

# Package ‘bayespref’

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**Type** Package

**Title** Hierarchical Bayesian analysis of ecological count data

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**Author** Zachariah Gompert and James A. Fordyce

**Maintainer** James A. Fordyce <jfordyce@utk.edu>

**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.

**License** GPL (>= 2)

**LazyLoad** yes

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**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**

Package:	bayespref
Type:	Package
Version:	1.0
Date:	2011-05-16
License:	GPL (>= 2)
LazyLoad:	yes

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

**Author(s)**

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

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bayesPref	<i>Hierarchical Bayesian model for count data</i>
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**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, calcdic = TRUE,
  constrain = FALSE, pmpriorLB = 1, pmpriorUB = 50, pprior = NULL,
  dicburn = 100, indc = TRUE, pops = TRUE, pmnit = NULL, ppnit = NULL,
  ipnit = 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.
calcdic	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 populationlevel 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.
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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)**

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

**Examples**

```
## Not run:
data(YGGV)
res <- bayesPref(pData=YGGV,mcmcL=1000)

## End(Not run)
```

---

calcdic

*Calculate DIC*


---

**Description**

THIS IS AN INTERNAL FUNCTION NOT CALLED BY USERS

**Usage**

```
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
```

popN  
 nPops  
 estip  
 measure

---

calcdicExtern                    *Calculates DIC*

---

### Description

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

### Usage

```
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

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

## End(Not run)
```

---

`calcP`*calcP*

---

**Description**

THIS IS AN INTERNAL FUNCTION NOT CALLED DIRECTLY BY USERS

**Usage**

```
calcP(step = NULL, prefsArray = NULL, popPrefsL = NULL, popMultL = NULL,  
lb = NULL, ub = NULL, pprior = NULL, N = NULL, pData = NULL,  
nPops = NULL, popN = NULL, estip = NULL)
```

**Arguments**

step  
prefsArray  
popPrefsL  
popMultL  
lb  
ub  
pprior  
N  
pData  
nPops  
popN  
estip

---

`credibleIntervals`*Calculates credible intervals for preferences*

---

**Description**

This function calculates the credible intervals for preference parameters for individuals and the population using the object created by the function bayesPref.

**Usage**

```
credibleIntervals(prefres = NULL, burn = 0, interval = 0.95)
```

**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@uwo.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

---

MHratioPopPref

*MHratioPopPref*

---

### Description

THIS IS AN INTERNAL FUNCTION NOT CALLED DIRECTLY BY USERS

### Usage

```
MHratioPopPref(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

---

MratioPopMult

*MratioPopMult*

---

### Description

THIS IS AN INTERNAL FUNCTION NOT CALLED DIRECTLY BY USERS

### Usage

```
MratioPopMult(step = NULL, nInd = NULL, prefsArray = NULL,  
popPrefs = NULL, popMult = NULL, lb = NULL, ub = NULL,  
estip = NULL, pData = NULL)
```



**Arguments**

step  
 nInd  
 prefsArray  
 popPrefs  
 popMult  
 lb  
 ub  
 estip  
 pData

---

pairwiseProb	<i>Pairwise probability for differences in preference</i>
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---

**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)**

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

**Examples**

```
## Not run:
data(YGGV)
res <- bayesPref(pData=YGGV,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.eps")
```

**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**

```
## 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**

Gompert, Z., J.A. Fordyce, M.L. Forister, A.M. Shapiro, & C.C. Nice. 2006. Homoploid hybrid speciation in an extreme habitat. *Science* 314:1923-1925.

**Examples**

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

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