

# Package ‘combi’

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**Type** Package

**Title** Compositional omics model based visual integration

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**Description** Combine quasi-likelihood estimation, compositional regression models and latent variable models for integrative visualization of several omics datasets. Both unconstrained and constrained integration is available, the results are shown as interpretable multiplots.

**License** GPL-2

**Encoding** UTF-8

**RoxygenNote** 6.1.1

**Imports** ggplot2, nleqslv, phyloseq, tensor, stats, limma, Matrix, BB, reshape2, alabama, cobs, Biobase, vegan, grDevices, graphics, methods, SummarizedExperiment

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**VignetteBuilder** knitr

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addLink	<i>Add a link on a compositional plot</i>
---------	---

---

## Description

Add a link on a compositional plot

## Usage

```
addLink(DIplot, links, Views, samples, variable = NULL, Dims = c(1, 2),
        addLabel = FALSE, labPos = NULL, projColour = "grey",
        latentSize = 0.25)
```

## Arguments

DIplot	A list with ggplot object where the links are to be added, and data frames with coordinates (obtained by setting plot(..., returnCoords = TRUE))
links	A matrix containing either feature names (two column matrix) or approximate coordinates (four column matrix)
Views	Indices or names of the views for which the links should be added
samples	Sample names or approximate sample coordinates
variable	Name of variable in environmental gradient for which link should be plotted
Dims	vector of length 2 referring to the model dimensions
addLabel	A boolean, should arrow with label be plotted?
labPos	The position of the label, as a numeric vector of length 2
projColour	The colour of the projection, as character string
latentSize	Size of the line from the origin to the latent variable dot

## Value

A ggplot object with the links added

**Examples**

```

data(Zhang)

#Unconstrained
microMetaboInt = combi(
  list("microbiome" = zhangMicrobio, "metabolomics" = zhangMetabo),
  distributions = c("quasi", "gaussian"), compositional = c(TRUE, FALSE),
  logTransformGaussian = FALSE, verbose = TRUE)

load(system.file("extdata", "zhangFits.RData", package = "combi"))
Plot = plot(microMetaboInt, samDf = zhangMetavars, samCol = "ABX",
  returnCoords = TRUE)
addLink(Plot, links = cbind("OTU0565b3", "OTUa14fb5"), Views = 1,
  samples = c(1,1))

```

---

arrayMult

*Array multiplication*


---

**Description**

Array multiplication

**Usage**

```
arrayMult(centralMat, outerMat, ncols = ncol(outerMat))
```

**Arguments**

centralMat	an nxp matrix
outerMat	an nxd matrix
ncols	an integer, the number of columns of outerMat

**Value**

an nxpxd matrix, the stacked matrices of centralMat multiplied to every column of outerMat

---

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 modelDI 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

---

buildCompMat	<i>Build the composition matrix for a certain dimension m dimensions</i>
--------------	--

---

**Description**

Build the composition matrix for a certain dimension m dimensions

**Usage**

```
buildCompMat(colMat, paramEsts, latentVar, m, norm = TRUE,
             id = seq_len(m), subtractMax = TRUE)
```

**Arguments**

colMat            The nxp independence model composition matrix

paramEsts        The matrix of feature parameter estimates

latentVar        The matrix of latent variables

m                the required dimension

norm            a boolean, should the composition matrix be normalized?

id                The vector of dimensions to consider

subtractMax     A boolean, should the maximum be subtracted from every composition prior to exponentiation? Recommended for numerical stability

**Value**

A matrix with compositions in the rows

---

buildConfMat	<i>Build confounder design matrices with and without intercepts</i>
--------------	---

---

**Description**

Build confounder design matrices with and without intercepts

**Usage**

```
buildConfMat(confounders)
```

**Arguments**

confounders	A dataframe of confounding variables #' 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

---

buildCovMat	<i>A function to build the covariate matrix of the constraints</i>
-------------	--

---

**Description**

A function to build the covariate matrix of the constraints

**Usage**

```
buildCovMat(datFrame)
```

**Arguments**

datFrame            the dataframe with which the covariate matrix is to be built  
 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

---

buildEmptyJac	<i>Prepare an empty Jacobian matrix, with useful entries prefilled. In case of distribution "gaussian", it returns the lhs matrix of the linear system for finding the feature parameters</i>
---------------	---

---

**Description**

Prepare an empty Jacobian matrix, with useful entries prefilled. In case of distribution "gaussian", it returns the lhs matrix of the linear system for finding the feature parameters

**Usage**

```
buildEmptyJac(n, m, lower, distribution = "quasi", normal = FALSE,
              nLambda1s = 1, centMat = NULL, weights = 1)
```

**Arguments**

n                    the number of parameters  
 m                    the dimension  
 lower                the current parameter estimates  
 distribution        A character string, the distributional assumption for the data  
 normal               a boolean, are normalization restrictions in place?  
 nLambda1s           The number of centering restrictions  
 centMat             The centering matrix  
 weights             Vector of feature weights

**Value**

an empty jacobian matrix, or the lhs of the system of estimating equations

---

`buildMarginalOffset`     *Build an offset matrix from an marginal model object*

---

### Description

Build an offset matrix from an marginal model object

### Usage

```
buildMarginalOffset(indepModel, invLink)
```

### Arguments

`indepModel`     The fitted marginal model, a list  
`invLink`         The inverse link function

### Value

an offset matrix of the size of the data

---

`buildMu`                 *A function to build the mu matrix*

---

### Description

A function to build the mu matrix

### Usage

```
buildMu(offSet, latentVar, paramEsts, distribution, paramMatrix = FALSE)
```

### Arguments

`offSet`             the offset matrix  
`latentVar, paramEsts, distribution`  
                       Latent variables, parameter estimates and distribution type  
`paramMatrix`     A boolean, are feature parameters provided as matrix

### Value

The mean matrix



---

buildMuMargins	<i>Build the marginal mu matrix</i>
----------------	-------------------------------------

---

**Description**

Build the marginal mu matrix

**Usage**

```
buildMuMargins(x, otherMargin, col)
```

**Arguments**

x	The marginal parameters begin estimated
otherMargin	The parameters of the other margin
col	A logical, are the column parameters being estimated?

**Value**

a matrix of means

---

buildOffsetModel	<i>Build a marginal offset matrix given a model</i>
------------------	---

---

**Description**

Build a marginal offset matrix given a model

**Usage**

```
buildOffsetModel(modelObj, View, distributions, compositional)
```

**Arguments**

modelObj	a modelDI object
View	The view for which to build the offset
distributions, compositional	belong to the view

**Value**

The offset matrix

---

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

---

checkMeanVarTrend	<i>Quickly check if the mean variance trend provides a good fit</i>
-------------------	---

---

**Description**

Quickly check if the mean variance trend provides a good fit

**Usage**

```
checkMeanVarTrend(data, meanVarFit = "spline", returnTrend = FALSE,
  ...)
```

**Arguments**

data	Data in any acceptable format (see details ?combi)
meanVarFit	The type of mean variance fit, either "cubic" or "spline"
returnTrend	A boolean, should the estimated trend be returned (TRUE) or only plotted (FALSE)?
...	passed on to the estMeanVarTrend() function

**Value**

A plot object

**Examples**

```
data(Zhang)
par(mfrow = c(1,2))
lapply(list("microbiome" = zhangMicrobio, "metabolome" = zhangMetabo),
  checkMeanVarTrend)
par(mfrow = c(1,1))
```

---

checkMonotonicity	<i>Check for monotonicity in compositional datasets fro given dimensions</i>
-------------------	--

---

**Description**

Check for monotonicity in compositional datasets fro given dimensions

**Usage**

```
checkMonotonicity(modelObj, Dim)
```

**Arguments**

modelObj	The combi fit
Dim	The dimensions considered

**Value**

A boolean matrix indicating monotonicity for every feature

---

combi	<i>Perform model-based data integration</i>
-------	---

---

**Description**

Perform model-based data integration

**Usage**

```
combi(data, M = 2L, covariates = NULL, distributions, compositional,
  maxIt = 300L, tol = 0.001, verbose = FALSE, prevCutoff = 0.95,
  minFraction = 0.1, logTransformGaussian = TRUE, confounders = NULL,
  compositionalConf = rep(FALSE, length(data)),
  nleq.control = list(maxit = 1000L, cndtol = 1e-16), record = TRUE,
  weights = NULL, fTol = 1e-05, meanVarFit = "spline",
  maxFeats = 2000, dispFreq = 10L, allowMissingness = FALSE,
  biasReduction = TRUE, maxItFeat = 20L)
```

**Arguments**

<code>data</code>	A list of data objects with the same number of samples. See details.
<code>M</code>	the required dimension of the fit, a non-negative integer
<code>covariates</code>	a dataframe of n samples with sample-specific variables.
<code>distributions</code>	a character vector describing which distributional assumption should be used. See details.
<code>compositional</code>	A logical vector with the same length as "data", indicating if the datasets should be treated as compositional
<code>maxIt</code>	an integer, the maximum number of iterations
<code>tol</code>	A small scalar, the convergence tolerance
<code>verbose</code>	Logical. Should verbose output be printed to the console?
<code>prevCutOff</code>	a scalar, the prevalence cutoff for the trimming.
<code>minFraction</code>	a scalar, each taxon's total abundance should equal at least the number of samples n times minFraction, otherwise it is trimmed.
<code>logTransformGaussian</code>	A boolean, should the gaussian data be logtransformed, i.e. are they log-normal?
<code>confounders</code>	A dataframe or a list of dataframes with the same length as data. In the former case the same dataframe is used for conditioning, In the latter case each view has its own conditioning variables (or NULL).
<code>compositionalConf</code>	A logical vector with the same length as "data", indicating if the datasets should be treated as compositional when correcting for confounders. Numerical problems may occur when set to TRUE
<code>nleq.control</code>	A list of arguments to the nleqslv function
<code>record</code>	A boolean, should intermediate estimates be stored? Can be useful to check convergence
<code>weights</code>	A character string, either 'marginal' or 'uniform', indicating rhow the feature parameters should be weighted in the normalization
<code>fTol</code>	The tolerance for solving the estimating equations
<code>meanVarFit</code>	The type of mean variance fit, see details
<code>maxFeats</code>	The maximal number of features for a Newton-Raphson procedure to be feasible
<code>dispFreq</code>	An integer, the period after which the variances should be reestimated
<code>allowMissingness</code>	A boolean, should NA values be allowed?
<code>biasReduction</code>	A boolean, should bias reduction be applied to allow for confounder correction in groups with all zeroes? Not guaranteed to work
<code>maxItFeat</code>	Integers, the maximum allowed number of iterations in the estimation of the feature parameters

**Details**

Data can be provided as raw matrices with features in the columns, or as phyloseq, Summarized-Experiment or ExpressionSet objects. Estimation of independence model and view wise parameters can be parametrized. See ?BiocParallel::bplapply and ?BiocParallel::register. meanVarFit = "spline" yields a cubic spline fit for the abundance-variance trend, "cubic" gives a third degree polynomial. Both converge to the diagonal line with slope 1 for small means. Distribution can be either "quasi" for quasi likelihood or "gaussian" for Gaussian data

**Value**

An object of the "combi" class, containing all information on the data integration and fitting procedure

**Examples**

```
data(Zhang)
#The method works on several datasets at once, and simply is not very fast.
#Hence the "Not run" statement

#Unconstrained
microMetaboInt = combi(
  list("microbiome" = zhangMicrobio, "metabolomics" = zhangMetabo),
  distributions = c("quasi", "gaussian"), compositional = c(TRUE, FALSE),
  logTransformGaussian = FALSE, verbose = TRUE)
#Constrained
microMetaboIntConstr = combi(
  list("microbiome" = zhangMicrobio, "metabolomics" = zhangMetabo),
  distributions = c("quasi", "gaussian"), compositional = c(TRUE, FALSE),
  logTransformGaussian = FALSE, covariates = zhangMetavars, verbose = TRUE)
```

---

convPlot

*Plot the convergence of the different parameter estimates in a line plot*


---

**Description**

Plot the convergence of the different parameter estimates in a line plot

**Usage**

```
convPlot(model, latent = is.null(View), nVars = Inf, Dim = 1L,
  View = NULL, size = 0.125)
```

**Arguments**

model	A fitted modelDI object
latent	A boolean, should latent variable trajectory be plotted
nVars	An integer, the number of variables to plot. By default all are plotted

Dim	An integer, the dimension to be plotted
View	An integer or character string, indicating the view to be plotted (if latent = FALSE)
size	The line size (see ?geom_path)

**Value**

A ggplot object containing the convergence plot

**Examples**

```
data(Zhang)
#Unconstrained
microMetaboInt = combi(
  list("microbiome" = zhangMicrobio, "metabolomics" = zhangMetabo),
  distributions = c("quasi", "gaussian"), compositional = c(TRUE, FALSE),
  logTransformGaussian = FALSE, verbose = TRUE)
load(system.file("extdata", "zhangFits.RData", package = "combi"))
convPlot(microMetaboInt)
convPlot(microMetaboInt, Dim = 2)
convPlot(microMetaboInt, View = "microbiome")
```

---

deriv2LagrangianFeatures

*The score function to estimate the latent variables*

---

**Description**

The score function to estimate the latent variables

**Usage**

```
deriv2LagrangianFeatures(x, data, distribution, offSet, latentVars, numVar,
  paramEstsLower, mm, Jac, meanVarTrend, weights, compositional,
  indepModel, ...)
```

**Arguments**

x	parameter estimates
data	A list of data matrices
distribution, compositional, meanVarTrend, offSet, numVar	Characteristics of the view
latentVars	A vector of latent variables
paramEstsLower	lower dimension estimates
mm	the current dimension
Jac	a prefab jacobian

weights	The normalization weights
indepModel	the independence model
...	Additional arguments passed on to the score and jacobian functions

**Value**

A vector of length n, the evaluation of the score functions of the latent variables

---

deriv2LagrangianLatentVars

*The jacobian function to estimate the latent variables*

---

**Description**

The jacobian function to estimate the latent variables

**Usage**

```
deriv2LagrangianLatentVars(x, data, distributions, offsets, paramEsts,
  paramMats, numVars, latentVarsLower, n, m, Jac, numSets, meanVarTrends,
  links, varPosts, indepModels, compositional, ...)
```

**Arguments**

x	The current estimates of the latent variables
data	Lists of information on all the views
distributions, links, compositional, meanVarTrends, offsets, numVars, numSets, paramMats, paramEsts, varPosts	Characteristics of the views
latentVarsLower	The parameter estimates of the lower dimensions
n, m	integers, number of samples and dimensions
Jac	an empty jacobian matrix
...	arguments to the jacobian function, currently ignored

**Value**

A vector of length n, the evaluation of the score functions of the latent variables

---

 deriv2LagrangianLatentVarsConstr

*The score function to estimate the latent variables*


---

### Description

The score function to estimate the latent variables

### Usage

```
deriv2LagrangianLatentVarsConstr(x, data, distributions, offsets,
  paramEsts, paramMats, numVars, latentVarsLower, nn, m, Jac, numSets,
  meanVarTrends, links, numCov, covMat, nLambdas, varPosts, compositional,
  indepModels, ...)
```

### Arguments

x	The current estimates of the latent variables
data	Lists of information on all the views
distributions, links, compositional, meanVarTrends, offsets, numVars, paramMats, paramEsts	Characteristics of the view
latentVarsLower	The parameter estimates of the lower dimensions
nn	number of samples
m	integers, number of samples and dimensions
Jac	an empty jacobian matrix
numSets	Characteristics of the views
numCov	The number of covariates
covMat	the covariates matrix
nLambdas	The number of centering restrictions
varPosts	Characteristics of the views
indepModels	Characteristics of the views
...	arguments to the jacobian function, currently ignored

### Value

A vector of length nn, the evaluation of the score functions of the latent variables



---

 derivLagrangianFeatures

*The score function to estimate the feature parameters*


---

### Description

The score function to estimate the feature parameters

### Usage

```
derivLagrangianFeatures(x, data, distribution, offSet, latentVars, numVar,
  paramEstsLower, mm, indepModel, meanVarTrend, weights, compositional,
  ...)
```

### Arguments

x	current parameter estimates
data	A list of data matrices
distribution, compositional, meanVarTrend, offSet, numVar, indepModel, paramEstsLower	Characteristics of the view
latentVars	A vector of latent variables
mm	the current dimension
weights	The normalization weights
...	arguments to the jacobian function, currently ignored

### Value

A vector with the evaluation of the score functions of the feature parameters

---

derivLagrangianLatentVars

*The score function to estimate the latent variables*


---

### Description

The score function to estimate the latent variables

### Usage

```
derivLagrangianLatentVars(x, data, distributions, offsets, paramEsts,
  paramMats, numVars, n, m, numSets, meanVarTrends, links, varPosts,
  latentVarsLower, compositional, indepModels, ...)
```

**Arguments**

x	The current estimates of the latent variables
n	The number of samples
m	The dimensions
numSets	The number of views
latentVarsLower	The parameter estimates of the lower dimensions
compositional, links, indepModels, meanVarTrends, numVars, distributions, data, offsets, varPosts, paramEsts, covMat, numCov, centMat, nLambdas	Lists of information on all the views
...	arguments to the jacobian function, currently ignored

**Value**

A vector of length n, the evaluation of the score functions of the latent variables

---

derivLagrangianLatentVarsConstr

*The score function to estimate the latent variables*

---

**Description**

The score function to estimate the latent variables

**Usage**

```
derivLagrangianLatentVarsConstr(x, data, distributions, offsets, paramEsts,
  numVars, latentVarsLower, n, m, numSets, meanVarTrends, links, covMat,
  numCov, centMat, nLambdas, varPosts, compositional, indepModels,
  paramMats, ...)
```

**Arguments**

x	The current estimates of the latent variables
latentVarsLower	The parameter estimates of the lower dimensions
n	The number of samples
m	The dimensions
numSets	The number of views
covMat	The covariance matrix
numCov	The number of covariates
centMat	A centering matrix
nLambdas	The number of dummy variables
compositional, links, indepModels, meanVarTrends, numVars, distributions, data, offsets, varPosts, paramEsts, covMat, numCov, centMat, nLambdas	Lists of information on all the views
...	arguments to the jacobian function, currently ignored

**Value**

A vector of length  $n$ , the evaluation of the score functions of the latent variables

---

estFeatureParameters *Estimate the feature parameters*

---

**Description**

Estimate the feature parameters

**Usage**

```
estFeatureParameters(paramEsts, lambdasParams, seqSets, data,
  distributions, offsets, nCores, m, JacFeatures, meanVarTrends,
  latentVars, numVars, control, weights, compositional, indepModels, fTol,
  allowMissingness, maxItFeat, ...)
```

**Arguments**

paramEsts	Current list of parameter estimates for the different views
lambdasParams	The lagrange multipliers
seqSets	A vector with view indices
data	A list of data matrices
distributions	A character vector describing the distributions
offsets	A list of offset matrices
nCores	The number of cores to use in multithreading
m	The dimension
JacFeatures	An empty Jacobian matrix
meanVarTrends	The mean-variance trends of the different views
latentVars	A vector of latent variables
numVars	The number of variables
control	A list of control arguments for the nleqslv function
weights	The normalization weights
compositional	A list of booleans indicating compositionality
indepModels	A list of independence model
fTol	A convergence tolerance
allowMissingness	A boolean indicating whether missing values are allowed
maxItFeat	An integer, the maximum number of iterations
...	Additional arguments passed on to the score and jacobian functions

**Value**

A vector with estimates of the feature parameters

---

<code>estIndepModel</code>	<i>Estimate the independence model belonging to one view</i>
----------------------------	--

---

**Description**

Estimate the independence model belonging to one view

**Usage**

```
estIndepModel(data, distribution, compositional, maxIt, tol, link, invLink,
              meanVarFit, newtonRaphson, dispFreq, ...)
```

**Arguments**

<code>data</code>	a list of data matrices with the same number of samples $n$ in the rows. Also phyloseq objects are acceptable
<code>distribution</code>	a character string describing which distributional assumption should be used.
<code>compositional</code>	A logical indicating if the dataset should be treated as compositional
<code>maxIt</code>	an integer, the maximum number of iterations
<code>tol</code>	A small scalar, the convergence tolerance
<code>link, invLink</code>	link and inverse link function
<code>meanVarFit</code>	mean variance model
<code>newtonRaphson</code>	a boolean, should newton-raphson be used
<code>dispFreq</code>	An integer, frequency of dispersion estimation
<code>...</code>	passed on to the <code>estOff()</code> function

**Value**

A list with elements

<code>rowOff</code>	The row offsets
<code>colOff</code>	The column offsets
<code>converged</code>	A logical flag, indicating whether the fit converged
<code>iter</code>	An integer, the number of iterations

---

estLatentVars	<i>Estimate the latent variables</i>
---------------	--------------------------------------

---

**Description**

Estimate the latent variables

**Usage**

```
estLatentVars(latentVars, lambdasLatent, constrained, fTol, ...)
```

**Arguments**

latentVars	A vector of latent variables
lambdasLatent	A vector of Lagrange multipliers
constrained	A boolean, is the ordination constrained?
fTol	The convergence tolerance
...	additional arguments passed on to score and jacobian functions

**Value**

A vector of length n, the estimates of the latent variables

---

estMeanVarTrend	<i>Estimate a column-wise mean-variance trend</i>
-----------------	---

---

**Description**

Estimate a column-wise mean-variance trend

**Usage**

```
estMeanVarTrend(data, meanMat, baseAbundances, libSizes, plot = FALSE,
  meanVarFit, degree = 2L, constraint = "none", ...)
```

**Arguments**

data	the data matrix with n rows
meanMat	the estimated mean matrix
baseAbundances	The baseline abundances
libSizes	Library sizes
plot	A boolean, should the trend be plotted?
meanVarFit	A character string describing the type of trend to be fitted: either "spline" or "cubic"

degree	The degree of the spline
constraint	Constraint to the spline
...	additional arguments passed on to the plot() function

**Value**

A list with components

meanVarTrend	An smoothed trend function, that can map a mean on a variance
meanVarTrendDeriv	A derivative function of this

---

estOff	<i>Estimate the row/column parameters of the independence model</i>
--------	---

---

**Description**

Estimate the row/column parameters of the independence model

**Usage**

```
estOff(data, distribution, rowOff, colOff, meanVarTrend, col,
       newtonRaphson, libSizes, ...)
```

**Arguments**

data	a list of data matrices with the same number of samples n in the rows. Also phyloseq objects are acceptable
distribution	a character string describing which distributional assumption should be used.
rowOff, colOff	current row and column offset estimates
meanVarTrend	The estimated mean-variance trend
col	A logical, should column offsets be estimated
newtonRaphson	A boolean, should Newton-Raphson be used to solve the estimating equations
libSizes	The library sizes, used to evaluate the mean-variance trend
...	passed onto nleqslv

**Value**

The estimated marginal parameters

---

extractCoords	<i>Extract coordinates from fitted object</i>
---------------	---

---

## Description

Extract coordinates from fitted object

## Usage

```
extractCoords(modelObj, Dim)
```

## Arguments

modelObj	The fitted model
Dim	the required dimensions

## Value

A list with components (matrices with two columns)

latentData	The latent variables
featureData	The feature parameters
varData	The variables

## Examples

```
data(Zhang)

#Unconstrained
microMetaboInt = combi(
  list("microbiome" = zhangMicrobio, "metabolomics" = zhangMetabo),
  distributions = c("quasi", "gaussian"), compositional = c(TRUE, FALSE),
  logTransformGaussian = FALSE, verbose = TRUE)

#Load the fits
load(system.file("extdata", "zhangFits.RData", package = "combi"))
extractCoords(microMetaboInt, Dim = c(1,2))
```

---

extractData	<i>Helper function to extract data matrix from phyloseq, expressionset objects etc. Also filters out all zero rows</i>
-------------	--

---

**Description**

Helper function to extract data matrix from phyloseq, expressionset objects etc. Also filters out all zero rows

**Usage**

```
extractData(data, logTransformGaussian = TRUE)
```

**Arguments**

data	The list of data objects, either matrix, phyloseq or ExpressionSet objects
logTransformGaussian	A boolean, should array data be logtransformed

**Value**

the raw data matrices, samples in the rows

**Examples**

```
data(Zhang)
matrixList = extractData(list("microbiome" = zhangMicrobio,
"metabolome" = zhangMetabo))
```

---

extractMat	<i>A function to extract a data matrix from a number of objects</i>
------------	---

---

**Description**

A function to extract a data matrix from a number of objects

**Usage**

```
extractMat(Y, ...)

## S4 method for signature 'ExpressionSet'
extractMat(Y, logTransformGaussian, ...)

## S4 method for signature 'SummarizedExperiment'
extractMat(Y, ...)

## S4 method for signature 'matrix'
extractMat(Y, ...)
```



**Arguments**

Y a phyloseq or eSet object, or another object, or a raw data matrix  
 ... additional arguments for the extractor function  
 logTransformGaussian A boolean, should array data be logtransformed

**Value**

A data matrix with samples in the rows and features in the columns

---

filterConfounders *Filter out the effect of known confounders*

---

**Description**

Filter out the effect of known confounders

**Usage**

```
filterConfounders(confMat, data, distribution, link, invLink,
  compositional, control, meanVarTrend, offSet, numVar, marginModel,
  biasReduction, allowMissingness)
```

**Arguments**

confMat A confounder design matrix  
 data data matrix  
 distribution, link, invLink, compositional, meanVarTrend, offSet, numVar, marginModel  
 Characteristics of the view  
 control A list of control elements to the nleqslv function  
 biasReduction A boolean, should bias reduction be applied  
 allowMissingness A boolean, are missing values allowed?

**Value**

Parameter estimates accounting for the effects of the confounders

---

getInflLatentVar	<i>Extract the influence on the estimation of the latent variable</i>
------------------	---

---

**Description**

Extract the influence on the estimation of the latent variable

**Usage**

```
getInflLatentVar(score, InvJac, i)
```

**Arguments**

score	The score matrix
InvJac	The inverse Jacobian
i	the sample index

**Value**

The influence of all observations on the i-th latent variable

---

gramSchmidtOrth	<i>Gram schmidt orhtogonalize a with respect to b, and normalize</i>
-----------------	--

---

**Description**

Gram schimdt orhtogonalize a with respect to b, and normalize

**Usage**

```
gramSchmidtOrth(a, b, weights = 1, norm = TRUE)
```

**Arguments**

a	the vector to be orthogonalized
b	the vector to be orthogonalized to
weights	weights vector
norm	a boolean, should the result be normalized?

**Value**

The orthogonalized vector

---

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 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

---

inflPlot	<i>A ggplot line plot showing the influences</i>
----------	--

---

**Description**

A ggplot line plot showing the influences

**Usage**

```
inflPlot(modelObj, plotType = ifelse(length(modelObj$data) <= 2,
  "pointplot", "boxplot"), pointFun = "sum", lineSize = 0.07,
  Dim = 1, samples = seq_len(nrow(if (is.null(modelObj$covariates))
    modelObj$latentVars else modelObj$alphas)), ...)
```

**Arguments**

modelObj	The fitted data integration
plotType	The type of plot requested, see details
pointFun	The function to calculate the summary measure to be plotted
lineSize	The line size
Dim	The dimension required
samples	index vector of which samples to be plotted
...	additional arguments passed on to the influence() function

**Details**

The options for plotType are: "pointPlot": Dot plot of total influence per view and sample, "boxplot": plot boxplot of influence of all observations per view and sample, "boxplotSingle": boxplot of log absolute total influence per view, "lineplot": line plot of total influence per view and sample. In the pointplot, dots crosses represent parameter estimates

**Value**

A ggplot object

**Examples**

```
data(Zhang)
#Unconstrained
microMetaboInt = combi(
  list("microbiome" = zhangMicrobio, "metabolomics" = zhangMetabo),
  distributions = c("quasi", "gaussian"), compositional = c(TRUE, FALSE),
  logTransformGaussian = FALSE, verbose = TRUE)
#Constrained
microMetaboIntConstr = combi(
  list("microbiome" = zhangMicrobio, "metabolomics" = zhangMetabo),
  distributions = c("quasi", "gaussian"), compositional = c(TRUE, FALSE),
  logTransformGaussian = FALSE, covariates = zhangMetavars, verbose = TRUE)
load(system.file("extdata", "zhangFits.RData", package = "combi"))
inflPlot(microMetaboInt)
#Constrained
inflPlot(microMetaboIntConstr)
```

---

influence.combi

*Evaluate the influence function*

---

**Description**

Evaluate the influence function

**Usage**

```
## S3 method for class 'combi'
influence(modelObj, samples = is.null(View), Dim = 1,
  View = NULL)
```

**Arguments**

modelObj	The model object
samples	A boolean, should we look at sample variables? Throws an error otherwise
Dim, View	Integers, the dimension and views required

**Details**

Especially the influence of the different views on the latent variable or gradient estimation may be of interest. The influence values are not all calculated. Rather, the score values and inverse jacobian are returned so they can easily be calculated

**Value**

A list with components

score	The evaluation of the score function
InvJac	The inverted jacobian matrix

---

jacConfounders	<i>Jacobian when estimating confounder variables</i>
----------------	--

---

**Description**

Jacobian when estimating confounder variables

**Usage**

```
jacConfounders(confMat, data, distribution, x, meanVarTrend, offSet,
  CompMat, libSizes, allowMissingness)
```

**Arguments**

confMat	Characteristics of the views
data	Characteristics of the views
distribution, offSet	distribution and offset of the view
x	the parameter estimates
meanVarTrend	Characteristics of the views
libSizes, CompMat	Library sizes and relative abundance
allowMissingness	a boolean, should missing values be allowed

**Value**

the jacobian matrix

---

jacConfoundersComp	<i>Jacobian for conditioning under compositionality</i>
--------------------	---

---

**Description**

Jacobian for conditioning under compositionality

**Usage**

```
jacConfoundersComp(x, confMat, data, meanVarTrend, marginModel,
  allowMissingness, biasReduction, subtractMax = TRUE)
```

**Arguments**

x	the parameter estimates
confMat	Characteristics of the views
data	Characteristics of the views
meanVarTrend	Characteristics of the views
marginModel, biasReduction, subtractMax	The marginal mode, and booleans indicating bias reduction and maximum subtraction
allowMissingness	a boolean, should missing values be allowed

**Value**

the jacobian matrix

---

jacFeatures	<i>Evaluate the jacobian for estimating the feature parameters for one view</i>
-------------	---

---

**Description**

Evaluate the jacobian for estimating the feature parameters for one view

**Usage**

```
jacFeatures(latentVars, data, distribution, paramEsts, meanVarTrend,
  offSet, compositional, indepModel, m, paramEstsLower, allowMissingness,
  ...)
```

**Arguments**

latentVars	A vector of latent variables
data	A list of data matrices
distribution, compositional, meanVarTrend, offSet, paramEsts, paramEstsLower, indepModel	Characteristics of each view
m	dimension
allowMissingness	a boolean, are missing values allowed?
...	Additional arguments passed on to the score and jacobian functions

**Value**

The jacobian matrix

---

jacLatentVars	<i>Evaluate the jacobian for estimating the latent variable for one view</i>
---------------	--

---

**Description**

Evaluate the jacobian for estimating the latent variable for one view

**Usage**

```
jacLatentVars(latentVar, data, distribution, paramEsts, paramMats, offSet,
  meanVarTrend, n, varPosts, mm, indepModel, latentVarsLower,
  compositional, allowMissingness, ...)
```

**Arguments**

latentVar	the latent variable estimates
data	Characteristics of the views
distribution, compositional, meanVarTrend, offSet, paramEsts, paramMats, indepModel	Characteristics of each view
n	the number of samples
varPosts	Characteristics of the views
mm	the current dimension
latentVarsLower	the lower dimensional latent variables
allowMissingness	a boolean, should missing values be allowed
...	additional arguments passed on to score and jacobian functions

**Value**

The diagonal of the jacobian matrix

---

jacLatentVarsConstr	<i>Evaluate the jacobian for estimating the latent variable for one view for constrained ordination</i>
---------------------	---

---

### Description

Evaluate the jacobian for estimating the latent variable for one view for constrained ordination

### Usage

```
jacLatentVarsConstr(latentVar, data, distribution, paramEsts, offSet,
  meanVarTrend, numCov, covMat, varPosts, compositional, mm, indepModel,
  latentVarsLower, ...)
```

### Arguments

latentVar	current latent variable estimates
distribution, compositional, meanVarTrend, offSet, paramEsts, indepModel, varPosts, data	Characteristics of each view
numCov	the number of covariates
covMat	the covariates matrix
mm	the dimension
latentVarsLower	latent variable estimates of lower dimensions
...	additional arguments passed on to score and jacobian functions

### Value

The jacobian matrix

---

plot.combi	<i>Make multiplots of the data integration object</i>
------------	---

---

### Description

Make multiplots of the data integration object



**Usage**

```
## S3 method for class 'combi'
plot(x, ..., Dim = c(1, 2), samDf = NULL,
     samShape = NULL, samCol = NULL, featurePlot = "threshold",
     featNum = 15L, samColValues = NULL, manExpFactorTaxa = 0.975,
     featSize = switch(featurePlot, threshold = 2.5, points = samSize * 0.7,
     density = 0.35), crossSize = 4, manExpFactorVar = 0.975,
     varNum = nrow(x$alphas), varSize = 2.5, samSize = 1.75,
     featCols = c("darkblue", "darkgreen", "grey10", "turquoise4", "blue",
     "green", "grey", "cornflowerblue", "lightgreen", "grey75"),
     strokeSize = 0.05, warnMonotonicity = FALSE, returnCoords = FALSE,
     squarePlot = TRUE, featAlpha = 0.5, featShape = 20, xInd = 0,
     yInd = 0, checkOverlap = FALSE, shapeValues = (21:(21 +
     length(unique(samDf[[samShape]]))))))
```

**Arguments**

x	the fit
...	additional arguments, currently ignored
Dim	the dimensions to be plotted
samDf	a dataframe of sample variables
samShape	A variable name from samDf used to shape the samples
samCol	A variable name from samDf used to colour the samples
featurePlot	A character string, either "threshold", "points" or "density". See details
featNum, varNum	The number of features and variables to plot
samColValues	Colours for the samples
manExpFactorTaxa, manExpFactorVar	Expansion factors for taxa and variables, normally calculated natively
featSize, crossSize, varSize, samSize, strokeSize	Size parameters for the features (text, dots or density contour lines), central cross, variable labels, sample dots, sample strokes and feature contour lines
featCols	Colours for the features
warnMonotonicity	A boolean, should a warning be thrown when the feature proportions of compositional views do not all vary monotonically with all latent variables?
returnCoords	A boolean, should coordinates be returned, e.g. for use in third party software
squarePlot	A boolean, should the axes be square? Strongly recommended
featAlpha	Controls the transparency of the features
featShape	Shape of feature dots when featurePlot = "points"
xInd, yInd	x and y indentations
checkOverlap	A boolean, should overlapping labels be omitted?
shapeValues	the shapes, as numeric values

**Details**

It is usually impossible to plot all features with their labels. Therefore, the default option of the 'featurePlot' parameter is "threshold", whereby only the 'featNum' features furthest away from the origin are shown. Alternatively, the "points" or "density" options are available to plot all features as a point or density cloud, but without labels.

**Value**

A ggplot object containing the plot

**Examples**

```
data(Zhang)

#Unconstrained
microMetaboInt = combi(
  list("microbiome" = zhangMicrobio, "metabolomics" = zhangMetabo),
  distributions = c("quasi", "gaussian"), compositional = c(TRUE, FALSE),
  logTransformGaussian = FALSE, verbose = TRUE)
#Constrained
microMetaboIntConstr = combi(
  list("microbiome" = zhangMicrobio, "metabolomics" = zhangMetabo),
  distributions = c("quasi", "gaussian"), compositional = c(TRUE, FALSE),
  logTransformGaussian = FALSE, covariates = zhangMetavars, verbose = TRUE)
#Load the fits
load(system.file("extdata", "zhangFits.RData", package = "combi"))
plot(microMetaboInt)
plot(microMetaboInt, samDf = zhangMetavars, samCol = "ABX")
#Plot all features as points or density
plot(microMetaboInt, samDf = zhangMetavars, samCol = "ABX",
  featurePlot = "points")
plot(microMetaboInt, samDf = zhangMetavars, samCol = "ABX",
  featurePlot = "density")
#Constrained
plot(microMetaboIntConstr, samDf = zhangMetavars, samCol = "ABX")
```

---

polyHorner

*Horner's method to evaluate a polynomial, copied from the polynom package. the most efficient way*

---

**Description**

Horner's method to evaluate a polynomial, copied from the polynom package. the most efficient way

**Usage**

```
polyHorner(coefs, x)
```

**Arguments**

coefs	the polynomial coefficients
x	the input values for the polynomial function

**Value**

the evaluated polynomial

---

predictSpline	<i>A custom spline prediction function, extending linearly with a slope such that prediction never drops below first bisectant</i>
---------------	--

---

**Description**

A custom spline prediction function, extending linearly with a slope such that prediction never drops below first bisectant

**Usage**

```
predictSpline(fit, newdata, linX, coefsQuad, deriv = 0L, meanVarFit,
              minFit, new.knots, degree)
```

**Arguments**

fit	The existing spline fit
newdata	points in which the spline needs to be evaluated
linX	The x at which the fit becomes linear and intersects the diagonal line
coefsQuad	parameters of a quadratic fit
deriv	An integer. Which derivative is required?
meanVarFit	A character string, indicating which type of mean variance fit is being used
minFit	The lower bound of the cubic fit
new.knots	The knots at which the spline is to be evaluated
degree	The degree of the polynomial fit

**Value**

The evaluation of the spline, i.e. the predicted variance

---

prepareJacMat      *prepare the jacobian matrix*

---

**Description**

prepare the jacobian matrix

**Usage**

```
prepareJacMat(mu, data, meanVarTrend, CompMat, libSizes)
```

**Arguments**

mu	the mean matrix
data	the count matrix
meanVarTrend	The mean variance trend
CompMat	The compisition matrix
libSizes	The library sizes

**Value**

the matrix which can be summed over

---

prepareJacMatComp      *prepare the jacobian for the latent variabls compostional*

---

**Description**

prepare the jacobian for the latent variabls compostional

**Usage**

```
prepareJacMatComp(mu, paramEsts, CompMat0, meanVarTrend, data, libSizes)
```

**Arguments**

mu	the mean matrix
paramEsts	Current parameter estimates
CompMat0	The compisition matrix
meanVarTrend	The mean variance trend
data	the count matrix
libSizes	The library sizesv

**Value**

The empty jacobian matrix with entries maximally filled out

---

prepareScoreMat	<i>Prepare a helper matrix for score function evaluation under quasi-likelihood</i>
-----------------	---

---

**Description**

Prepare a helper matrix for score function evaluation under quasi-likelihood

**Usage**

```
prepareScoreMat(data, mu, meanVarTrend, CompMat, libSizes)
```

**Arguments**

data	the count matrix
mu	the mean matrix
meanVarTrend	The mean variance trend
CompMat	The composition matrix
libSizes	The library sizes

**Value**

The helper matrix

---

print.combi	<i>Print an overview of a fitted combi x</i>
-------------	--

---

**Description**

Print an overview of a fitted combi x

**Usage**

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

**Arguments**

x	a fitted combi x
...	Further arguments, currently ignored

**Value**

An overview of the number of dimensions, views and parameters, type of ordination and importance parameters

**Examples**

```

data(Zhang)

#Unconstrained
microMetaboInt = combi(
  list("microbiome" = zhangMicrobio, "metabolomics" = zhangMetabo),
  distributions = c("quasi", "gaussian"), compositional = c(TRUE, FALSE),
  logTransformGaussian = FALSE, verbose = TRUE)
#Constrained
microMetaboIntConstr = combi(
  list("microbiome" = zhangMicrobio, "metabolomics" = zhangMetabo),
  distributions = c("quasi", "gaussian"), compositional = c(TRUE, FALSE),
  logTransformGaussian = FALSE, covariates = zhangMetavars, verbose = TRUE)
#Load the fits
load(system.file("extdata", "zhangFits.RData", package = "combi"))
print(microMetaboInt)
print(microMetaboIntConstr)
#Or simply
microMetaboInt

```

---

quasiJacIndep

*The jacobian for column offset estimation*


---

**Description**

The jacobian for column offset estimation

**Usage**

```
quasiJacIndep(x, data, otherMargin, meanVarTrend, col, libSizes, ...)
```

**Arguments**

x	the initial guess for the current margin
data	the data matrix
otherMargin	The other margin
meanVarTrend	the function describing the mean-variance trend
col	A logical, is the column being estimated?
libSizes	The library sizes
...	passed on to prepareJacMat

**Value**

the jacobian matrix

---

quasiScoreIndep	<i>Quasi score equations for column offset parameters of sequence count data</i>
-----------------	--

---

**Description**

Quasi score equations for column offset parameters of sequence count data

**Usage**

```
quasiScoreIndep(x, data, otherMargin, meanVarTrend, col, libSizes, ...)
```

**Arguments**

x	the initial guess for the current margin
data	the data matrix
otherMargin	The other margin
meanVarTrend	the function describing the mean-variance trend
col	A logical, is the column being estimated?
libSizes	The library sizes
...	passed on to prepareJacMat

**Value**

the evaluated estimating equation

---

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

---

scaleCoords	<i>A helper function to rescale coordinates</i>
-------------	---

---

**Description**

A helper function to rescale coordinates

**Usage**

```
scaleCoords(featsCoords, latentData, manExpFactorTaxa, featNum = NULL)
```

**Arguments**

featsCoords	the feature coordinates to be rescaled
latentData	latent variables
manExpFactorTaxa	an expansion factor
featNum	the number of features to retain

**Value**

The rescaled feature coordinates

---

scoreConfounders	<i>Score functions for confounder variables</i>
------------------	---

---

**Description**

Score functions for confounder variables

**Usage**

```
scoreConfounders(x, data, distribution, offSet, confMat, meanVarTrend,
  allowMissingness, libSizes, CompMat)
```



**Arguments**

x                    the parameter estimates  
 data, distribution, offSet, confMat, meanVarTrend  
                          Characteristics of the views  
 allowMissingness  
                          a boolean, should missing values be allowed  
 libSizes, CompMat  
                          Library sizes and relative abundance

**Value**

The evaluation of the estimating equations

---

scoreConfoundersComp    *Score equations for conditioning under compositionality*

---

**Description**

Score equations for conditioning under compositionality

**Usage**

```
scoreConfoundersComp(x, confMat, data, meanVarTrend, marginModel,
  biasReduction, allowMissingness, subtractMax = TRUE)
```

**Arguments**

x                    Confounder parameter estimates  
 confMat            confounder matrix  
 data                data  
 meanVarTrend    mean variance trend  
 marginModel     marginal models  
 biasReduction    A boolean, should a bias reduced estimation be applied?  
 allowMissingness  
                          A boolean, are missing values allowed  
 subtractMax      A boolean, should the maximum be subtracted before softmax transformation?  
                          Recommended for numerical stability

**Value**

The evaluation of the estimating equations

---

scoreFeatureParams	<i>Evaluate the score functions for the estimation of the feature parameters for a single dataset</i>
--------------------	---

---

**Description**

Evaluate the score functions for the estimation of the feature parameters for a single dataset

**Usage**

```
scoreFeatureParams(x, data, distribution, offSet, latentVar, meanVarTrend,
  mm, indepModel, compositional, paramEstsLower, allowMissingness, ...)
```

**Arguments**

x	the parameter estimates
data, distribution, offSet, meanVarTrend, indepModel, compositional, paramEstsLower	Characteristics of the views
latentVar	the latent variables
mm	the dimension
allowMissingness	a boolean, should missing values be allowed
...	Additional arguments passed on to the score and jacobian functions

**Value**

A vector with evaluated score function

---

scoreLatentVars	<i>Evaluate the score functions for the estimation of the latent variables for a single dataset</i>
-----------------	---

---

**Description**

Evaluate the score functions for the estimation of the latent variables for a single dataset

**Usage**

```
scoreLatentVars(data, distribution, paramEsts, paramMats, offSet,
  latentVar, meanVarTrend, constrained = FALSE, covMat = NULL,
  varPosts, compositional, indepModel, mm, latentVarsLower,
  allowMissingness, ...)
```

**Arguments**

data, distribution, offSet, meanVarTrend, indepModel, varPosts, paramEsts, paramMats, compositional	Characteristics of the views
latentVar	the latent variable estimates
constrained	a boolean, is this a constrained analysis
covMat	a matrix of constraining covariates
mm	the current dimension
latentVarsLower	the lower dimensional latent variables
allowMissingness	a boolean, should missing values be allowed
...	additional arguments passed on to score and jacobian functions

**Value**

A vector of length n, with evaluated score function

---

 seqM

*A small auxiliary function for the indices of the lagrange multipliers*

---

**Description**

A small auxiliary function for the indices of the lagrange multipliers

**Usage**

```
seqM(y, normal = TRUE, nLambdas = 1)
```

**Arguments**

y	an integer, the current dimension
normal	a logical, is there a normalization restriction?
nLambdas	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, data, prevCutOff, minFraction, n)
```

**Arguments**

confounders	a n <sub>x</sub> t confounder matrix
data	the 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'

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zhangMetabo	<i>Metabolomes of mice that underwent Pulsed Antibiotic Treatment (PAT) and controls</i>
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**Description**

Metabolome of mice that underwent Pulsed Antibiotic Treatment (PAT) and controls

**Usage**

```
data(Zhang)
```

**Format**

SummarizedExperiment with metabolome data

**zhangMetabo** The metabolome data as a SummarizedExperiment object

**Source**

<https://www.ibdmdb.org/>

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`zhangMetavars`*Baseline sample variables of PAT and control mice*

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**Description**

Baseline covariates of PAT mice and healthy controls

**Usage**

```
data(Zhang)
```

**Format**

A dataframe with baseline sample variables

**zhangMetavars** The metadata on the mice

**Source**

<https://www.ibdmdb.org/>

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`zhangMicrobio`*Microbiomes of mice that underwent Pulsed Antibiotic Treatment (PAT) and controls*

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**Description**

Microbiome of mice that underwent Pulsed Antibiotic Treatment (PAT) and controls. The data were extracted from the source <https://www.ibdmdb.org/>, and then only the samples matching between microbiome and metabolome were retained.

**Usage**

```
data(Zhang)
```

**Format**

A phyloseq object containing microbiome data

**zhangMicrobio** The microbiome dataset pruned for matches with the metabolome object

**Source**

<https://www.ibdmdb.org/>

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