

# Package ‘RCM’

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**Type** Package

**Title** Fit row-column association models with the negative binomial distribution for the microbiome

**Version** 1.23.0

**Description** Combine ideas of log-linear analysis of contingency table, flexible response function estimation and empirical Bayes dispersion estimation for explorative visualization of microbiome datasets. The package includes unconstrained as well as constrained analysis. In addition, diagnostic plot to detect lack of fit are available.

**License** GPL-2

**Encoding** UTF-8

**LazyData** true

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**Imports** RColorBrewer, alabama, edgeR, reshape2, tseries, stats, VGAM, ggplot2 (>= 2.2.1.9000), nleqslv, phyloseq, tensor, MASS, grDevices, graphics, methods

**Depends** R (>= 4.0), DBI

**Suggests** knitr, rmarkdown, testthat

**VignetteBuilder** knitr

**biocViews** Metagenomics, DimensionReduction, Microbiome, Visualization

**BugReports** <https://github.com/CenterForStatistics-UGent/RCM/issues>

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---

addOrthProjection	<i>This function adds orthogonal projections to a given plot</i>
-------------------	--

---

## Description

This function adds orthogonal projections to a given plot

## Usage

```
addOrthProjection(
  RCMplot,
  sample = NULL,
  species = NULL,
  variable = NULL,
  Dims = c(1, 2),
  addLabel = FALSE,
  labPos = NULL
)
```

**Arguments**

RCMplot            the RCMplot object  
 sample, species, variable            names or approximate coordinates of sample, species or variable  
 Dims                The dimensions of the solutions that have been plotted  
 addLabel           a boolean, should the r-s-psi label be added?  
 labPos              the position of the label. Will be calculated if not provided

**Value**

a modified ggplot object that contains the geom\_segment object that draws the projection

**See Also**

[plot.RCM](#)

**Examples**

```
data(Zeller)
require(phyloseq)
tmpPhy = prune_taxa(taxa_names(Zeller)[seq_len(100)],
prune_samples(sample_names(Zeller)[seq_len(50)], Zeller))
zellerRCM = RCM(tmpPhy, k = 2, round = TRUE)
zellerPlot = plot(zellerRCM, returnCoords = TRUE)
addOrthProjection(zellerPlot, species = c(-0.35,1.1), sample = c(1,1.2))
```

---

arrayprod	<i>An auxiliary R function to 'array' multiply an array with a vector, kindly provided by Joris Meys</i>
-----------	--

---

**Description**

An auxiliary R function to 'array' multiply an array with a vector, kindly provided by Joris Meys

**Usage**

```
arrayprod(x, y)
```

**Arguments**

x                    a axbxc array  
 y                    a vector of length c

**Value**

a axb matrix. The ij-th element equals  $\text{sum}(x[i,j,]*y)$

---

buildCentMat	<i>A function to build a centering matrix based on a dataframe</i>
--------------	--

---

**Description**

A function to build a centering matrix based on a dataframe

**Usage**

```
buildCentMat(object)
```

**Arguments**

object	an rcm object or dataframe
--------	----------------------------

**Value**

a centering matrix consisting of ones and zeroes, or a list with components

centMat	a centering matrix consisting of ones and zeroes
datFrame	The dataframe with factors with one level removed

---

buildConfMat	<i>A function to build the confounder matrices</i>
--------------	--

---

**Description**

A function to build the confounder matrices

**Usage**

```
buildConfMat(x, ...)
```

**Arguments**

x	a matrix, data frame or character string
...	further arguments passed on to other methods

For the preliminary trimming, we do not include an intercept, but we do include all the levels of the factors using contrasts=FALSE: we want to do the trimming in every subgroup, so no hidden reference levels For the filtering we just use a model with an intercept and treatment coding, here the interest is only in adjusting the offset

**Value**

a list with components

confModelMatTrim

A confounder matrix without intercept, with all levels of factors present. This will be used to trim out taxa that have zero abundances in any subgroup defined by confounders

confModelMat

A confounder matrix with intercept, and with reference levels for factors absent. This will be used to fit the model to modify the independence model, and may include continuous variables

---

buildConfMat.character

*buildConfMat.character*

---

**Description**

buildConfMat.character

**Usage**

```
## S3 method for class 'character'
buildConfMat(confounders, physeq)
```

**Arguments**

confounders      a numeric matrix of confounders

physeq            a physeq object with a sample\_data slot

**Value**

see buildConfMat.numeric

---

buildConfMat.data.frame

*buildConfMat.data.frame*

---

**Description**

buildConfMat.data.frame

**Usage**

```
## S3 method for class 'data.frame'
buildConfMat(confounders, n)
```

**Arguments**

confounders      a data frame of confounders  
 n                    the number of rows of the count matrix

**Value**

see buildConfMat

---

buildCovMat                    *A function to build the covariate matrix of the constraints*

---

**Description**

A function to build the covariate matrix of the constraints

**Usage**

```
buildCovMat(covariates, dat)
```

**Arguments**

covariates      the covariates, either as dataframe or as character string  
 dat              the phyloseq object  
 In this case we will 1) Include dummy's for every level of the categorical variable, and force them to sum to zero. This is needed for plotting and required for reference level independent normalization. 2) Exclude an intercept. The density function f() will provide this already.

**Value**

a list with components

covModelMat      The model matrix  
 datFrame         The dataframe used to construct the model matrix

---

buildDesign	<i>A function to build the design matrix</i>
-------------	--

---

**Description**

A function to build the design matrix

**Usage**

```
buildDesign(sampleScore, responseFun)
```

**Arguments**

sampleScore	a vector of environmental scores
responseFun	A character string, indicating the shape of the response function For dynamic response function estimation, the same desing matrix as for the quadratic one is returned. Will throw an error when an unknown reponse function is provided

**Value**

A design matrix of dimension n-by-f

---

checkAlias	<i>Check for alias structures in a dataframe, and throw an error when one is found</i>
------------	--

---

**Description**

Check for alias structures in a dataframe, and throw an error when one is found

**Usage**

```
checkAlias(datFrame, covariatesNames)
```

**Arguments**

datFrame	the data frame to be checked for alias structure
covariatesNames	The names of the variables to be considered

**Value**

Throws an error when an alias structure is detected, returns invisible otherwise



## Examples

```
#Make a dataframe with aliased variables
df = data.frame(foo = rnorm(10), baa = rep(c(TRUE, FALSE), each = 5),
foo2 = factor(rep(c("male", "female"), each = 5)))
checkAlias(df, c("foo", "baa"))
#Check test files for the error being thrown
```

---

constrCorresp

*Constrained correspondence analysis with adapted powers*

---

## Description

Constrained correspondence analysis with adapted powers

## Usage

```
constrCorresp(
  X,
  Y,
  rowExp,
  colExp,
  muMarg = outer(rowSums(X), colSums(X))/sum(X)
)
```

## Arguments

X	outcome matrix
Y	constraining matrix
rowExp, colExp	see ?RCM_NB
muMarg	mean matrix under independence model

## Details

the vegan version, adapted for flexible powers rowExp and colExp

## Value

a list with eigenvalues, aliased variables and environmentam gradients

---

`correctXMissingness`     *Replace missing entries in X by their expectation to set their contribution to the estimating equations to zero*

---

### Description

Replace missing entries in X by their expectation to set their contribution to the estimating equations to zero

### Usage

```
correctXMissingness(X, mu, allowMissingness, naId)
```

### Arguments

<code>X</code>	the matrix of counts
<code>mu</code>	the matrix of expectations
<code>allowMissingness</code>	A boolean, are missing values present
<code>naId</code>	The numeric index of the missing values in X

### Value

The matrix X with the NA entries replaced by the corresponding entries in mu

### Note

This may seem like a hacky approach, but it avoids having to deal with NAs in functions like `crossprod()`.

---

`deviances`     *A function to extract deviances for all dimension, including after filtering on confounders*

---

### Description

A function to extract deviances for all dimension, including after filtering on confounders

### Usage

```
deviances(rcm, squaredSum = FALSE)
```

**Arguments**

rcm	an object of the RCM class
squaredSum	a boolean, should total deviance be returned? Total deviances can be deceptive and not correspond to the differences in log-likelihood. As the dispersion is different for each model. To compare models it is better to compare likelihoods.

**Value**

If Sum is FALSE, a named array of deviance residuals of the independence model and all models with dimension 1 to k, including after filtering on confounders. Otherwise a table with total deviances (the sum of squared deviance residuals), deviance explained and cumulative deviance explained.

---

dLR_nb	<i>A function that returns the value of the partial derivative of the log-likelihood ratio to alpha, keeping the response functions fixed</i>
--------	---

---

**Description**

A function that returns the value of the partial derivative of the log-likelihood ratio to alpha, keeping the response functions fixed

**Usage**

```
dLR_nb(
  Alpha,
  X,
  CC,
  responseFun = c("linear", "quadratic", "nonparametric", "dynamic"),
  psi,
  NB_params,
  NB_params_noLab,
  d,
  alphaK,
  k,
  centMat,
  nLambda,
  nLambda1s,
  thetaMat,
  muMarg,
  ncols,
  envGradEst,
  allowMissingness,
  naId,
  ...
)
```

**Arguments**

Alpha	a vector of length $d + k*(2+(k-1)/2)$ , the environmental gradient plus the lagrangian multipliers
X	the n-by-p count matrix
CC	a n-by-d covariate vector
responseFun	a character string indicating the type of response function
psi	a scalar, an importance parameter
NB_params	Starting values for the NB_params
NB_params_noLab	Starting values for the NB_params without label
d	an integer, the number of covariate parameters
alphaK	a matrix of environmental gradients of lower dimensions
k	an integer, the current dimension
centMat	a nLambdas-by-d centering matrix
nLambdas	an integer, number of lagrangian multipliers
nLambdas	an integer, number of centering restrictions
thetaMat	a matrix of size n-by-p with estimated dispersion parameters
muMarg	an n-by-p offset matrix
ncols	a scalar, the number of columns of X
envGradEst	a character string, indicating how the environmental gradient should be fitted. 'LR' using the likelihood-ratio criterion, or 'ML' a full maximum likelihood solution
allowMissingness	A boolean, are missing values present
naId	The numeric index of the missing values in X
...	further arguments passed on to other methods

**Value**

: The value of the lagrangian and the constraining equations

---

dNBabundsOld *A score function for the column components of the independence model (mean relative abundances)*

---

**Description**

A score function for the column components of the independence model (mean relative abundances)

**Usage**

dNBabundsOld(beta, X, reg, thetas, allowMissingness, naId)

**Arguments**

beta	a vector of length p with current abundance estimates
X	a n-by-p count matrix
reg	a vector of length n with library sizes estimates
thetas	a n-by-p matrix with overdispersion estimates in the rows
allowMissingness	A boolean, are missing values present
naId	The numeric index of the missing values in X

**Value**

a vector of length p with evaluations of the score function

---

dNLibSizes	<i>A score function for the row components of the independence model (library sizes)</i>
------------	--

---

**Description**

A score function for the row components of the independence model (library sizes)

**Usage**

```
dNLibSizes(beta, X, reg, thetas, allowMissingness, naId)
```

**Arguments**

beta	a vector of length n with current library size estimates
X	a n-by-p count matrix
reg	a vector of length p with relative abundance estimates
thetas	a n-by-p matrix with overdispersion estimates in the rows
allowMissingness	A boolean, are missing values present
naId	The numeric index of the missing values in X

**Value**

a vector of length n with evaluations of the score function

---

dNBllcolNP	<i>Estimation of the parameters of a third degree GLM</i>
------------	---

---

**Description**

Estimation of the parameters of a third degree GLM

**Usage**

```
dNBllcolNP(beta, X, reg, theta, muMarg, allowMissingness, naId, ...)
```

**Arguments**

beta	A vector of any length
X	the data vector of length n
reg	a n $\times$ length(beta) regressor matrix
theta	a scalar, the overdispersion
muMarg	the offset of length n
allowMissingness	A boolean, are missing values present
naId	The numeric index of the missing values in X
...	further arguments passed on to the jacobian

**Value**

A vector of the same length as beta with evaluations of the score function

---

dNBllcolOld	<i>A score function for the estimation of the column scores in an unconstrained RC(M) model</i>
-------------	---

---

**Description**

A score function for the estimation of the column scores in an unconstrained RC(M) model

**Usage**

```
dNBllcolOld(
  beta,
  X,
  reg,
  thetas,
  muMarg,
  k,
  p,
  n,
  colWeights,
  nLambda,
  cMatK,
  allowMissingness,
  naId,
  ...
)
```

**Arguments**

beta	vector of length $p+1+1+(k-1)$ : p row scores, 1 centering, one normalization and (k-1) orthogonality lagrangian multipliers
X	the nxp data matrix
reg	a nx1 regressor matrix: outer product of rowScores and psis
thetas	nxp matrix with the dispersion parameters (converted to matrix for numeric reasons)
muMarg	the nxp offset
k	an integer, the dimension of the RC solution
p	an integer, the number of taxa
n	an integer, the number of samples
colWeights	the weights used for the restrictions
nLambda	an integer, the number of restrictions
cMatK	the lower dimensions of the colScores
allowMissingness	A boolean, are missing values present
naId	The numeric index of the missing values in X
...	further arguments passed on to the jacobian

**Value**

A vector of length  $p+1+1+(k-1)$  with evaluations of the derivative of lagrangian

---

dNBllcol\_constr      *The score function of the response function for 1 taxon at the time*

---

### Description

The score function of the response function for 1 taxon at the time

### Usage

```
dNBllcol_constr(betas, X, reg, theta, muMarg, psi, allowMissingness, naId)
```

### Arguments

betas	a vector of $v$ parameters of the response function of a single taxon
X	the count vector of length $n$
reg	a $n$ -by- $v$ matrix of regressors
theta	The dispersion parameter of this taxon
muMarg	offset of length $n$
psi	a scalar, the importance parameter
allowMissingness	A boolean, are missing values present
naId	The numeric index of the missing values in X

Even though this approach does not imply normalization over the parameters of all taxa, it is very fast and they can be normalized afterwards

### Value

A vector of length  $v$  with the evaluation of the score functions

---

dNBllcol\_constr\_noLab      *The score function of the general response function*

---

### Description

The score function of the general response function



**Usage**

```
dNBllcol_constr_noLab(
  betas,
  X,
  reg,
  thetasMat,
  muMarg,
  psi,
  allowMissingness,
  naId,
  ...
)
```

**Arguments**

betas	a vector of regression parameters with length $v$
X	the $n \times p$ data matrix
reg	a matrix of regressors of dimension $n \times v$
thetasMat	A matrix of dispersion parameters
muMarg	offset matrix of dimension $n \times p$
psi	a scalar, the importance parameter
allowMissingness	A boolean, are missing values present
naId	The numeric index of the missing values in X
...	further arguments passed on to the jacobian

**Value**

The evaluation of the score functions (a vector length  $v$ )

---

dNBllrow	<i>A score function of the NB for the row scores</i>
----------	--

---

**Description**

A score function of the NB for the row scores

**Usage**

```
dNBllrow(
  beta,
  X,
  reg,
  thetas,
```

```

    muMarg,
    k,
    n,
    p,
    rowWeights,
    nLambda,
    rMatK,
    allowMissingness,
    naId,
    ...
)

```

### Arguments

beta	a vector of of length $n + k + 1$ regression parameters to optimize
X	the data matrix of dimensions $n \times p$
reg	a $1 \times p$ regressor matrix: outer product of column scores and psis
thetas	$n \times p$ matrix with the dispersion parameters (converted to matrix for numeric reasons)
muMarg	an $n \times p$ offset matrix
k	a scalar, the dimension of the RC solution
n	a scalar, the number of samples
p	a scalar, the number of taxa
rowWeights	a vector of length $n$ , the weights used for the restrictions
nLambda	an integer, the number of lagrangian multipliers
rMatK	the lower dimension row scores
allowMissingness	A boolean, are missing values present
naId	The numeric index of the missing values in X
...	Other arguments passed on to the jacobian

### Value

A vector of length  $n + k + 1$  with evaluations of the derivative of the lagrangian

---

dNBpsis

*A score function for the psi of a given dimension*

---

### Description

A score function for the psi of a given dimension

### Usage

```
dNBpsis(beta, X, reg, theta, muMarg, allowMissingness, naId, ...)
```

**Arguments**

beta	a scalar, the initial estimate
X	the n-by-p count matrix
reg	the regressor matrix, the outer product of current row and column scores
theta	a n-by-p matrix with the dispersion parameters
muMarg	the nxp offset matrix
allowMissingness	A boolean, are missing values present
naId	The numeric index of the missing values in X
...	other arguments passed on to the jacobian

**Value**

The evaluation of the score function at beta, a scalar

---

ellipseCoord      *A function that returns the coordinates of an ellipse*

---

**Description**

A function that returns the coordinates of an ellipse

**Usage**

```
ellipseCoord(a, b, c, quadDrop = 0.95, nPoints = 100)
```

**Arguments**

a, b, c	parameters of the quadratic function $a^2x+bx+c$
quadDrop	A scalar, fraction of peak height at which to draw the ellipse
nPoints	an integer, number of points to use to draw the ellipse

**Value**

a matrix with x and y coordinates of the ellipse

---

 estDisp

*Estimate the overdispersion*


---

**Description**

Estimate the overdispersion

**Usage**

```
estDisp(
  X,
  cMat = NULL,
  rMat = NULL,
  muMarg,
  psis,
  trended.dispersion = NULL,
  prior.df = 10,
  dispWeights = NULL,
  rowMat = NULL,
  allowMissingness = FALSE,
  naId
)
```

**Arguments**

X	the data matrix of dimensions n x p
cMat	a 1 x p column scores matrix
rMat	a n x 1 rowscores matrix, if unconstrained
muMarg	an n x p offset matrix
psis	a scalar, the current psi estimate
trended.dispersion	a vector of length p with pre-calculated trended.dispersion estimates. They do not vary in function of the offset anyway
prior.df	an integer, number of degrees of freedom of the prior for the Bayesian shrinkage
dispWeights	Weights for estimating the dispersion in a zero-inflated model
rowMat	matrix of row scores in case of constrained ordination
allowMissingness	A boolean, are missing values present
naId	The numeric index of the missing values in X

**Details**

Information between taxa is shared with empirical Bayes using the edgeR package, where the time-limiting steps are programmed in C.

**Value**

A vector of length p with dispersion estimates

---

 estNBparams

*A function to estimate the taxon-wise NB-params*


---

**Description**

A function to estimate the taxon-wise NB-params

**Usage**

```
estNBparams(
  design,
  thetas,
  muMarg,
  psi,
  X,
  nleqslv.control,
  ncols,
  initParam,
  v,
  dynamic = FALSE,
  envRange,
  allowMissingness,
  naId
)
```

**Arguments**

design	an n-by-v design matrix
thetas	a vector of dispersion parameters of length p
muMarg	an offset matrix
psi	a scalar, the importance parameter
X	the data matrix
nleqslv.control	a list of control elements, passed on to nleqslv()
ncols	an integer, the number of columns of X
initParam	a v-by-p matrix of initial parameter estimates
v	an integer, the number of parameters per taxon
dynamic	a boolean, should response function be determined dynamically? See details
envRange	a vector of length 2, giving the range of observed environmental scores
allowMissingness	A boolean, are missing values present

naId            The numeric index of the missing values in  $X$   
 If dynamic is TRUE, quadratic response functions are fitted for every taxon. If the optimum falls outside of the observed range of environmental scores, a linear response function is fitted instead

### Value

a v-by-p matrix of parameters of the response function

---

estNBparamsNoLab            *A function to estimate the NB-params ignoring the taxon labels*

---

### Description

A function to estimate the NB-params ignoring the taxon labels

### Usage

```
estNBparamsNoLab(
  design,
  thetasMat,
  muMarg,
  psi,
  X,
  nleqslv.control,
  initParam,
  n,
  v,
  dynamic,
  envRange,
  preFabMat,
  allowMissingness,
  naId
)
```

### Arguments

design            an n-by-v design matrix  
 thetasMat        A matrix of dispersion parameters  
 muMarg           an offset matrix  
 psi              a scalar, the importance parameter  
 X                the data matrix  
 nleqslv.control    a list of control elements, passed on to nleqslv()  
 initParam        a vector of length v of initial parameter estimates

n	an integer, the number of samples
v	an integer, the number of parameters per taxon
dynamic	a boolean, should response function be determined dynamically? See details
envRange	a vector of length 2, giving the range of observed environmental scores
preFabMat	a pre-fabricated auxiliary matrix
allowMissingness	A boolean, are missing values present
naId	The numeric index of the missing values in X If dynamic is TRUE, quadratic response functions are fitted for every taxon. If the optimum falls outside of the observed range of environmental scores, a linear response function is fitted instead

**Value**

a v-by-p matrix of parameters of the response function

---

 estNPresp

---

*Estimate the taxon-wise response functions non-parametrically*


---

**Description**

Estimate the taxon-wise response functions non-parametrically

**Usage**

```
estNPresp(
  sampleScore,
  muMarg,
  X,
  ncols,
  thetas,
  n,
  coefInit,
  coefInitOverall,
  dfSpline,
  vgamMaxit,
  degree,
  verbose,
  allowMissingness,
  naId,
  ...
)
```

**Arguments**

sampleScore	a vector of length n with environmental scores
muMarg	the offset matrix
X	the n-by-p data matrix
ncols	an integer, the number of columns of X
thetas	a vector of length p with dispersion parameters
n	an integer, the number of samples
coefInit	a 2-by-p matrix with current taxon-wise parameter estimates
coefInitOverall	a vector of length 2 with current overall parameters
dfSpline	a scalar, the degrees of freedom for the smoothing spline.
vgamMaxit	Maximal number of iterations in the fitting of the GAM model
degree	The degree if the parametric fit if the VGAM fit fails
verbose	a boolean, should number of failed fits be reported
allowMissingness	A boolean, are missing values present
naId	The numeric index of the missing values in X
...	further arguments, passed on to the VGAM:::vgam() function

The negative binomial likelihood is still maximized, but now the response function is a non-parametric one. To avoid a perfect fit and overly flexible functions, we enforce smoothness restrictions. In practice we use a generalized additive model (GAM), i.e. with splines. The same fitting procedure is carried out ignoring species labels. We do not normalize the parameters related to the splines: the psis can be calculated afterwards.

**Value**

A list with components

taxonCoef	The fitted coefficients of the sample-wise response curves
splinesList	A list of all the B-spline objects
rowMar	The row matrix
overall	The overall fit ignoring taxon labels, as a list of coefficients and a spline
rowVecOverall	The overall row vector, ignoring taxon labels



---

extractCoord	<i>A function to extract plotting coordinates, either for plot.RCM or to export to other plotting software</i>
--------------	--

---

### Description

A function to extract plotting coordinates, either for plot.RCM or to export to other plotting software

### Usage

```
extractCoord(RCM, Dim = c(1, 2))
```

### Arguments

RCM	an RCM object
Dim	an integer vector of required dimensions

The parameters for the ellipses of the quadratic response function come from the parametrization  $f(x) = a \cdot x^2 + b \cdot x + c$ . For an unconstrained object the row and column coordinates are returned in separate matrices. The row names will correspond to the labels. For a constrained analysis also the variable points are returned. All variables still need to be scaled to optimally fill the available space

### Value

A list with components

samples	A dataframe of sample scores
species	A dataframe of column scores, with origin, slope, end and ellipse coordinates as needed
variables	A dataframe of variable scores, loadings of the environmental gradient

### Examples

```
data(Zeller)
require(phyloseq)
tmpPhy = prune_taxa(taxa_names(Zeller)[1:100],
prune_samples(sample_names(Zeller)[1:50], Zeller))
zellerRCM = RCM(tmpPhy, k = 2, round = TRUE)
coordsZeller = extractCoord(zellerRCM)
```

---

extractE	<i>A function to extract a matrix of expected values for any dimension of the fit</i>
----------	---

---

**Description**

A function to extract a matrix of expected values for any dimension of the fit

**Usage**

```
extractE(rcm, Dim = rcm$k)
```

**Arguments**

rcm	an object of class RCM
Dim	the desired dimension. Defaults to the maximum of the fit. Choose 0 for the independence model, 0.5 for the confounders filter model.

**Value**

The matrix of expected values

---

filterConfounders	<i>Filters out the effect of known confounders. This is done by fitting interactions of every taxon with the levels of the confounders. It returns a modified offset matrix for the remainder of the fitting procedure.</i>
-------------------	---

---

**Description**

Filters out the effect of known confounders. This is done by fitting interactions of every taxon with the levels of the confounders. It returns a modified offset matrix for the remainder of the fitting procedure.

**Usage**

```
filterConfounders(
  muMarg,
  confMat,
  X,
  thetas,
  p,
  n,
  nleqslv.control,
  trended.dispersion,
  tol = 0.001,
```

```

    maxIt = 20,
    allowMissingness,
    naId
  )

```

### Arguments

muMarg	a nxp matrix, the current offset
confMat	a nxt confounder matrix
X	the nxp data matrix
thetas	a vector of length p with the current dispersion estimates
p	an integer, the number of columns of X
n	an integer, the number of rows of X
nleqslv.control	see nleqslv()
trended.dispersion	a vector of length p with trended dispersion estimates
tol	a scalar, the convergence tolerance
maxIt	maximum number of iterations
allowMissingness	A boolean, are missing values present
naId	The numeric index of the missing values in X Fits the negative binomial mean parameters and overdispersion parameters iteratively. Convergence is determined based on the L2-norm of the absolute change of mean parameters

### Value

a list with components:

thetas	new theta estimates
NB_params	The estimated parameters of the interaction terms

---

getDevianceRes	<i>A function to calculate the matrix of deviance residuals.</i>
----------------	--

---

### Description

A function to calculate the matrix of deviance residuals.

### Usage

```
getDevianceRes(RCM, Dim = RCM$k)
```

**Arguments**

RCM	an RCM object
Dim	The dimensions to use For the deviance residuals we use the overdispersions from the reduced model. Standard dimensions used are only first and second, since these are also plotted

**Value**

A matrix with deviance residuals of the same size as the original data matrix

**Examples**

```
data(Zeller)
require(phyloseq)
tmpPhy = prune_taxa(taxa_names(Zeller)[1:120],
prune_samples(sample_names(Zeller)[1:75], Zeller))
#Subset for a quick fit
zellerRCM = RCM(tmpPhy, k = 2, round = TRUE, prevCutOff = 0.03)
devRes = getDevianceRes(zellerRCM)
```

---

getDevMat

*ACalculate the matrix of deviance residuals*


---

**Description**

ACalculate the matrix of deviance residuals

**Usage**

```
getDevMat(X, thetaMat, mu)
```

**Arguments**

X	the data matrix
thetaMat	the matrix of dispersions
mu	the matrix of means

**Value**

The matrix of deviance residuals

---

getInflCol	<i>A function to extract the influence for a given parameter index</i>
------------	--

---

**Description**

A function to extract the influence for a given parameter index

**Usage**

```
getInflCol(score, InvJac, taxon)
```

**Arguments**

score	a score matrix
InvJac	The inverted jacobian
taxon	The taxon name or index

**Value**

A matrix with all observations' influence on the given taxon

---

getInflRow	<i>Extract the influence of all observations on a given row score</i>
------------	---

---

**Description**

Extract the influence of all observations on a given row score

**Usage**

```
getInflRow(score, InvJac, sample)
```

**Arguments**

score	the score function evaluated for every observation
InvJac	The inverse jacobian
sample	the row score or sample index

**Value**

A matrix with all observations' influence on the row score

---

getInt *Integrate the spline of an vgam object*

---

**Description**

Integrate the spline of an vgam object

**Usage**

```
getInt(coef, spline, sampleScore, stop.on.error = FALSE, ...)
```

**Arguments**

coef	A vector of coefficients
spline	The cubic smoothing spline
sampleScore	the observed environmental scores
stop.on.error	see ?integrate
...	additional arguments passed on to integrate()

**Value**

a scalar, the value of the integral

---

getLogLik *Extract the logged likelihood of every count*

---

**Description**

Extract the logged likelihood of every count

**Usage**

```
getLogLik(rcm, Dim)
```

**Arguments**

rcm	an RCM object
Dim	A vector of integers indicating which dimensions to take along, or Inf for the saturated model, or 0 for the independence model

**Value**

A matrix with logged likelihood of the size of the data matrix

---

getModelMat	<i>A function to construct a model matrix of a certain degree</i>
-------------	---

---

**Description**

A function to construct a model matrix of a certain degree

**Usage**

```
getModelMat(y, degree)
```

**Arguments**

y	the variable
degree	the degree

**Value**

A model matrix with degree+1 columns and as many rows as length(y)

---

getRowMat	<i>Return a matrix of row scores</i>
-----------	--------------------------------------

---

**Description**

Return a matrix of row scores

**Usage**

```
getRowMat(sampleScore, responseFun, NB_params, taxonCoef, spline)
```

**Arguments**

sampleScore	a vector of length n with sample scores
responseFun	a character string, the type of response function, either 'linear' or 'quadratic'
NB_params	a v-by-p matrix of parameters of the response function
taxonCoef	A vector of coefficients
spline	The cubic smoothing spline

Multiplying the old offset with the exponent matrix times the importance parameter obtains the new one based on lower dimension

**Value**

a n-by-p matrix of scores

---

GramSchmidt	<i>Gram-Schmidt orthogonalization of vectors</i>
-------------	--

---

**Description**

Gram-Schmidt orthogonalization of vectors

**Usage**

```
GramSchmidt(x, otherVecs, weights = rep(1, length(x)))
```

**Arguments**

x	The vector that is to be orthogonalized
otherVecs	a matrix; x is orthogonalized with respect to its rows
weights	The weights used in the orthogonalization

**Value**

The orthogonalized vector

---

heq_nb	<i>Define linear equality constraints for env. gradient</i>
--------	---

---

**Description**

Define linear equality constraints for env. gradient

**Usage**

```
heq_nb(Alpha, alphaK, d, k, centMat, ...)
```

**Arguments**

Alpha	the current estimate of the environmental gradient
alphaK	a matrix with the environmental gradients of the lower dimensions
d	an integer, the number of environmental variables, including dummies
k	an integer, the current dimension
centMat	a centering matrix
...	further arguments for other methods, not needed in this one

The centering matrix centMat ensures that the parameters of the dummies of the same categorical variable sum to zero

**Value**

a vector of with current values of the constraints, should evolve to zeroes only



---

heq_nb_jac	<i>The jacobian of the linear equality constraints</i>
------------	--

---

**Description**

The jacobian of the linear equality constraints

**Usage**

```
heq_nb_jac(Alpha, alphaK, d, k, centMat, ...)
```

**Arguments**

Alpha	the current estimate of the environmental gradient
alphaK	a matrix with the environmental gradients of the lower dimensions
d	an integer, the number of environmental variables, including dummies
k	an integer, the current dimension
centMat	a centering matrix
...	further arguments for other methods, not needed in this one

**Value**

The jacobian matrix

---

indentPlot	<i>Functions to indent the plot to include the entire labels</i>
------------	--

---

**Description**

Functions to indent the plot to include the entire labels

**Usage**

```
indentPlot(plt, xInd = 0, yInd = 0)
```

**Arguments**

plt	a ggplot object
xInd	a scalar or a vector of length 2, specifying the indentation left and right of the plot to allow for the labels to be printed entirely
yInd	a scalar or a vector of length 2, specifying the indentation top and bottom of the plot to allow for the labels to be printed entirely

**Value**

a ggplot object, squared

---

inertia	<i>Calculate the log-likelihoods of all possible models</i>
---------	---

---

**Description**

Calculate the log-likelihoods of all possible models

**Usage**

```
inertia(rcm)
```

**Arguments**

rcm                    an object of the RCM class

**Value**

A table with inertias, proportion inertia explained and cumulative proportion of inertia explained.

**Examples**

```
data(Zeller)
require(phyloseq)
tmpPhy = prune_taxa(taxa_names(Zeller)[1:100],
prune_samples(sample_names(Zeller)[1:50], Zeller))
zellerRCM = RCM(tmpPhy, round = TRUE)
inertia(zellerRCM)
```

---

JacCol_constr	<i>Jacobian of the constrained analysis with linear response function.</i>
---------------	--

---

**Description**

Jacobian of the constrained analysis with linear response function.

**Usage**

```
JacCol_constr(betas, X, reg, theta, muMarg, psi, allowMissingness, naId)
```

**Arguments**

betas	a vector of $v$ parameters of the response function of a single taxon
X	the count vector of length $n$
reg	a $n$ -by- $v$ matrix of regressors
theta	The dispersion parameter of this taxon
muMarg	offset of length $n$
psi	a scalar, the importance parameter
allowMissingness	A boolean, are missing values present
naId	The numeric index of the missing values in X Even though this approach does not imply normalization over the parameters of all taxa, it is very fast and they can be normalized afterwards

**Value**

The jacobian, a square symmetric matrix of dimension  $v$

---

JacCol\_constr\_noLab     *The jacobian of the response function without taxon labels*

---

**Description**

The jacobian of the response function without taxon labels

**Usage**

```
JacCol_constr_noLab(
  betas,
  X,
  reg,
  thetasMat,
  muMarg,
  psi,
  n,
  v,
  preFabMat,
  allowMissingness,
  naId
)
```

**Arguments**

betas	a vector of regression parameters with length v
X	the nxp data matrix
reg	a matrix of regressors of dimension nxv
thetasMat	A matrix of dispersion parameters
muMarg	offset matrix of dimension nxp
psi	a scalar, the importance parameter
n	an integer, number of rows of X
v	an integer, the number of parameters of the response function
preFabMat	a prefabricated matrix
allowMissingness	A boolean, are missing values present
naId	The numeric index of the missing values in X

**Value**

The jacobian (a v-by-v matrix)

---

likes	<i>Calculate the log-likelihoods of all possible models</i>
-------	---

---

**Description**

Calculate the log-likelihoods of all possible models

**Usage**

```
likes(rcm, Sum = TRUE)
```

**Arguments**

rcm	an object of the RCM class
Sum	a boolean, should log-likelihoods be summed?

**Value**

If Sum is FALSE, a named array log-likelihoods of the independence model and all models with dimension 1 to k, including after filtering on confounders. Otherwise a table with log-likelihoods, deviance explained and cumulative deviance explained.

**Examples**

```

data(Zeller)
require(phyloseq)
tmpPhy = prune_taxa(taxa_names(Zeller)[1:100],
prune_samples(sample_names(Zeller)[1:50], Zeller))
zellerRCM = RCM(tmpPhy, round = TRUE)
liks(zellerRCM)

```

---

LR\_nb

*Get the value of the log-likelihood ratio of alpha*


---

**Description**

Get the value of the log-likelihood ratio of alpha

**Usage**

```

LR_nb(
  Alpha,
  X,
  CC,
  responseFun = c("linear", "quadratic", "nonparametric", "dynamic"),
  muMarg,
  psi,
  nleqslv.control = list(trace = FALSE),
  n,
  NB_params,
  NB_params_noLab,
  thetaMat,
  ncols,
  nonParamRespFun,
  envGradEst,
  ...
)

```

**Arguments**

Alpha	a vector of length d, the environmental gradient
X	the n-by-p count matrix
CC	the n-by-d covariate matrix
responseFun	a character string indicating the type of response function
muMarg	an n-by-p offset matrix
psi	a scalar, an importance parameter
nleqslv.control	the control list for the nleqslv() function

n	number of samples
NB_params	Starting values for the NB_params
NB_params_noLab	Starting values for the NB_params without label
thetaMat	a matrix of size n-by-p with estimated dispersion parameters
ncols	a scalar, the number of columns of X
nonParamRespFun	A list, the result of the estNPresp() function
envGradEst	a character string, indicating how the environmental gradient should be fitted. 'LR' using the likelihood-ratio criterion, or 'ML' a full maximum likelihood solution
...	Further arguments passed on to other functions DON'T USE 'p' as variable name, partial matching in the grad-function in the numDeriv package

**Value**

: a scalar, the evaluation of the log-likelihood ratio at the given alpha

---

LR\_nb\_Jac

*A function that returns the Jacobian of the likelihood ratio*


---

**Description**

A function that returns the Jacobian of the likelihood ratio

**Usage**

```
LR_nb_Jac(
  Alpha,
  X,
  CC,
  responseFun = c("linear", "quadratic", "nonparametric", "dynamic"),
  psi,
  NB_params,
  NB_params_noLab,
  d,
  alphaK,
  k,
  centMat,
  nLambda,
  nLambda1s,
  thetaMat,
  muMarg,
  n,
```

```

ncols,
preFabMat,
envGradEst,
allowMissingness,
naId,
...
)

```

### Arguments

Alpha	a vector of length $d + k*(2+(k-1)/2)$ , the environmental gradient plus the lagrangian multipliers
X	the n-by-p count matrix
CC	a n-by-d covariate vector
responseFun	a character string indicating the type of response function
psi	a scalar, an importance parameter
NB_params	Starting values for the NB_params
NB_params_noLab	Starting values for the NB_params without label
d	an integer, the number of covariate parameters
alphaK	a matrix of environmental gradients of lower dimensions
k	an integer, the current dimension
centMat	a nLambdas-by-d centering matrix
nLambda	an integer, number of lagrangian multipliers
nLambdas	an integer, number of centering restrictions
thetaMat	a matrix of size n-by-p with estimated dispersion parameters
muMarg	an n-by-p offset matrix
n	an integer, the number of rows of X
ncols	a scalar, the number of columns of X
preFabMat	a prefabricated matrix
envGradEst	a character string, indicating how the environmental gradient should be fitted. 'LR' using the likelihood-ratio criterion, or 'ML' a full maximum likelihood solution
allowMissingness	A boolean, are missing values present
naId	The numeric index of the missing values in X
...	Further arguments passed on to other functions

### Value

A symmetric matrix, the evaluated Jacobian

---

NBalphaInfl	<i>Calculate the components of the influence functions</i>
-------------	--

---

**Description**

Calculate the components of the influence functions

**Usage**

```
NBalphaInfl(rcm, Dim)
```

**Arguments**

rcm	an rcm object
Dim	the required dimension

**Value**

An n-by-p-by-d array with the influence of every observation on every alpha parameter

---

NBcolInfl	<i>The influence function for the column scores</i>
-----------	---

---

**Description**

The influence function for the column scores

**Usage**

```
NBcolInfl(rcm, Dim = 1)
```

**Arguments**

rcm	an rcm object
Dim	the required dimension

**Value**

A list with components

score	a matrix with components of the score function
InvJac	A square matrix of dimension p with the components of the Jacobian related to the column scores



---

NBjacobianAbundsOld     *Jacobian for the column components of the independence model*

---

**Description**

Jacobian for the column components of the independence model

**Usage**

NBjacobianAbundsOld(beta, X, reg, thetas, allowMissingness, naId)

**Arguments**

beta	a vector of length p with current abundance estimates
X	a n-by-p count matrix
reg	a vector of length n with library sizes estimates
thetas	a n-by-p matrix with overdispersion estimates in the rows
allowMissingness	A boolean, are missing values present
naId	The numeric index of the missing values in X

**Value**

a diagonal matrix of dimension p with evaluations of the jacobian function

---

NBjacobianColNP     *Jacobian function for the estimation of a third degree GLM*

---

**Description**

Jacobian function for the estimation of a third degree GLM

**Usage**

NBjacobianColNP(beta, X, reg, theta, muMarg)

**Arguments**

beta	vector of any length
X	the data vector of length n
reg	a nlength(beta) regressor matrix
theta	a scalar, the overdispersion
muMarg	the offset of length n

**Value**

A matrix of dimension 8-by-8

---

NBjacobianColOld      *Jacobian for the estimation of the column scores*

---

**Description**

Jacobian for the estimation of the column scores

**Usage**

```
NBjacobianColOld(
  beta,
  X,
  reg,
  thetas,
  muMarg,
  k,
  n,
  p,
  colWeights,
  nLambda,
  cMatK,
  preFabMat,
  Jac,
  allowMissingness,
  naId
)
```

**Arguments**

beta	vector of length $p+1+1+(k-1)$ : $p$ row scores, 1 centering, one normalization and $(k-1)$ orthogonality lagrangian multipliers
X	the $n \times p$ data matrix
reg	a $n \times 1$ regressor matrix: outer product of rowScores and psis
thetas	$n \times p$ matrix with the dispersion parameters (converted to matrix for numeric reasons)
muMarg	the $n \times p$ offset
k	an integer, the dimension of the RC solution
n	an integer, the number of samples
p	an integer, the number of taxa
colWeights	the weights used for the restrictions
nLambda	an integer, the number of restrictions

cMatK	the lower dimensions of the colScores
preFabMat	a prefab matrix, $(1+X/\text{thetas})$
Jac	an empty Jacobian matrix
allowMissingness	A boolean, are missing values present
naId	The numeric index of the missing values in X

**Value**

A matrix of dimension  $p+1+1+(k-1)$  with evaluations of the Jacobian

---

NBjacobianLibSizes     *Jacobian for the raw components of the independence model*

---

**Description**

Jacobian for the raw components of the independence model

**Usage**

NBjacobianLibSizes(beta, X, reg, thetas, allowMissingness, naId)

**Arguments**

beta	a vector of length n with current library size estimates
X	a n-by-p count matrix
reg	a vector of length p with relative abundance estimates
thetas	a n-by-p matrix with overdispersion estimates in the rows
allowMissingness	A boolean, are missing values present
naId	The numeric index of the missing values in X

**Value**

a diagonal matrix of dimension n: the Fisher information matrix

---

NBjacobianPsi	<i>Jacobian for the psi of a given dimension</i>
---------------	--

---

**Description**

Jacobian for the psi of a given dimension

**Usage**

```
NBjacobianPsi(beta, X, reg, muMarg, theta, preFabMat, allowMissingness, naId)
```

**Arguments**

beta	a scalar, the current estimate
X	the n-by-p count matrix
reg	the regressor matrix, the outer product of current row and column scores
muMarg	the nxp offset matrix
theta	a n-by-p matrix with the dispersion parameters
preFabMat	a prefab matrix, $(1+X/\theta)$
allowMissingness	A boolean, are missing values present
naId	The numeric index of the missing values in X

**Value**

The evaluation of the jacobian function at beta, a 1-by-1 matrix

---

NBjacobianRow	<i>A jacobian function of the NB for the row scores</i>
---------------	---

---

**Description**

A jacobian function of the NB for the row scores

**Usage**

```
NBjacobianRow(
  beta,
  X,
  reg,
  thetas,
  muMarg,
  k,
```

```

    n,
    p,
    rowWeights,
    nLambda,
    rMatK,
    preFabMat,
    Jac,
    allowMissingness,
    naId
  )

```

### Arguments

beta	a vector of of length $n + k + 1$ regression parameters to optimize
X	the data matrix of dimensions $n \times p$
reg	a $1 \times p$ regressor matrix: outer product of column scores and psis
thetas	$n \times p$ matrix with the dispersion parameters (converted to matrix for numeric reasons)
muMarg	an $n \times p$ offset matrix
k	a scalar, the dimension of the RC solution
n	a scalar, the number of samples
p	a scalar, the number of taxa
rowWeights	a vector of length $n$ , the weights used for the restrictions
nLambda	an integer, the number of lagrangian multipliers
rMatK	the lower dimension row scores
preFabMat	a prefab matrix, $(1+X)/\text{thetas}$
Jac	an empty Jacobian matrix
allowMissingness	A boolean, are missing values present
naId	The numeric index of the missing values in $X$

### Value

a symmetric jacobian matrix of size  $n+k + 1$

---

NBpsiInfl

*The influence function for the psis*

---

### Description

The influence function for the psis

**Usage**

```
NBpsiInfl(rcm, Dim = 1)
```

**Arguments**

rcm	an rcm object
Dim	the required dimensions

**Value**

The influence of every single observation on the psi value of this dimension

---

NBrowInfl	<i>The influence function for the row scores</i>
-----------	--

---

**Description**

The influence function for the row scores

**Usage**

```
NBrowInfl(rcm, Dim = 1)
```

**Arguments**

rcm	an rcm object
Dim	the required dimension

**Value**

A list with components

score	a matrix with components of the score function
InvJac	A square matrix of dimension n with the components of the Jacobian related to the row scores

---

plot.RCM

*Plot RC(M) ordination result with the help of ggplot2*


---

### Description

Plot RC(M) ordination result with the help of ggplot2

### Usage

```
## S3 method for class 'RCM'
plot(
  x,
  ...,
  Dim = c(1, 2),
  plotType = c("samples", "species", "variables"),
  samColour = if (is.null(inflVar)) NULL else "Influence",
  taxNum = if (all(plotType == "species") || !is.null(taxRegExp)) { ncol(x$X) }
  else { 10 },
  taxRegExp = NULL,
  varNum = 15,
  arrowSize = 0.25,
  inflDim = 1,
  inflVar = NULL,
  returnCoords = FALSE,
  alpha = TRUE,
  varPlot = NULL,
  colLegend = if (!is.null(inflVar)) paste0("Influence on\n", inflVar,
  "\nparameter \nin dimension", inflDim) else samColour,
  samShape = NULL,
  shapeLegend = samShape,
  samSize = 2,
  scalingFactor = NULL,
  quadDrop = 0.995,
  plotEllipse = TRUE,
  taxaScale = 0.5,
  Palette = if (!all(plotType == "species")) "Set1" else "Paired",
  taxLabels = !all(plotType == "species"),
  taxDots = FALSE,
  taxCol = "blue",
  taxColSingle = "blue",
  nudge_y = 0.08,
  axesFixed = TRUE,
  aspRatio = 1,
  xInd = if (all(plotType == "samples")) c(0, 0) else c(-0.75, 0.75),
  yInd = c(0, 0),
  taxLabSize = 4,
  varLabSize = 3.5,
```

```

alphaRange = c(0.2, 1),
varExpFactor = 10,
manExpFactorTaxa = 0.975,
nPhyl = 10,
phylOther = c(""),
legendSize = samSize,
noLegend = is.null(samColour),
crossSize = 4,
contCol = c("orange", "darkgreen"),
legendLabSize = 15,
legendTitleSize = 16,
axisLabSize = 14,
axisTitleSize = 16,
plotPsi = "psi",
breakChar = "\n"
)

```

### Arguments

x	an RCM object
...	further arguments, passed on to aes in the the ggplot() function
Dim	An integer vector of length two, which dimensions to plot
plotType	a character string: which components to plot. Can be any combination of 'samples', 'species' and 'variables'
samColour	a character string, the variable to use for the colour of the sample dots. Can also be a richness measure, or "influence". Alternatively, a vector equal to the number of samples in the RCM object can be supplied. See details.
taxNum	an integer, the number of taxa to be plotted
taxRegExp	a character vector indicating which taxa to plot. Any taxa matching this regular expression will be plotted
varNum	an integer, number of variable arrows to draw
arrowSize	a scalar, the size of the arrows
inflDim	an integer, the dimension for which the influence should be calculated
inflVar	the variable on which the influence should be plotted. See details.
returnCoords	a boolean, should final coordinates be returned?
alpha	a boolean, should small arrows be made transparent?
varPlot	the names of the variable arrows to plot. Overrides the varNum argument
colLegend	a character string, the legend text for the sample colour. Defaults to the name of the colour variable
samShape	a character string, the variable to use for the shape of the sample dots
shapeLegend	a character string, the text to use for the shapeLegend. Defaults to the name of the shape variable
samSize	a scalar, the size of the sample dots



scalingFactor	a scalar, a user supplied scaling factor for the taxon arrows. If not supplied it will be calculated to make sample and taxon plots on the same scale
quadDrop	a number between 0 and 1. At this fraction of the peak height are the ellipses of the quadratic response functions drawn
plotEllipse	a boolean, whether to add the ellipses
taxaScale	a scalar, by which to scale the rectangles of the quadratic taxon plot
Palette	the colour palette
taxLabels	a boolean, should taxon labels be plotted?
taxDots	a boolean, should taxa be plotted as dots?
taxCol	the taxon colour
taxColSingle	the taxon colour if there is only one
nudge_y	a scalar, the offset for the taxon labels
axesFixed	A boolean, should the aspect ratio of the plot (the scale between the x and y-axis) be fixed. It is highly recommended to keep this argument at TRUE for honest representation of the ordination. If set to FALSE, the plotting space will be optimally used but the plot may be deformed in the process.
aspRatio	The aspect ratio of the plot when 'axesfixed' is TRUE (otherwise this argument is ignored), passed on to ggplot2::coord_fixed(). It is highly recommended to keep this argument at 1 for honest representation of the ordination.
xInd	a scalar or a vector of length 2, specifying the indentation left and right of the plot to allow for the labels to be printed entirely. Defaults to 0.75 at every side
yInd	a scalar or a vector of length 2, specifying the indentation top and bottom of the plot to allow for the labels to be printed entirely. Defaults to 0 at every side
taxLabSize	the size of taxon labels
varLabSize	the size of the variable label
alphaRange	The range of transparency
varExpFactor	a scalar, the factor by which to expand the variable coordinates
manExpFactorTaxa	a manual expansion factor for the taxa. Setting it to a high value allows you to plot the taxa around the samples
nPhyl	an integer, number of phylogenetic levels to show
phylOther	a character vector of phylogenetic levels to be included in the 'other' group
legendSize	a size for the coloured dots in the legend
noLegend	a boolean indicating you do not want a legend
crossSize	the size of the central cross
contCol	a character vector of length two, giving the low and high values of the continuous colour scale
legendLabSize	size of the legend labels
legendTitleSize	size of the legend title

axisLabSize	size of the axis labels
axisTitleSize	size of the axis title
plotPsi	a character vector, describing what to plot on the axis. Can be either 'psi', 'none' or 'loglik'. The latter plots the log-likelihood explained
breakChar	a character string indicating how the taxon names should be broken

### Details

This function relies on the ggplot2 machinery to produce the plots, and the result can be modified accordingly. Monoplots, biplots and for constrained analysis even triplots can be produced, depending on the 'plotType' argument.

When one of either 'Observed', 'Chao1', 'ACE', 'Shannon', 'Simpson', 'InvSimpson' or 'Fisher' are supplied to the 'samColour' argument, the according richness measure (as calculated by phyloseq::estimate\_richness) is mapped to the sample colour. When "influence" is supplied, the influence on the variable supplied is plotted. This 'inflVar' variable should be either "psi", or a variable name.

### Value

plots a ggplot2-object to output

### Note

Supplying only few categorical variables as constraining variables may cause the samples to be plotted on top of each other, since the number of unique sample scores is limited. The plot is still valid, but consider adding more sample variables to spread out the samples

### See Also

[RCM](#), [addOrthProjection](#), [extractCoord](#), [plotRespFun](#)

### Examples

```
data(Zeller)
require(phyloseq)
tmpPhy = prune_taxa(taxa_names(Zeller)[1:100],
prune_samples(sample_names(Zeller)[1:50], Zeller))
# Subset for a quick fit
zellerRCM = RCM(tmpPhy)
plot(zellerRCM)
```

---

plotRespFun

*Plot the non-parametric response functions*


---

### Description

Plots a number of response functions over the observed range of the environmental score. If no taxa are provided those who react most strongly to the environmental score are chosen.

### Usage

```
plotRespFun(
  RCM,
  taxa = NULL,
  type = "link",
  logTransformYAxis = FALSE,
  addSamples = TRUE,
  samSize = NULL,
  Dim = 1L,
  nPoints = 100L,
  labSize = 2.5,
  yLocVar = NULL,
  yLocSam = NULL,
  Palette = "Set3",
  addJitter = FALSE,
  nTaxa = 9L,
  angle = 90,
  legendLabSize = 15,
  legendTitleSize = 16,
  axisLabSize = 14,
  axisTitleSize = 16,
  lineSize = 0.75,
  ...
)
```

### Arguments

RCM	an RCM object
taxa	a character vector of taxa to be plotted
type	a character string, plot the response function on the log-scale ('link') or the abundance scale 'response', similar to predict.glm().
logTransformYAxis	a boolean, should y-axis be log transformed?
addSamples	a boolean, should sample points be shown?
samSize	a sample variable name or a vector of length equal to the number of samples, for the sample sizes

Dim	An integer, the dimension to be plotted
nPoints	the number of points to be used to plot the lines
labSize	the label size for the variables
yLocVar	the y-location of the variables, recycled if necessary
yLocSam	the y-location of the samples, recycled if necessary
Palette	which color palette to use
addJitter	A boolean, should variable names be jittered to make them more readable
nTaxa	an integer, number of taxa to plot
angle	angle at which variable labels should be turned
legendLabSize	size of the legend labels
legendTitleSize	size of the legend title
axisLabSize	size of the axis labels
axisTitleSize	size of the axis title
lineSize	size of the response function lines
...	Other arguments passed on to the <code>ggplot()</code> function

**Value**

Plots a `ggplot2`-object to output

**See Also**

[RCM](#), [plot.RCM](#), [residualPlot](#)

**Examples**

```
data(Zeller)
require(phyloseq)
tmpPhy = prune_taxa(taxa_names(Zeller)[1:100],
prune_samples(sample_names(Zeller)[1:50], Zeller))
#Subset for a quick fit
zellerRCMnp = RCM(tmpPhy, k = 2,
covariates = c('BMI', 'Age', 'Country', 'Diagnosis', 'Gender'),
round = TRUE, responseFun = 'nonparametric')
plotRespFun(zellerRCMnp)
```

RCM

*Wrapper function for the RCM() function***Description**

This is a wrapper function, which currently only fits the negative binomial distribution, but which could easily be extended to other ones.

**Usage**

```
RCM(dat, ...)

## S4 method for signature 'phyloseq'
RCM(dat, covariates = NULL, confounders = NULL, ...)

## S4 method for signature 'matrix'
RCM(
  dat,
  k = 2,
  round = FALSE,
  prevCutOff = 0.05,
  minFraction = 0.1,
  rowWeights = "uniform",
  colWeights = "marginal",
  confModelMat = NULL,
  confTrimMat = NULL,
  covModelMat = NULL,
  centMat = NULL,
  allowMissingness = FALSE,
  ...
)
```

**Arguments**

<code>dat</code>	an nxp count matrix or a phyloseq object with an <code>otu_table</code> slot
<code>...</code>	Further arguments passed on to the <code>RCM.NB()</code> function
<code>covariates</code>	In case 'dat' is a phyloseq object, the names of the sample variables to be used as covariates in the constrained analysis, or 'all' to indicate all variables to be used. In case 'dat' is a matrix, a nxp matrix or dataframe of covariates. Character variables will be converted to factors, with a warning. Defaults to NULL, in which case an unconstrained analysis is carried out.
<code>confounders</code>	In case 'dat' is a phyloseq object, the names of the sample variables to be used as confounders to be filtered out. In case 'dat' is a matrix, a nxp dataframe of confounders. Character variables will be converted to factors, with a warning. Defaults to NULL, in which case no filtering occurs.
<code>k</code>	an integer, the number of dimensions of the RCM solution

**round** a boolean, whether to round to nearest integer. Defaults to FALSE.  
**prevCutOff** a scalar, the prevalence cutoff for the trimming. Defaults to 2.5e-2  
**minFraction** a scalar, each taxon's total abundance should equal at least the number of samples  $n$  times minFraction, otherwise it is trimmed. Defaults to 10%  
**rowWeights, colWeights** character strings, the weighting procedures for the normalization of row and column scores. Defaults to 'uniform' and 'marginal' respectively  
**confTrimMat, confModelMat, covModelMat, centMat** Dedicated model matrices constructed based on phyloseq object.  
**allowMissingness** A boolean, should NA values be tolerated?

### Details

This function should be called on a raw count matrix, without rarefying or normalization to proportions. This function trims on prevalence and total abundance to avoid instability of the algorithm. Covariate and confounder matrices are constructed, so that everything is passed on to the workhorse function RCM.NB() as matrices.

### Value

see [RCM\\_NB](#)

### See Also

[RCM\\_NB](#), [plot.RCM](#), [residualPlot](#), [plotRespFun](#)

### Examples

```

data(Zeller)
require(phyloseq)
tmpPhy = prune_taxa(taxa_names(Zeller)[1:100],
prune_samples(sample_names(Zeller)[1:50], Zeller))
zellerRCM = RCM(tmpPhy, round = TRUE)
  
```

---

RCM\_NB

*Fit the RC(M) model with the negative binomial distribution.*

---

### Description

Fit the RC(M) model with the negative binomial distribution.

**Usage**

```
RCM_NB(
  X,
  k,
  rowWeights = "uniform",
  colWeights = "marginal",
  tol = 0.001,
  maxItOut = 1000L,
  Psitol = 0.001,
  verbose = FALSE,
  global = "dbldog",
  nleqslv.control = list(maxit = 500L, cndtol = 1e-16),
  jacMethod = "Broyden",
  dispFreq = 10L,
  convNorm = 2,
  prior.df = 10,
  marginEst = "MLE",
  confModelMat = NULL,
  confTrimMat = NULL,
  prevCutOff,
  minFraction = 0.1,
  covModelMat = NULL,
  centMat = NULL,
  responseFun = c("linear", "quadratic", "dynamic", "nonparametric"),
  record = FALSE,
  control.outer = list(trace = FALSE),
  control.optim = list(),
  envGradEst = "LR",
  dfSpline = 3,
  vgamMaxit = 100L,
  degree = switch(responseFun[1], nonparametric = 3, NULL),
  rowExp = if (is.null(covModelMat)) 1 else 0.5,
  colExp = rowExp,
  allowMissingness = FALSE
)
```

**Arguments**

X	a nxp data matrix
k	an scalar, number of dimensions in the RC(M) model
rowWeights	a character string, either 'uniform' or 'marginal' row weights.
colWeights	a character string, either 'uniform' or 'marginal' column weights.
tol	a scalar, the relative convergencde tolerance for the row scores and column scores parameters.
maxItOut	an integer, the maximum number of iterations in the outer loop.
Psitol	a scalar, the relative convergence tolerance for the psi parameters.

verbose	a boolean, should information on iterations be printed?
global	global strategy for solving non-linear systems, see ?nleqslv
nleqslv.control	a list with control options, see nleqslv
jacMethod	Method for solving non-linear equations, ?see nleqslv. Defaults to Broyden. The difference with the newton method is that the Jacobian is not recalculated at every iteration, thereby speeding up the algorithm
dispFreq	an integer, how many iterations the algorithm should wait before reestimating the dispersions.
convNorm	a scalar, the norm to use to determine convergence
prior.df	an integer, see estDisp()
marginEst	a character string, either 'MLE' or 'marginSums', indicating how the independence model should be estimated
confModelMat	an nxg matrix with confounders, with no reference levels and with intercept
confTrimMat	an nxh matrix with confounders for filtering, with all levels and without intercept
prevCutOff	a scalar the minimum prevalence needed to retain a taxon before the the confounder filtering
minFraction	a scalar, total taxon abundance should equal minFraction*n if it wants to be retained before the confounder filtering
covModelMat	an nxd matrix with covariates. If set to null an unconstrained analysis is carried out, otherwise a constrained one. Factors must have been converted to dummy variables already
centMat	a fxd matrix containing the contrasts to center the categorical variables. f equals the number of continuous variables + the total number of levels of the categorical variables.
responseFun	a characters string indicating the shape of the response function
record	A boolean, should intermediate parameter estimates be stored?
control.outer	a list of control options for the outer loop constrOptim.nl function
control.optim	a list of control options for the optim() function
envGradEst	a character string, indicating how the environmental gradient should be fitted. 'LR' using the likelihood-ratio criterion, or 'ML' a full maximum likelihood solution
dfSpline	a scalar, the number of degrees of freedom for the splines of the non-parametric response function, see VGAM::s()
vgamMaxit	an integer, the maximum number of iteration in the vgam() function
degree	an integer, the degree of the polynomial fit if the spline fit fails
rowExp, colExp	exponents for the row and column weights of the singular value decomposition used to calculate starting values. Can be played around with in case of numerical troubles.
allowMissingness	See RCM()



**Details**

Includes fitting of the independence model, filtering out the effect of confounders and fitting the RC(M) components in a constrained or an unconstrained way for any dimension  $k$ . Not intended to be called directly but only through the RCM() function

**Value**

A list with elements

converged	a vector of booleans of length $k$ indicating if the algorithm converged for every dimension
rMat	if not constrained a $n \times k$ matrix with estimated row scores
cMat	a $k \times p$ matrix with estimated column scores
psis	a vector of length $k$ with estimates for the importance parameters $\psi$
thetas	a vector of length $p$ with estimates for the overdispersion
rowRec	(if not constrained) a $n \times k \times \text{maxItOut}$ array with a record of all rMat estimates through the iterations
colRec	a $k \times p \times \text{maxItOut}$ array with a record of all cMat estimates through the iterations
psiRec	a $k \times \text{maxItOut}$ array with a record of all $\psi$ estimates through the iterations
thetaRec	a matrix of dimension $p \times \text{maxItOut}$ with estimates for the overdispersion along the way
iter	number of iterations
Xorig	(if confounders provided) the original fitting matrix
X	the trimmed matrix if confounders provided, otherwise the original one
fit	type of fit, either 'RCM_NB' or 'RCM_NB_constr'
lambdaRow	(if not constrained) vector of Lagrange multipliers for the rows
lambdaCol	vector of Lagrange multipliers for the columns
rowWeights	(if not constrained) the row weights used
colWeights	the column weights used
alpha	(if constrained) the $k \times d$ matrix of environmental gradients
alphaRec	(if constrained) the $k \times d \times \text{maxItOut}$ array of alpha estimates along the iterations
covariates	(if constrained) the matrix of covariates
libSizes	a vector of length $n$ with estimated library sizes
abunds	a vector of length $p$ with estimated mean relative abundances
confounders	(if provided) the confounder matrix
confParams	the parameters used to filter out the confounders
nonParamRespFun	A list of the non parametric response functions
degree	The degree of the alternative parametric fit
NApresent	A boolean, were NA values present?

**Note**

Plotting is not supported for quadratic response functions

**See Also**

[RCM](#)

**Examples**

```
data(Zeller)
require(phyloseq)
tmpPhy = prune_taxa(taxa_names(Zeller)[seq_len(100)],
prune_samples(sample_names(Zeller)[seq_len(50)], Zeller))
mat = as(otu_table(tmpPhy), "matrix")
mat = mat[rowSums(mat)>0, colSums(mat)>0]
zellerRCM = RCM_NB(mat, k = 2)
#Needs to be called directly onto a matrix
```

---

residualPlot

*Make residual plots*

---

**Description**

Make residual plots

**Usage**

```
residualPlot(
  RCM,
  Dim = 1,
  whichTaxa = "response",
  resid = "Deviance",
  numTaxa = 9,
  mfrow = NULL,
  samColour = NULL,
  samShape = NULL,
  legendLabSize = 15,
  legendTitleSize = 16,
  axisLabSize = 14,
  axisTitleSize = 16,
  taxTitle = TRUE,
  h = 0
)
```

**Arguments**

RCM	an RCM object
Dim	an integer, which dimension?
whichTaxa	a character string or a character vector, for which taxa to plot the diagnostic plots
resid	the type of residuals to use, either 'Deviance' or 'Pearson'
numTaxa	an integer, the number of taxa to plot
mfrow	passed on to par(). If not supplied will be calculated based on numTaxa
samColour, samShape	Vectors or character strings denoting the sample colour and shape respectively. If character string is provided, the variables with this name is extracted from the phyloseq object in RCM
legendLabSize	size of the legend labels
legendTitleSize	size of the legend title
axisLabSize	size of the axis labels
axisTitleSize	size of the axis title
taxTitle	A boolean, should taxon title be printed
h	Position of reference line. Set to NA for no line

**Details**

If whichTaxa is 'run' or 'response' the taxa with the highest run statistics or steepest slopes of the response function are plotted, numTax indicates the number. If whichTaxa is a character vector, these are interpreted as taxon names to plot. This function is mainly meant for linear response functions, but can be used for others too. The runs test statistic from the tseries package is used.

**Value**

Plots a ggplot2-object to output

**See Also**

[RCM](#)

**Examples**

```
data(Zeller)
require(phyloseq)
tmpPhy = prune_taxa(taxa_names(Zeller)[1:120],
prune_samples(sample_names(Zeller)[1:75], Zeller))
#Subset for a quick fit
zellerRCMlin = RCM(tmpPhy, k = 2,
covariates = c('BMI', 'Age', 'Country', 'Diagnosis', 'Gender'),
responseFun = 'linear', round = TRUE, prevCutOff = 0.03)
residualPlot(zellerRCMlin)
```

---

respFunJacMat                      *Calculates the Jacobian of the parametric response functions*

---

### Description

Calculates the Jacobian of the parametric response functions

### Usage

```
respFunJacMat(
  betas,
  X,
  reg,
  thetaMat,
  muMarg,
  psi,
  v,
  p,
  IDmat,
  IndVec,
  allowMissingness,
  naId
)
```

### Arguments

betas	a vector of length $(deg+1)*(p+1)$ with regression parameters with deg the degree of the response function and the lagrangian multipliers
X	the nxp data matrix
reg	a vector of regressors with the dimension n-by-v
thetaMat	The n-by-p matrix with dispersion parameters
muMarg	offset matrix of size nxp
psi	a scalar, the importance parameter
v	an integer, one plus the degree of the response function
p	an integer, the number of taxa
IDmat	an logical matrix with indices of non-zero elements
IndVec	a vector with indices with non-zero elements
allowMissingness	A boolean, are missing values present
naId	The numeric index of the missing values in X

### Value

The jacobian, a square matrix of dimension  $(deg+1)*(p+1)$

---

respFunScoreMat      *Derivative of the Lagrangian of the parametric response function*

---

### Description

Derivative of the Lagrangian of the parametric response function

### Usage

```
respFunScoreMat(
  betas,
  X,
  reg,
  thetaMat,
  muMarg,
  psi,
  p,
  v,
  allowMissingness,
  naId,
  ...
)
```

### Arguments

betas	a vector of length $(deg+1)*(p+1)$ with regression parameters with deg the degree of the response function and the lagrangian multipliers
X	the nxp data matrix
reg	a matrix of regressors with the dimension $n \times (deg+1)$
thetaMat	The n-by-p matrix with dispersion parameters
muMarg	offset matrix of size nxp
psi	a scalar, the importance parameter
p	an integer, the number of taxa
v	an integer, one plus the degree of the response function
allowMissingness	A boolean, are missing values present
naId	The numeric index of the missing values in X
...	further arguments passed on to the jacobian

The parameters are restricted to be normalized, i.e. all squared intercepts, first order and second order parameters sum to 1

### Value

The evaluation of the score functions, a vector of length  $(p+1) * (deg+1)$

---

rowMultiply	<i>A function to efficiently row multiply a matrix and a vector</i>
-------------	---

---

**Description**

A function to efficiently row multiply a matrix and a vector

**Usage**

```
rowMultiply(matrix, vector)
```

**Arguments**

matrix	a numeric matrix of dimension a-by-b
vector	a numeric vector of length b t(t(matrix)*vector) but then faster

**Details**

Memory intensive but that does not matter with given matrix sizes

**Value**

a matrix, row multiplied by the vector

---

seq_k	<i>A small auxiliary function for the length of the lambdas</i>
-------	---

---

**Description**

A small auxiliary function for the length of the lambdas

**Usage**

```
seq_k(y, nLambda1s = 1)
```

**Arguments**

y	an integer, the current dimension
nLambda1s	the number of centering restrictions

**Value**

a vector containing the ranks of the current lagrangian multipliers

---

trimOnConfounders	<i>Trim based on confounders to avoid taxa with only zero counts</i>
-------------------	--

---

**Description**

Trim based on confounders to avoid taxa with only zero counts

**Usage**

```
trimOnConfounders(confounders, X, prevCutOff, minFraction, n)
```

**Arguments**

confounders	a n <sub>x</sub> t confounder matrix
X	the n <sub>x</sub> p data matrix
prevCutOff	a scalar between 0 and 1, the prevalence cut off
minFraction	a scalar between 0 and 1, each taxon's total abundance should equal at least the number of samples n times minFraction, otherwise it is trimmed
n	the number of samples

Should be called prior to fitting the independence model

**Value**

A trimmed data matrix n<sub>x</sub>p'

---

Zeller	<i>Microbiomes of colorectal cancer patients and healthy controls</i>
--------	---

---

**Description**

Microbiome sequencing data of colorectal cancer patients, patients with small adenoma and healthy controls, together with other baseline covariates

**Usage**

Zeller

**Format**

A phyloseq object with an OTU-table and sample data

**otu\_table** Count data matrix of 709 taxa in 194 samples

**sample\_data** Data frame of patient covariates

**Source**

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4299606/>

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