

# Package: BayesComm (via r-universe)

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**Type** Package

**Title** Bayesian Community Ecology Analysis

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**Description** Bayesian multivariate binary (probit) regression models  
for analysis of ecological communities.

**License** GPL (>= 2)

**Imports** Rcpp (>= 0.11.6), abind, coda, mvtnorm, progress

**Suggests** testthat

**LinkingTo** Rcpp, RcppArmadillo

**Repository** <https://goldingn.r-universe.dev>

**RemoteUrl** <https://github.com/goldingn/bayescomm>

**RemoteRef** HEAD

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## Description

BayesComm fits Bayesian multivariate binary (probit) regression models for analysis of ecological communities. These models can be used to make inference about underlying inter-species interactions in communities and to separate the effects of environmental covariates and inter-species interactions on community assembly. This package accompanies the paper (in preparation) by Golding et al. (2013) and is based on a model described by Edwards and Allenby (2003).

## Details

Package: BayesComm  
Type: Package  
Version: 0.1-1  
Date: 2014-03-07  
License: GPL (>=2)

BayesComm models take as input a matrix of species presence/absence records and optionally a matrix of environmental covariates. `BC` is the main function for setting up models. It is a wrapper function to `BCfit` and returns a `bayescomm` object. `bayescomm` objects have associated `summary`, `plot`, `print`, `window` and `residuals` functions. Functions are also provided to calculate Deviance Information Criteria (`DIC`) and run a deviance partitioning procedure on model outputs (`devpart`).

Full details of formulation of the model are given in Golding et al. (2013).

## Author(s)

Nick Golding <[nick.golding@zoo.ox.ac.uk](mailto:nick.golding@zoo.ox.ac.uk)> & Dave Harris

## References

- Golding (2013) Mapping and understanding the distributions of potential vector mosquitoes in the UK: New methods and applications. (Chapter 3) <http://dx.doi.org/10.6084/m9.figshare.767289>
- Edwards, Y., Allenby, G. (2003) Multivariate analysis of multiple response data. *Journal of Marketing Research*, 40 (3) 321-34.

## See Also

`BC`, `BCfit`, `window.bayescomm`, `plot.bayescomm`, `print.bayescomm`, `summary.bayescomm`, `residuals.bayescomm`, `DIC`, `devpart`,

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BC *Run a BayesComm model*

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### Description

BC is the main function for running BayesComm models. It is a wrapper function for BCfit; it checks inputs, sets up the model types and specifies a number of default BCfit settings.

### Usage

```
BC(Y, X = NULL, model = "null", covlist = NULL, condition = NULL, its = 100, ...)
```

### Arguments

Y	matrix of species presence/absence data
X	matrix of environmental covariates
model	type of model to run
covlist	optional list of which covariates to assign to each species
condition	matrix of conditioning variables
its	number of iterations for sampling phase
...	further arguments to pass to BCfit

### Details

Y must be a matrix with records as rows and species as columns and X a matrix with records as rows and covariates as columns. model must be one of: "null" (intercept only), "environment" (intercept & covariates), "community" (intercept & community matrix) or "full" (intercept, covariates & community matrix). covlist must have the same length as the number of species with, each element a vector of column indices for X. covlist defaults to NULL, which includes all covariates for all species. For more details of arguments for model fitting see [BCfit](#). condition is an optional matrix of conditioning variables. These are fitted in the same way as X but are not removed in null and community models.

### Value

An object of class bayescomm containing the model call and parameter chains which can be viewed and manipulated using window, plot, print and summary.

### See Also

[BCfit](#)

**Examples**

```

# create fake data
n <- 500
nsp <- 4
k <- 3

X <- matrix(c(rep(1, n), rnorm(n * k)), n) # covariate matrix

# Random covariance matrix
W <- 10 * solve(rWishart(1, nsp + 1, diag(nsp))[, , 1])

B <- matrix(rnorm(nsp * (k + 1), 0, 1), nsp) # true covariates
mu <- apply(B, 1, function(b, x) x %*% b, X) # true mean
e <- matrix(rnorm(n * nsp), n) %*% chol(W) # true e
z <- mu + e # true z
Y <- ifelse(z > 0, 1, 0) # true presence/absence

# run BC (after removing intercept column from design matrix)
m1 <- BC(Y, X[, -1], model = "full", its = 100)

```

BCfit

*Fit a BayesComm model***Description**

BCfit is the workhorse function for the BayesComm model. It is highly recommended to use the wrapper function `BC` which checks inputs and sets up different model types and initial values. BCfit arguments can be accessed through BC using the `...` argument.

**Usage**

```

BCfit(y, X, covlist, R, z, mu, updateR, iters, thin = 1, burn = 0,
      priW = c(nrow(z) + 2 * ncol(z), 2 * ncol(z)), updateMu = TRUE,
      verbose = 0)

```

**Arguments**

<code>y</code>	matrix of species presence/absence data
<code>X</code>	matrix of environmental covariates
<code>covlist</code>	optional list of which covariates to assign to each species
<code>R</code>	initial values for correlation matrix
<code>z</code>	initial values for $z$
<code>mu</code>	initial values for $\mu$
<code>updateR</code>	logical; if true the correlation matrix is updated, if false it is fixed at $R$
<code>iters</code>	total number of iterations
<code>thin</code>	amount to thin the posterior chains. Defaults to 1 (no thinning)

burn	number of iterations to discard at the beginning of the chain
priW	prior specification for correlation matrix W
updateMu	logical; if true, the mean matrix is updated; if false, it is fixed at mu (and B is not estimated). Defaults to TRUE. Note that this argument cannot be passed from <a href="#">BC</a> ; it can only be used in <code>BCfit</code> directly
verbose	how often to print updates to the console. 0 for no updates. 1 for updates every thin iterations after burnin. 2 for updates every iteration.

### Details

`priW` specifies the inverse Wishart prior on the unknown and unidentifiable covariance matrix  $W$  from which the correlation matrix  $R$  is derived. `priW` is a vector of length two, the first element specifies the degrees of freedom, the second element is multiplied by an identity matrix to form the scale matrix. The default for `priW` is  $c(n + 2p, 2p)$ , where  $n$  is the number of records and  $p$  is the number of species in the community; this therefore forms the prior:  $iW(n + 2p, 2pI)$ . This prior was determined to exert minimal influence on the posterior of  $R$  whilst limiting dependence of  $R$  on the unidentifiable variance parameters of  $W$ .

For further details on how to specify  $Y$ ,  $X$  and `covlist` see [BC](#).

### Value

A list containing elements:

R	samples from posteriors of the correlation matrix
B	samples from posteriors of regression coefficients (a list of matrices)
z	samples from posteriors of latent variables $z$

### See Also

[BC](#)

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devpart	<i>Deviance partitioning</i>
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### Description

Runs a deviance partitioning procedure on a set of four `bayescomm` objects.

### Usage

```
devpart(null, environment, community, full)
```

**Arguments**

null	a bayescomm object containing a 'null' model
environment	a bayescomm object containing an 'environment' model
community	a bayescomm object containing a 'community' model
full	a bayescomm object containing a 'full' model

**Details**

The deviance partitioning procedure determines the proportion of the null deviance explained by each of the other three model types. The four model types are those created by BC.

**Value**

A list containing elements

devpart	matrix containing the proportion of the null deviance explained by each model for each species
null	a matrix containing the mean and 95% credible intervals for the deviance for each species in the null model
environment	a matrix containing the mean and 95% credible intervals for the deviance for each species in the environment model
community	a matrix containing the mean and 95% credible intervals for the deviance for each species in the community model
full	a matrix containing the mean and 95% credible intervals for the deviance for each species in the full model

**See Also**

[BC](#)

**Examples**

```
# create fake data
n <- 100
nsp <- 4
k <- 3

X <- matrix(c(rep(1, n), rnorm(n * k)), n) # covariate matrix
W <- matrix(rnorm(nsp * nsp), nsp)
W <- W %>% t(W) / 2 # true covariance matrix
B <- matrix(rnorm(nsp * (k + 1), 0, 3), nsp) # true covariates
mu <- apply(B, 1, function(b, x) x %>% b, X) # true mean
e <- matrix(rnorm(n * nsp), n) %>% chol(W) # true e
z <- mu + e # true z
Y <- ifelse(z > 0, 1, 0) # true presence/absence

# run BC (after removing intercept column from design matrix)
null <- BC(Y, X[, -1], model = "null", its = 100)
```

```
comm <- BC(Y, X[, -1], model = "community", its = 100)
envi <- BC(Y, X[, -1], model = "environment", its = 100)
full <- BC(Y, X[, -1], model = "full", its = 100)

devpart(null, envi, comm, full)
```

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DIC

*Deviance Information Criterion*

---

### Description

Calculates Deviance Information Criteria for bayescomm objects.

### Usage

```
DIC(BC)
```

### Arguments

BC                    a bayescomm object

### References

Spiegelhalter, D.J., Best, N.G., Carlin, B.P., van der Linde, A. (2002). Bayesian measures of model complexity and fit. *Journal of the Royal Statistical Society, Series B*, 64 (4): 583-639.

### See Also

[BC](#)

### Examples

```
m1 <- example(BC)[[1]]
DIC(m1)
```

---

plot.bayescomm

*Plot bayescomm parameter chains*

---

### Description

plot.bayescomm creates summary plots of a subset of the parameter chains in a bayescomm object using the coda package.

### Usage

```
## S3 method for class 'bayescomm'
plot(x, chain, ...)
```

**Arguments**

x a bayescomm object  
 chain a character string of the parameter chains to plot  
 ... further arguments to pass to plot.mcmc

**Details**

chain should be one of 'R' (for correlation coefficients) or 'B\$sp' where sp is the species of interest (for regression coefficients).

**See Also**

[BC](#), [plot.mcmc](#)

**Examples**

```
m1 <- example(BC)[[1]]
plot(m1, 'R')
plot(m1, 'B$sp1')
```

---

predict.bayescomm      *Function to make predictions at new locations*

---

**Description**

For each set of parameter values sampled by the model (including values of Z), simulate the occurrence probabilities for each species at each new location.

**Usage**

```
## S3 method for class 'bayescomm'
predict(object, newdata, ...)
```

**Arguments**

object A bayescomm object  
 newdata A data.frame with the same columns as X from the original BC model  
 ... Further arguments passed to or from other methods.

**Value**

An array of occurrence probabilities. Rows index locations. Columns index species. Slices index MCMC samples.

**Author(s)**

David J. Harris (<http://davharris.github.io>)



### Examples

```
# load model from first example
m1 <- example(BC)[[1]]

# use the first five sites of the training data as newdata
newdata <- X[1:5, -1]

# get predictions
prob <- predict(m1, newdata)
```

---

<code>print.bayescomm</code>	<i>Print a bayescomm object</i>
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### Description

`print.bayescomm` prints a brief summary of a bayescomm object.

### Usage

```
## S3 method for class 'bayescomm'
print(x, ...)
```

### Arguments

<code>x</code>	a bayescomm object
<code>...</code>	further arguments to pass to print

### See Also

[BC](#)

### Examples

```
m1 <- example(BC)[[1]]
print(m1)
m1
```

residuals.bayescomm *Extract bayescomm model residuals*

---

### Description

residuals.bayescomm extracts model residuals from a bayescomm object. Residuals are calculated based on the mean of the posterior probability of presence.

### Usage

```
## S3 method for class 'bayescomm'  
residuals(object, ...)
```

### Arguments

object	a bayescomm object
...	other arguments

### See Also

[BC](#)

### Examples

```
m1 <- example(BC)[[1]]  
m1.res <- residuals(m1)
```

---

summary.bayescomm *Summarise bayescomm parameter chains*

---

### Description

summary.bayescomm creates summaries of a subset of the parameter chains in a bayescomm object using the coda package.

### Usage

```
## S3 method for class 'bayescomm'  
summary(object, chain, ...)
```

### Arguments

object	a bayescomm object
chain	a character string of the parameter chains to plot
...	further arguments to pass to summary.mcmc

**Details**

chain should be one of 'R' (for correlation coefficients) or 'B\$sp' where sp is the species of interest (for regression coefficients).

**See Also**

[BC](#), [summary.mcmc](#)

**Examples**

```
m1 <- example(BC)[[1]]
summary(m1, 'R')
summary(m1, 'B$sp1')
```

---

window.bayescomm	<i>Window bayescomm objects</i>
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**Description**

window.bayescomm is window function for bayescomm objects, it calls window.mcmc from the coda package. Parameter chains are subsetted by start and end and thinned by thin.

**Usage**

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

**Arguments**

x	a bayescomm object
start	start iteration
end	end iteration
thin	thinning interval
...	further arguments to pass to window.mcmc

**Details**

If start = NULL (default) the start is taken as the first iteration. If end = NULL (default) the end is taken as the final iteration. If thin = 1 (default) all iterations within the window are retained.

**Value**

A bayescomm object with windowed parameter chains.

**See Also**

[BC](#), [window.mcmc](#)

**Examples**

```
m1 <- example(BC)[[1]]  
m2 <- window(m1, 51, 150, 10)
```

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