Package 'RCM'

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Type Package

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

Version 1.25.1

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

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Depends R (>= 4.5.0)

Suggests knitr, rmarkdown, testthat

VignetteBuilder knitr

biocViews Metagenomics, DimensionReduction, Microbiome, Visualization

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Contents

`addOrthProjection` *This function adds orthogonal projections to a given plot*

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

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 sum(x[i,j,]*y)

`buildCentMat` *A function to build a centering matrix based on a dataframe*

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` *A function to build the confounder matrices*

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-method

buildConfMat.character

Description

buildConfMat.character

Usage

```
## S4 method for signature 'character'
buildConfMat(x, physeq)
```

Arguments

x	a numeric matrix of confounders
physeq	a physeq object with a sample_data slot

Value

see buidConfMat.numeric

---

buildConfMat,data.frame-method

buildConfMat.data.frame

Description

buildConfMat.data.frame

Usage

```
## S4 method for signature 'data.frame'
buildConfMat(x, n)
```

Arguments

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

Value

see buidConfMat

`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` *A function to build the design matrix*

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 repsonse function is provided

Value

A design matrix of dimension n-by-f

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

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

`X`	the matrix of counts
`mu`	the matrix of expectations
`allowMissingness`	A boolean, are missing values present
`naId`	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 *A function that returns the value of the partial derivative of the log-likelihood ratio to alpha, keeping the response functions fixed*

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 nLambda1s-by-d centering matrix
nLambda	an integer, number of lagrangian multipliers
nLambda1s	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

---

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

Description

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

Usage

```
dNBlibSizes(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 *Estimation of the parameters of a third degree GLM*

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

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) orhtogonality 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 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
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 *A score function of the NB for the row scores*

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 nxp
reg	a 1xp regressor matrix: outer product of column scores and psis
thetas	nxp matrix with the dispersion parameters (converted to matrix for numeric reasons)
muMarg	an nxp 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 nxp
cMat	a 1xp colum scores matrix
rMat	a nx1 rowscores matrix, if unconstrained
muMarg	an nxp 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 pacakage, 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` *A function to extract plotting coordinates, either for plot.RCM or to export to other plotting software*

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*x^2 + b*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` *A function to extract a matrix of expected values for any dimension of the fit*

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` *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.*

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 *A function to calculate the matrix of deviance residuals.*

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

getDistCoord — *Get coordinates of a distance object of n observations for the provided indices*

Description

Get coordinates of a distance object of n observations for the provided indices

Usage

```
getDistCoord(indices, n)
```

Arguments

indices	The row indices for which distance indices are wanted
n	The total number of objects in the distance matrix

Value

a vector of coordinates

getInflCol — *A function to extract the influence for a given parameter index*

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 *Extract the influence of all observations on a given row score*

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 *A function to construct a model matrix of a certain degree*

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 lenght(y)

getRowMat *Return a matrix of row scores*

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 theresponse 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 *Gram-Schmidt orthogonalization of vectors*

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 *Define linear equality constraints for env. gradient*

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 *The jacobian of the linear equality constraints*

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` *Functions to indent the plot to include the entire labels*

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 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` *Calculate the log-likelihoods of all possible models*

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` *Jacobian of the constrained analysis with linear response function.*

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)

liks *Calculate the log-likelihoods of all possible models*

Description

Calculate the log-likelihoods of all possible models

Usage

```
liks(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 nLambda1s-by-d centering matrix
nLambda	an integer, number of lagrangian multipliers
nLambda1s	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 *Calculate the components of the influence functions*

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 *The influence function for the column scores*

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 nxlength(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) orhtogonality 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
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/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 *Jacobian for the psi of a given dimension*

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/thetas)
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 *A jacobian function of the NB for the row scores*

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 nxp
reg	a 1xp regressor matrix: outer product of column scores and psis
thetas	nxp matrix with the dispersion parameters (converted to matrix for numeric reasons)
muMarg	an nxp 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/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 *The influence function for the row scores*

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

---

permanova *Perform a PERMANOVA analysis for group differences of a predefined cofactor using the pseudo F-statistic*

Description

Perform a PERMANOVA analysis for group differences of a predefined cofactor using the pseudo F-statistic

Usage

```
permanova(
  rcmObj,
  groups,
  nPerm = 10000,
  Dim = seq_len(rcmObj$k),
  verbose = TRUE
)
```

Arguments

rcmObj	an RCM object
groups	a factor of length n with cluster memberships, or a name of a variable contained in the RCM object
nPerm	Number of permutations in the PERMANOVA
Dim	Dimensions on which the test should be performed. Defaults to all dimensions of the fitted RCM object.
verbose	a boolean, should output be printed?

Value

A list with components

statistic	The pseudo F-statistic
p.value	The p-value of the PERMANOVA

See Also

RCM

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)
zellerPermanova = permanova(zellerRCM, "Diagnosis")
```

---

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 matcing this regular expression will be plotted
varNum	an integehr, 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 offet 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), passde 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 argumens passed on to the ggplot() 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

dat	an nxp count matrix or a phyloseq object with an otu_table slot
...	Further arguments passed on to the RCM.NB() function
covariates	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 nxf 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.
confounders	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 nxf dataframe of confounders. Character variables will be converted to factors, with a warning. Defaults to NULL, in which case no filtering occurs.
k	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 prevalance 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 functions 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 convergende 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 reestimationg 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 nxk matrix with estimated row scores
cMat	a kxp 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 x k x maxItOut array with a record of all rMat estimates through the iterations
colRec	a k x p x maxItOut array with a record of all cMat estimates through the iterations
psiRec	a k x maxItOut array with a record of all psi estimates through the iterations
thetaRec	a matrix of dimension pxmaxItOut 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 kxd matrix of environmental gradients
alphaRec	(if constrained) the kxdxmaxItOut 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 nx(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 *A function to efficiently row multiply a matrix and a vector*

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 multplied by the vector

seq_k *A small auxiliary function for the length of the lambdas*

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 *Trim based on confounders to avoid taxa with only zero counts*

Description

Trim based on confounders to avoid taxa with only zero counts

Usage

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

Arguments

confounders	a nxt confounder matrix
X	the nxp 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 nxp'

Zeller *Microbiomes of colorectal cancer patients and healthy controls*

Description

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

Usage

```
data(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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