunction` to generate random starting values for use with `bugs`. If `ragged` has a spatial component, starting values for a spatial random effect will also be computed.

Value

A list of vectors, one for each set of parameters or random effects, and a list of estimated standard deviations.

Author(s)

Patrick Brown <patrick.brown@utoronto.ca>

See Also

`glmmPQLstrings`, `startingFunction`, `bugs`, `glmmBUGS`

Description

Creates ragged arrays, writes a model file, and generates sensible starting estimates.

Usage

```r
glmmBUGS(formula, data, effects, modelFile = "model.txt",
  initFile = "getInits.R",
  family = c("bernoulli", "binomial", "poisson", "gaussian"),
  spatial=NULL, spatialEffect = NULL,
  reparam=NULL, prefix=NULL, priors=NULL,
  brugs=length(grep("unix|xlinux",
    .Platform$OS.type,
    ignore.case=TRUE)))
```
Arguments

formula A formula for the fixed effects portion of the model
data A data frame containing the response, covariates, and group membership
effects A vector of character strings containing the grouping levels, from most general to most specific
modelFile File for saving the bugs model
initFile File for saving the function for generating initial values
family distribution of responses
spatial For Markov Random Field models, a polygons or adjacency matrix. For Geostatistical models, a SpatialPoints objects, a matrix or data frame with columns "x" and "y", or a vector of complex numbers.
spatialeffect spatial variable from data
reparam vector of random effect names, subtract covariates at this level from the intercept.
prefix string to append to object names
priors List or vector where names refer to parameters and elements are prior distributions, for example list(SDsite="dunif(0,10)").
brugs compatibility with OpenBUGS, using the inprod function in place of inprod2, defaults to FALSE on windows and TRUE on unix platforms.

Details

Consider the following model, where \( Y_{ijk} \) is the number of absences from individual \( k \) from class \( j \) in school \( k \).

\[
Y_{ijk} \sim \text{Poisson}(\mu_i)
\]

\[
\log(\mu_i) = \delta \text{age}_{ijk} \beta + \text{classSize}_{ij} \alpha + \text{schoolCategory}_i \gamma + U_i + V_{ij}
\]

\[
U_i \sim N(0, \sigma^2)
\]

\[
V_{ij} \sim N(0, \nu^2)
\]

Here there are covariates which apply to each of the three levels, and random effects at the school and class level. If data is a data frame with one line per individual, the following would implement this model:

```r
glmmBUGS(data, effects=c("school","class"), covariates = list(school="schoolCategory", class="classsize"), observations = "absences", family="poisson")
```

To aid in convergence, the bugs model is actually the following:

\[
\log(\mu_i) = \delta \text{age}_{ijk} \beta + V_{ij}
\]

\[
V_{ij} \sim N(U_i + \text{classSize}_{ij} \alpha, \nu^2)
\]
and the function `restoreParams` subtracts the means from the random effects to restore the original set of equations.

`glmmBUGS` calls the following functions:

- `getDesignMatrix` to convert factors and interactions to indicator variables and find which covariates apply at which levels
- `win BugsRaggedArray` to prepare the ragged array
- `glmmPQLstrings` estimate starting values
- `writeBugsModel` to create a model file
- `getStartingValues` to extract starting values from the `glmmPQL` result
- `startingFunction` to write a function to generate random starting values

Type `glmmBUGS` on the R command line to see the source code, it provides a good summary of the roles of the various functions in the `glmmBUGS` package.

**Value**

Returns a list with the ragged array, from `win BugsRaggedArray`, and the list of starting values from `getStartingValues`. Writes a model file and an initial value function. Note that the initial value function in `initFile` will look for an object called `startingValues`, which does not exist as this is part of a list. Either create `startingValues <- result$startingValues` or edit `initFile`.

**Warning**

You are strongly encouraged to modify the model file and the initial value function file prior to using them.

**Note**

`glmmBUGS` uses the `inprod2` function, which isn’t implemented in OpenBugs, the model file will have to be modified for use with OpenBUGS.

**Author(s)**

Patrick Brown. <patrick.brown@utoronto.ca>

**References**

"Handling unbalanced datasets" in the "Tricks: Advanced Use of the BUGS Language" section of the bugs manual, at [http://www.openbugs.net/Manuals/Tricks.html](http://www.openbugs.net/Manuals/Tricks.html)

**See Also**

`win BugsRaggedArray, glmmPQLstrings, writeBugsModel, getStartingValues, startingFunction, bugs`
Examples

```
library(nlme)
data(Muscle)

muscleRagged = glmmBUGS(conc ~ length, data=Muscle, 
effects="Strip", family="gaussian", 
modelFile='model.bug', reparam='Strip')
startingValues = muscleRagged$startingValues

## Not run:
# run with winbugs
source("getInits.R")
require('R2WinBUGS')
muscleResult = bugs(muscleRagged$ragged, getInits, 
parameters.to.save = names(getInits()), 
model.file="model.bug", n.chain=3, n.iter=1000, 
n.burnin=100, n.thin=10, program="winbugs", 
working.directory=getwd())

# a jags example
require('R2jags')
muscleResultJags = jags(
muscleRagged$ragged, getInits, parameters.to.save = names(getInits()), 
model.file="model.bug", n.chain=3, n.iter=1000, 
n.burnin=100, n.thin=10, 
working.directory=getwd())
muscleParamsJags = restoreParams(
muscleResultJags$BUGSoutput, 
muscleRagged$ragged)
checkChain(muscleParamsJags)

## End(Not run)

data(muscleResult)

muscleParams = restoreParams(muscleResult, muscleRagged$ragged)
summaryChain(muscleParams)
checkChain(muscleParams)

# a spatial example
## Not run:
library(diseaseasemapping)
data('popdata')
data('casedata')
```
model = getRates(casedata, popdata, -age*sex)
ontario = getSMR(popdata, model, casedata)
ontario = ontario@data[.c("CSDUID","observed","logExpected")]

popDataAdjMat = spdep::poly2nb(popdata, row.names=as.character(popdata[["CSDUID"]]))
data('popDataAdjMat')
data('ontario')

forBugs = glmmBUGS(formula=observed + logExpected ~ 1,
effects="CSDUID", family="poisson", spatial=popDataAdjMat, data=ontario)

startingValues = forBugs$startingValues

source("getInits.R")
# find patrick's OpenBUGS executable file
if(Sys.info()["user"] == "patrick") {
obExec = system("find /store/patrick/ -name OpenBUGS", TRUE)
obExec = obExec[length(obExec)]
} else {
obExec = NULL
}

bugsResult = bugs(forBugs$ragged, getInits,
parameters.to.save = names(getInits()),
model.file="model.bug", n.chain=3, n.iter=50, n.burnin=10,
n.thin=2,
program="winbugs", debug=T, working.directory=getwd())
data('ontarioResult')

ontarioParams = restoreParams(ontarioResult, forBugs$ragged)

ontarioSummary = summaryChain(ontarioParams)

# posterior probability of having 10x excess risk
postProb = apply(ontarioParams$FittedRCSDUID, 3, function(x) mean(x>log(10)) )
hist(postProb)

ontario = mergeBugsData(popdata, ontarioSummary)

spplot(ontario, "FittedRateCSDUID.mean")

ontario = mergeBugsData(ontario, postProb, newcol="postProb", by.x="CSDUID")
spplot(ontario, "postProb")
```

## End(Not run)

# geostatistical example

## Not run:
library(geoRglm)
data(rongelap)

rongelap= read.table(url(
paste("http://www.leg.ufpr.br/lib/exe/fetch.php/",
"pessoais:paulojus:mbgbook:datasets:rongelap.txt",
sep=""), header=TRUE)
)
library('spdep')
coordinates(rongelap) = ~cX+cY

rongelap$logOffset = log(rongelap$time)
rongelap$site = seq(1, length(rongelap$time))

forBugs = glmmBUGS(
  formula=counts + logOffset ~ 1, family="poisson",
  data=rongelap$data, effects="site", spatial=rongelap,
  priors=list(phisite=dgamma(100,1))
)

startingValues = forBugs$startingValues
startingValues$phi$site = 100

source("getInits.R")

rongelapResult = bugs(forBugs$ragged, getInits,
  parameters.to.save = names(getInits()),
  model.file="model.bug", n.chain=2, n.iter=20, n.burnin=4, n.thin=2,
  program="winbugs", debug=TRUE,
  working.directory=getwd())

data('rongelapResult')

rongelapParams = restoreParams(rongelapResult, forBugs$ragged)

cHECKChain(rongelapParams)

rongelapParams$siteGrid = CondSimuPosterior(rongelapParams, rongelap,
  gridSize=100)
	nongelapSummary=summaryChain(rongelapParams)
```

glmmPQLstrings

# plot posterior probabilities of being above average
image(rongelapSummary$siteGrid$pgt@

## End(Not run)

### glmmPQLstrings

*An alternat interface to glmmPQL*

#### Description

Calls glmmPQL in the MASS library, with the model being specified in the same manner as `writeBugsModel`

#### Usage

```r
glmmPQLstrings(effects, covariates, observations, data = NULL,
family=c("bernoulli", "binomial", "poisson", "gaussian"), ...)
```

#### Arguments

- **effects**: A vector of character strings containing the grouping levels, from most general to most specific
- **covariates**: A list with names corresponding to effects and each element being a vector of covariates applicable at that level
- **observations**: A character string giving the column of observations, or a vector where the first element is the observations and the remaining are offsets. For binomial responses, the first element is the counts (of successes), and the second element is the total number of trials. Note this differs from glmmPQL and glm's notation, but is consistent with WinBUGS.
- **data**: A data frame containing the response, covariates, and group membership.
- **family**: The distribution to use. Either using glmmPQL’s specifications or `writeBugsModel`
- **...**: further arguments to `glmmPQL`

#### Details

This function is useful for generating starting values for an MCMC chain.

#### Value

In addition to the output from glmmPQL, the following are returned

- **effects**, **covariates**, **observations**
  
  As input

#### Author(s)

Patrick Brown, patrick.brown@utoronto.ca
mergeBugsData-methods

See Also
getStartingValues, glmmPQL

Examples

library(nlme)
data(Muscle)
glmmPQL(strings(effects="Strip", observations="conc", covariates=list(observations="length"), data=Muscle, family="gaussian"))

mergeBugsData-methods  Merge results from BUGS into a data.frame or SPDF

Description
merge the result from bugs function

Usage

## S4 method for signature 'data.frame'
mergeBugsData(
x, bugsSummary, by.x = NULL, newcol = "mean", ...
)
## S4 method for signature 'SpatialPolygonsDataFrame'
mergeBugsData(
x, bugsSummary, by.x = NULL, newcol = "mean", ...
)

Arguments

x  spatial polygon object i.e population data set (popdata)
bugsSummary posterior distribution result from summaryChain function
by.x  the common term from the spatial polygon object and the bugs function result
newcol  the summary statistic that to be merged back to the data frame
... additional arguments

Author(s)
Patrick Brown

Examples

if(require('diseasemapping')){
data('popdata')
newdata = c("3560102"=2, "3560104"=3)
popdatatry = mergeBugsData(popdata, newdata, by.x="CSDUID")
}
**muscleResult**

*data set contains muscle result*

**Description**

Results from running the muscle example in *glmmBUGS*.

**Usage**

```r
data(muscleResult)
```

**Format**

A list as returned by the *bugs* function.

**Details**

See *glmmBUGS* and *Muscle*.

**Examples**

```r
data(muscleResult)
```

---

**ontario**

*Ontario data on molar cancer*

**Description**

Data frame showing expected and observed counts of molar cancer in Ontario.

**Usage**

```r
data(ontario)
```

**Format**

A data frame with 585 observations on the following 3 variables.

- **CSDUID**: factor of Ontario census subdivision ID numbers
- **observed**: Observed molar cancer cases
- **logExpected**: expected cases

**Details**

See the documentation for *glmmBUGS* for how this was created.
Example

```r
data(ontario)
head(ontario)
```

---

**Description**

Results from running Winbugs on the ontario data

**Usage**

```r
data(ontarioResult)
```

**Format**

A list, as produced by the `bugs` function.

**Examples**

```r
data(ontarioResult)
ontarioParams = restoreParams(ontarioResult)
ontarioSummary = summaryChain(ontarioParams)
```

---

**popDataAdjMat**

*Data set containing an adjacency matrix*

**Description**

The `popDataAdjMat` Data set contains the adjacency matrix which calculated from the `poly2nb` function.

**Usage**

```r
data('popDataAdjMat')
```

**Details**

It is a adjacency matrix denoting the neighbours of Ontario census subdivisions.
### Examples

```r
## Not run:
library('diseasemapping')
data('popdata')
popDataAdjMat = spdep::poly2nb(popdata,
row.names=as.character(popdata$CSUID))

## End(Not run)
data('popDataAdjMat')
summary(popDataAdjMat)
attributes(popDataAdjMat)$region.id[1:10]
```

### Description

Undoes the parametrisation used in `writeBugsModel`, and gives the original names to random effect levels.

### Usage

```r
restoreParams(bugsResult, ragged = NULL, extraX = NULL)
```

### Arguments

- **bugsResult**: Output from `bugs`, using a ragged array generated by `winBugsRaggedArray` and a model generated by `writeBugsModel`.
- **ragged**: The ragged array used to call `bugs`.
- **extraX**: Possible extra covariates for spatial regions with no data but do have predicted spatial effects.

### Value

A list where each element is a matrix or an array. The first dimension is the number of realisations, the second the number of chains, and for vector-valued parameters and random effects, the third dimension is the length of the parameter.

If the model contains a spatial component, the result will have list entries the following:

- **$reffect**: The random effect. In the case of spatial models this is the sum of the spatial and non-spatial random effects $U+V$.
- **$reffectSpatial**: The spatial random effect for each region, if any.
- **$fittedreffect**: The predicted values on the link scale, being the random effect plus intercept and effect of covariates.
Note

For spatial models, one fitted rate is computed for each region in the adjacency matrix, even though some of these regions may not have spatial or non-spatial random effects simulated in the bugs model. If a spatial random effect is missing (as happens with islands), a zero is added. If a non-spatial random effect is missing (as happens when a regions does not have data), a value is simulated unconditionally from each iteration’s intercept and standard deviation for that effect. Note that this does not add on the effect of possible covariates for that region. This can be added via the extraX argument.

Author(s)

Patrick Brown patrick.brown@utoronto.ca

See Also

bugs

Description

A SpatialPointsDataFrame containing the Rongelap data, in a UTM projection.

Usage

data("rongelapUTM")
data("rongelapResult")

Details

These coordinates were obtained by translating and rotating the original Rongelap data until all the coordinates fit into the Rongelap border given by www.gadm.org. So they are not exact.

Source

See the help file for rongelap, or http://www.leg.ufpr.br/doku.php/pessoais:paulejus:mbbook:datasets

Examples

data("rongelapUTM")
if(require("sp", quietly=TRUE)){
  plot(rongelapUTM)
}

## Not run:
rongelapBorderLL = raster::getData("GADM",

startingFunction

```r

country="MHL", level=0
library("rgdal")
rongelapBorderUTM = spTransform(rongelapBorderLL, CRS(proj4string(rongelapUTM)))
plot(rongelapBorderUTM, add=TRUE)

## End(Not run)

rongelapUTM$logOffset = log(rongelapUTM$time)
rongelapUTM$site = seq(1, length(rongelapUTM$time))

forBugs = glmmBUGS(
  formula=count + logOffset ~ 1, family="poisson",
  data=rongelapUTM@data, effects="site",
  spatial=rongelapUTM,
  priors=list(phisite="dgamma(100,1)"")
)

startingValues = forBugs$startingValues
startingValues$phi=list(site = 100)

source("getInits.R")

## Not run:
rongelapResult = bugs(forBugs$ragged, getInits,
  parameters.to.save = names(getInits()),
  model.file="model.bug", n.chain=2, n.iter=20, n.burnin=4, n.thin=2,
  program="winbugs", debug=TRUE,
  working.directory=getwd())
rongelapParams = restoreParams(rongelapResult, forBugs$ragged)

## End(Not run)

data("rongelapResult")
rongelapParams = restoreParams(rongelapResult)

checkChain(rongelapParams)
rongelapSummary=summaryChain(rongelapParams)
```

**Description**

The code for the resulting function is saved in a file, to be edited and sourced in before calling WinBUGS.
startingFunction

Usage

startingFunction(startingValues, file = "getInits.R")

Arguments

startingValues  list returned from getStartingValues
file  character string giving the name of the file to write to

Details

Given a list containing initial estimates of parameters and random effects, a text file is produced containing code for a function to generate random starting values for use with the bugs() function. It is intended that the file produced be checked and edited prior to use.

Value

A file, with the name given by the 'file' argument, is written.

Warning

You are strongly encouraged to edit the file to ensure the result is sensible.

Author(s)

Patrick Brown, patrick.brown@utoronto.ca

See Also

getStartingValues, bugs

Examples

### Should be DIRECTLY executable !! ----
###---> Define data, use random,
###--or do help(data=index) for the standard data sets.
sval = list(intercept=0, beta = 1:2, Rperson = rep(0, 5), vars=list(person=1))
startingFunction(sval)
summaryChain

**Compute mean, standard deviation, and quantiles of an MCMC run**

### Description

Computes summary statistics for each parameter.

### Usage

```r
summaryChain(chain, probs = c(0.005, 0.025, 0.05, 0.5))
```

### Arguments

- **chain**: The result from `restoreParams`, or the `sims.array` component of a `bugs` call.
- **probs**: Quantiles for the posterior credible interval

### Value

A list of matrices, with rows corresponding to summary statistics and columns to parameters.

- **scalar**: Matrix for the scalar parameters
- **...**: One matrix for each vector valued parameter
- **FittedRateEffect**: For spatial models only, summaries on the natural scale (exponential of FittedRateEffect).

### Author(s)

Patrick Brown

### See Also

`restoreParams`

### Examples

```r
# create a simple chain
thechain = list(beta = array(1, c(10, 3, 4)),
dimnames = list(NULL, NULL, paste("beta[", 1:4, "]", sep=""))),
intercept = matrix(1, 10, 3))

summaryChain(thechain)
```
Description

Suitable for unbalanced data.

Usage

winBugsRaggedArray(data, effects = names(data)[-length(names(data))],
covariates = NULL, observations = names(data)[length(names(data))],
returnData = FALSE,
prefix= NULL, reparam=FALSE)

Arguments

data A data frame containing the response, covariates, and group membership.
effects A vector of character strings containing the grouping levels, from most general to most specific. Defaults to the column names of data, excluding the last column.
covariates A list with names corresponding to effects and each element being a vector of covariates applicable at that level
observations A character string giving the column of observations, or a vector where the first element is the observations and the remaining are offsets.
returnData If true, returns the re-ordered data frame as well as the data frame
prefix Character string to be appended to variable names
reparam Vector of effect names, reparametrize the intercept by subtracting the mean of covariates at this level.

Details

This function creates a list of data suitable for passing to the bugs function, suitable for implementation as a ragged array. The output can be passed to getStartingValues to manipulate the output from glmPQLstrings, and to restoreParams to restore the original parametrisation from bugs output.

Value

A list with the following components

Nxx The number of levels in the most general grouping
Syy Indexing sequences, one for each level. If yy is level n, level n+1 has elements Syy[1] to Syy[2]-1 belonging to the first category of level n.
Xyy Matrix or vector of covariates belonging to level yy
vector of observations.
writeBugsModel

Author(s)
Patrick Brown, <patrick.brown@utoronto.ca>

References
"Handling unbalanced datasets" in the "Tricks: Advanced Use of the BUGS Language" section of the bugs manual, at http://www.openbugs.net/Manuals/Tricks.html

See Also
bugs

Examples
library(nlme)
data(Muscle)
muscleRagged = winBugsRaggedArray(Muscle, effects="Strip",
observations="conc",
covariates=list(observations="length"))

writeBugsModel(file, effects, covariates, observations, family = c("bernoulli", "binomial", "poisson", "normal", "other"), spatial = NULL, geostat=FALSE, prefix = "", reparam=NULL, brugs=TRUE, priors=NULL)

Arguments
file a character string denoting the name of the bugs model file written.
effects vector of effect groups
covariates A list with names corresponding to effects and each element being a vector of covariates applicable at that level
observations A character string giving the column of observations, or a vector where the first element is the observations and the remaining are offsets.
family Response distribution
spatial: name of the spatial random effect
geostat: Is this a geostatistical random effect? Defaults to FALSE for the Besag, York and Mollie discrete spatial variation model
prefix: the prefix
reparam: vector of random effect names, subtract covariates at this level from the intercept.
brugs: make the model file compatible with OpenBugs by using the inprod function in place of inprod2
priors: character string of prior distributions, with the name of each element referring to the parameter it is the prior for

Details

The arguments to the function specify a generalised linear mixed model. A file containing code for a corresponding bugs model is written. The model uses ragged arrays to specify grouping factors, and includes covariates at the appropriate levels to aid in chain convergence. It is intended that the user will edit this file before its use. The prior distributions in particular may not be appropriate.

Value

A file, suitable for passing to the bugs function in R2WinBUGS.

Warning

You are strongly encouraged to modify the model file prior to using it.

Author(s)

Patrick Brown, <patrick.brown@utoronto.ca>

References

"Handling unbalanced datasets" in the "Tricks: Advanced Use of the BUGS Language" section of the bugs manual, at http://www.openbugs.net/Manuals/Tricks.html

Examples

```r
writeBugsModel("model.bug", effects="Strip", observations="conc",
covariates=list(observations="length"),
family="normal", priors=c(intercept="dunif(-10,10)"))

cat(scan("model.bug", "a",sep='\n'),sep='\n')
```
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