Package ‘bayespref’

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Description This program implements a hierarchical Bayesian analysis
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Hierarchical Bayesian analysis of ecological count data

Description

This program implements a hierarchical Bayesian analysis of count data, such as preference experiments. It provides population-level and individual-level preference parameter estimates obtained via MCMC. It also allows for model comparison using Deviance Information Criterion.

Details

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Version: 1.0
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License: GPL (>= 2)
LazyLoad: yes

For information regarding functions implemented in bayespref, please see the appropriate function help pages.

Author(s)

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Hierarchical Bayesian model for count data

Description

This function implements a hierarchical Bayesian model for count data. Preference parameters are estimated using MCMC.

Usage

bayesPref(pData = NULL, mcmcL = 1000, dirvar = 2, calc dic = TRUE, constrain = FALSE, pm priorLB = 1, pm priorUB = 50, ppprior = NULL, dicburn = 100, indc = TRUE, pops = TRUE, pminit = NULL, ppinit = NULL, ipinit = NULL, constrainP = NULL, diradd = 0.1, univar = 2, estip = TRUE, measure = "mean")
Arguments

- **pData**: A matrix of count data, rows are replicates or individuals and columns are categories.
- **mcmcl**: A value indicating the length of the mcmc chain (recommended > 5000).
- **dirvar**: A value for multiplier for population preference proposals. Increase to decrease proposal distances.
- **calc dic**: A Boolean for returning DIC.
- **constrain**: A Boolean for constraining population-level preferences to be equal.
- **pmpriorLB**: A value setting the lower bounds of uniform prior for popmult.
- **pmpriorUB**: A value setting the upper bounds of uniform prior for popmult.
- **ppprior**: A vector of alphas for Dirichlet prior on population preference.
- **dicburn**: A value indicating the number of burnin samples discarded for DIC calculation.
- **indc**: A Boolean indicating an independence chain (default) vs. random-walk for population-level preferences.
- **pops**: A Boolean indicating whether the first column of the matrix are values indicating populations.
- **pminit**: A value indicating the initial value for the population multiplier.
- **ppinit**: A vector or matrix of initial values population preferences.
- **ipinit**: A vector or matrix of initial values for individual-level preferences.
- **constrainP**: A vector with one entry per population giving the group each population belongs to.
- **diradd**: A value added to the Dirichlet proposal for population preferences.
- **univar**: A value that is the jump distance for univorm variance parameter.
- **estip**: A boolean indicating whether to attempt to estimate individual preferences or only estimate population preference (the latter used a multivariate Polya).
- **measure**: Indicates whether the "mean" or "median" is used for calculating DIC.

Details

Populations are indicated in the first column (if present) as integers. constrainP provides a way to group populations with the goal of comparing among various models. For example, if there are 3 populations in the data (indicated as 1, 2, 3) and it is desired to examine a model where populations 1 and 3 are constrained to have the same population-level preference parameters, constrainP=c(1,2,1).

The mixing of the chains should be observed by plotting each step in the chain against a population-level preference parameter, for example. Tuning parameters (e.g., dirvar), or initial starting conditions (e.g., ppinit) can be modified for better mixing if needed.

Value

A list containing the following for each population in the analysis.

- **IndPref**: An array containing the individual-level preference parameter estimates for each step in the MCMC.
PopPref  An array containing the population-level preference parameter estimates for each step in the MCMC.

likelihood  The log-likelihood of the model given the parameter estimates for each step in the MCMC.

dic  The deviance information criterion score for the model.

Note

Even if only one population is present, the values are returned in a list of length one.

Author(s)

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Examples

```r
## not run:
data(YGGV)
res <- bayesPref(pData=YGGV,mcmc=1000)
## End(Not run)
```

calcdic  Calculate DIC

Description

THIS IS AN INTERNAL FUNCTION NOT CALLED BY USERS

Usage

```r
calcdic(lnL = NULL, popP = NULL, popM = NULL, indP = NULL, dicburn = NULL, mcmc = NULL, N = NULL, pData = NULL, popN = NULL, nPops = NULL, estip = NULL, measure = NULL)
```

Arguments

- `lnL`
- `popP`
- `popM`
- `indP`
- `dicburn`
- `mcmc`
- `N`
- `pData`
calcdicExtern

popN
nPops
estip
measure

---

**Description**

This function calculates the DIC score for an object return by bayesPref.

**Usage**

```r
calcdicExtern(pData = NULL, prefres = NULL, pops = TRUE, dicburn = 0, estip = TRUE, measure = "median", constrainP = NULL)
```

**Arguments**

- **pData**: A matrix of count data, rows are replicates or individuals and columns are categories.
- **prefres**: An object returned by bayesPref.
- **pops**: A Boolean indicating whether the first column of the matrix are values indicating populations.
- **dicburn**: A value indicating the number of burnin samples discarded for DIC calculation.
- **estip**: A boolean indicating whether to attempt to estimate individual preferences or only estimate population preference (the latter used a multivariate Polya).
- **measure**: Indicates whether the "mean" or "median" is used for calculating DIC.
- **constrainP**: A vector with one entry per population giving the group each population belongs to.

**Author(s)**

Zachariah Gompert <zgompert@uwyo.edu>, James A. Fordyce <jfordyce@utk.edu>

**Examples**

```r
## Not run:
data(YGGV)
res <- bayesPref(pData=YGGV,mcmcL=1000)
calcdicExtern(pData=YGGV,prefres=res,pops=TRUE,dicburn=100)

## End(Not run)
```
**credibilityIntervals**

**Description**

THIS IS AN INTERNAL FUNCTION NOT CALLED DIRECTLY BY USERS

**Usage**

credibilityIntervals(prefres = NULL, burn = 0, interval = 0.95)
dpolya

Arguments

prefres An object returned by bayesPref.
burn A value indicating the number of burnin samples discarded.
interval A value between 0 and 1 indicating the size of the credible interval calculated.

Value

A list containing the following:

IndPref An array containing the lower credible interval, the median, and upper credible interval for the individual-level preference parameters.

PopPref An array containing the lower credible interval, the median, and upper credible interval for the population-level preference parameters.

PopVar A vector for the lower credible interval, the median, and upper credible interval for the variance of the population-level preference parameters (variance of alphas in Dirichlet).

Author(s)

Zachariah Gompert <zgompert@uwyo.edu>, James A. Fordyce <jfordyce@utk.edu>

Examples

## Not run:
data(YGGV)
res <- bayesPref(pData=YGGV,mcmcl=1000)
credibleIntervals(prefres=res[[1]],burn=100) #credible intervals for population 1

## End(Not run)

dpolya  Multivariate polya pdf

Description

THIS IS AN INTERNAL FUNCTION NOT CALLED DIRECTLY BY USERS

Usage

dpolya(x = NA, alpha = NA)

Arguments

x
alpha
MratioPopMult

Description

THIS IS AN INTERNAL FUNCTION NOT CALLED DIRECTLY BY USERS

Usage

```
MratioPopMult(step = NULL, nInd = NULL, prefsArray = NULL, popPrefs = NULL, popMult = NULL, popprior = NULL, dirvar = NULL, indc = NULL, pData = NULL, diradd = NULL, estip = NULL)
```

Arguments

- `step`
- `nInd`
- `prefsArray`
- `popPrefs`
- `popMult`
- `popprior`
- `dirvar`
- `indc`
- `pData`
- `diradd`
- `estip`
pairwiseProb

Arguments

- step
- nInd
- prefsArray
- popPrefs
- popMult
- lb
- ub
- estip
- pData

**pairwiseProb**  *Pairwise probability for differences in preference*

**Description**

This function calculates the pairwise probability that preference among items differs. It provides the probability that row > column.

**Usage**

pairwiseProb(prefres = NULL, burn = 0)

**Arguments**

- prefres An object returned by bayesPref.
- burn A value indicating the number of burnin samples discarded.

**Details**

This function examines the proportion of times a certain preference parameter is ranked over an alternate preference parameter across each post burnin MCMC step. It can be interpreted as a post-hoc test to the results obtained from bayesPref.

**Value**

A square matrix of pairwise comparisons giving the probability that row > column.

**Author(s)**

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Examples

## Not run:
data(YGV)
res <- bayesPref(pData=YGV,mcmcL=1000)
pairwiseProb(prefres=res[[1]],burn=100) #pairwise probability for population 1

## End(Not run)

prefPlot

Plot population and individual preferences

Description

This function will plot the posterior densities for population-level and individual-level preferences based upon a bayespref analysis.

Usage

prefPlot(prefres = NULL, burn = 0, ind = TRUE, pop = TRUE, dist = FALSE, ymax = 5, xmin = 0, xmax = 1, dadj = 2, colors = NULL, leg = FALSE, lx = 0.8, ly = 4, catname = NULL, ps = FALSE, file = ".prefplot.ep")

Arguments

prefres An object returned by bayesPref.
burn A value indicating the number of burnin samples discarded.
ind A boolean indicating whether to plot individual-level preferences.
pop A boolean indicating whether to plot population-level preferences.
dist A boolean indicating whether to plot population-level preferences based on density of the posterior (default), or whether to plot population-level preferences based on the estimate of the Dirichlet alphas.
ymax A value indicating the maximum value for the y-axis.
xmin A value indicating the minimum value for the x-axis.
xmax A value indicating the maximum value for the x-axis.
dadj A value indicating the bandwidth used for the smoothing of the density plot.
colors A vector indicating the colors used for plotting.
leg A Boolean indicating whether to include a legend in the plot.
lx A value indicating where the legend begins on the horizontal (x-axis).
ly A value indicating where the legend begins on the vertical (y-axis).
catname A vector indicating the names associated with the legend.
ps A Boolean indicating whether to write the plot to a file.
file The name of the file the plot is written to.
Author(s)
Zachariah Gompert <zgompert@uwyo.edu>, James A. Fordyce <jfordyce@utk.edu>

Examples

```r
## not run:
data(YGGV)
res <- bayesPref(pData=YGGV,mcmcL=1000)
prefPlot(prefres=res[[1]],burn=100,pop=TRUE)
prefPlot(prefres=res[[1]],burn=100,pop=TRUE,ymax=15,leg=TRUE,
catname=c("Astragalus","Lotus","Lupine","Medicago"),lx=0.6,ly=14) # includes legend
prefPlot(prefres=res[[1]],burn=100,ind=FALSE,pop=TRUE,ymax=15,leg=TRUE,
catname=c("Astragalus","Lotus","Lupine","Medicago"),lx=0.6,ly=14) # includes only
population posterior and legend
## end(not run)
```

YGGV

**Oviposition preference data from Yuba Gap, CA and Gardnerville, NV.**

Description
A data matrix of experimental host plant choice data from two population of Lycaeides.

Usage

data(YGGV)

Format
A data frame with 26 observations on the following 5 variables.

- **Pop** a numeric vector
- **Ast** a numeric vector
- **Lotus** a numeric vector
- **Lupine** a numeric vector
- **Medicago** a numeric vector

Details
Pop 1 is Yuba Gap, CA and Pop 2 is Gardnerville, NV.
Source


Examples

```r
data(YGGV)
boxplot(YGGV[,2:5])
str(YGGV)
```
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