

Package ‘parafac4microbiome’

July 31, 2025

Title Parallel Factor Analysis Modelling of Longitudinal Microbiome Data

Version 1.3.2

Description Creation and selection of PARAllel FACtor Analysis (PARAFAC) models of longitudinal microbiome data. You can import your own data with our import functions or use one of the example datasets to create your own PARAFAC models. Selection of the optimal number of components can be done using `assessModelQuality()` and `assessModelStability()`. The selected model can then be plotted using `plotPARAFACmodel()`. The Parallel Factor Analysis method was originally described by Carroll and Chang (1970) <[doi:10.1007/BF02310791](https://doi.org/10.1007/BF02310791)> and Harshman (1970) <<https://www.psychology.uwo.ca/faculty/harshman/wpppfac0.pdf>>.

License MIT + file LICENSE

Encoding UTF-8

RoxygenNote 7.3.2

Imports compositions, cowplot, doParallel, dplyr, foreach, ggplot2, ggpubr, lifecycle, magrittr, methods, multiway, parallel, pracma, rlang, rTensor, stats, tidy

Depends R (>= 2.10)

LazyData true

Suggests knitr, phyloseq, rmarkdown, TreeSummarizedExperiment (>= 2.16.1), SummarizedExperiment (>= 1.38.1), testthat (>= 3.0.0), withr, NPLStoolbox

Config/testthat/edition 3

VignetteBuilder knitr

URL <https://grvanderploeg.com/parafac4microbiome/>,
<https://github.com/GRvanderPloeg/parafac4microbiome/>

BugReports <https://github.com/GRvanderPloeg/parafac4microbiome/issues>

NeedsCompilation no

Author Geert Roelof van der Ploeg [aut, cre] (ORCID: <https://orcid.org/0009-0007-5204-3386>),
 Johan Westerhuis [ctb] (ORCID: <https://orcid.org/0000-0002-6747-9779>),
 Anna Heintz-Buschart [ctb] (ORCID: <https://orcid.org/0000-0002-9780-1933>),
 Age Smilde [ctb] (ORCID: <https://orcid.org/0000-0002-3052-4644>),
 University of Amsterdam [cph, fnd]

Maintainer Geert Roelof van der Ploeg <g.r.ploeg@uva.nl>

Repository CRAN

Date/Publication 2025-07-31 10:00:08 UTC

Contents

assessModelQuality	3
assessModelStability	4
calculateFMS	5
calculateSparsity	6
calculateVarExp	7
calcVarExpPerComponent	7
corcondia	8
fac_to_vect	9
flipLoadings	9
Fujita2023	10
importPhyloseq	11
importTreeSummarizedExperiment	12
initializePARAFAC	13
multiwayCenter	14
multiwayCLR	14
multiwayScale	15
parafac	15
parafac_core_als	16
parafac_fun	17
plotModelMetric	18
plotModelStability	18
plotModelITCCs	20
plotPARAFACmodel	20
processDataCube	22
reinflateFac	23
reinflateTensor	24
reshapeData	24
Shao2019	25
sortComponents	26
transformPARAFACloadings	27
vanderPloeg2024	27
vect_to_fac	28

Index	29
--------------	-----------

assessModelQuality	<i>Create randomly initialized models to determine the correct number of components by assessing model quality metrics.</i>
--------------------	---

Description

Create randomly initialized models to determine the correct number of components by assessing model quality metrics.

Usage

```
assessModelQuality(
  X,
  minNumComponents = 1,
  maxNumComponents = 5,
  numRepetitions = 100,
  ctol = 1e-04,
  maxit = 500,
  numCores = 1
)
```

Arguments

X	Input data
minNumComponents	Minimum number of components (default 1).
maxNumComponents	Maximum number of components (default 5).
numRepetitions	Number of randomly initialized models to create (default 100).
ctol	Relative change in loss tolerated to call the algorithm converged in the ALS case (default 1e-4).
maxit	Maximum number of iterations allowed without convergence (default 500).
numCores	Number of cores to use. If set larger than 1, it will run the job in parallel (default 1)

Value

A list object of the following:

- plots: Plots of all assessed metrics and an overview plot showing a summary of all of them.
- metrics: metrics of every created model (number of iterations, sum of squared errors, CORCONDIA score and variance explained).
- models: all created models.

Examples

```
X = Fujita2023$data

# Run assessModelQuality with less strict convergence parameters as example
assessment = assessModelQuality(X,
                                minNumComponents=1,
                                maxNumComponents=3,
                                numRepetitions=5)

assessment$plots$overview
```

`assessModelStability` *Bootstrapping procedure to determine PARAFAC model stability for a given number of components.*

Description

Bootstrapping procedure to determine PARAFAC model stability for a given number of components.

Usage

```
assessModelStability(
  dataset,
  minNumComponents = 1,
  maxNumComponents = 5,
  numFolds = dim(dataset$data)[1],
  considerGroups = FALSE,
  groupVariable = "",
  colourCols = NULL,
  legendTitles = NULL,
  xLabels = NULL,
  legendColNums = NULL,
  arrangeModes = NULL,
  maxit = 500,
  ctol = 1e-04,
  numCores = 1
)
```

Arguments

<code>dataset</code>	See Fujita2023 , Shao2019 or vanderPloeg2024 .
<code>minNumComponents</code>	Minimum number of components (default 1).
<code>maxNumComponents</code>	Maximum number of components (default 5).
<code>numFolds</code>	Number of bootstrapped models to create.

considerGroups	Consider subject groups in calculating sparsity (default FALSE)
groupVariable	Column name in dataset\$mode1 that should be used to consider groups (default "")
colourCols	Vector of strings stating which column names should be factorized for colours per mode.
legendTitles	Vector of strings stating the legend title per mode.
xLabels	Vector of strings stating the x-axis labels per mode.
legendColNums	Vector of integers stating the desired number of columns for the legends per mode.
arrangeModes	Vector of boolean values per mode, stating if the loadings should be arranged according to colourCols (TRUE) or not (FALSE).
maxit	Maximum number of iterations allowed without convergence (default 500).
ctol	Relative change in loss tolerated to call the algorithm converged in the ALS case (default 1e-4).
numCores	Number of cores to use. If set larger than 1, it will run the job in parallel (default 1)

Value

A list containing the following:

- models: All stabilized sign-flipped bootstrapped PARAFAC models.
- modelPlots: A list of plots of the median model with error bars for each number of components.
- FMSplot: A bar plot showing the Factor Match Scores per number of components (see Li et al., 2024).
- FMS: FMS values that the FMS plot is based on.

Examples

```
processedFujita = processDataCube(Fujita2023, sparsityThreshold=0.99, centerMode=1, scaleMode=2)
modelStability = assessModelStability(processedFujita,
                                     minNumComponents=1,
                                     maxNumComponents=2)
```

calculateFMS

Calculate Factor Match Score for all initialized models.

Description

Calculate Factor Match Score for all initialized models.

Usage

```
calculateFMS(models)
```

Arguments

models Output of `parafac()` using `output="all"`.

Value

Vector containing FMS scores of all comparisons

Examples

```
A = array(rnorm(108*2), c(108, 2))
B = array(rnorm(100*2), c(100, 2))
C = array(rnorm(10*2), c(10, 2))
X = reinflateTensor(A, B, C)
models = parafac(X, 2, initialization="random", nstart=10, maxit=2, output="all")
calculateFMS(models)
```

calculateSparsity *Calculate sparsity across the feature mode of a multi-way array.*

Description

Calculate sparsity across the feature mode of a multi-way array.

Usage

```
calculateSparsity(dataset, considerGroups = FALSE, groupVariable = "")
```

Arguments

dataset See [Fujita2023](#), [Shao2019](#) or [vanderPloeg2024](#).

considerGroups Consider subject groups in calculating sparsity (default FALSE)

groupVariable Column name in `dataset$mode1` that should be used to consider groups (default "")

Value

Vector of sparsity fractions ($N \times J$) where N is the number of groups and J is the number of features.

Examples

```
# No groups
sparsity = calculateSparsity(Fujita2023)
length(sparsity)
hist(sparsity)

# Consider groups
colnames(Shao2019$mode1)
sparsity = calculateSparsity(Shao2019, considerGroups=TRUE, groupVariable="Delivery_mode")
```

```
dim(sparsity)
hist(sparsity[,1])
hist(sparsity[,2])
```

calculateVarExp	<i>Calculate the variation explained by a PARAFAC model.</i>
-----------------	--

Description

Calculate the variation explained by a PARAFAC model.

Usage

```
calculateVarExp(Fac, X)
```

Arguments

Fac	Fac object output from the <code>parafac()</code> function.
X	Input data of the PARAFAC model.

Value

The variation explained by the model, expressed as a fraction (between 0-1).

Examples

```
X = Fujita2023$data
model = parafac(X, nfac=1, nstart=1)
calculateVarExp(model$Fac, X)
```

calcVarExpPerComponent	<i>Calculate the variance explained of a PARAFAC model, per component</i>
------------------------	---

Description

Calculate the variance explained of a PARAFAC model, per component

Usage

```
calcVarExpPerComponent(Fac, X)
```

Arguments

Fac	Fac object output of a model
X	Input dataset

Value

Vector of scalars of the percentage of variation explained per component

Examples

```
X = array(rnorm(108*100*10), c(108,100,10))
model = parafac(X, 2)
calcVarExpPerComponent(model$Fac, X)
```

corcondia

Core Consistency Diagnostic (CORCONDIA) calculation

Description

Core Consistency Diagnostic (CORCONDIA) calculation

Usage

```
corcondia(X, Fac)
```

Arguments

X	Input data matrix
Fac	PARAFAC model Fac object

Value

Scalar of the CORCONDIA value

Examples

```
X = Fujita2023$data
model = parafac(X, 2)
corcondia(X, model$Fac)
```

fac_to_vect	<i>Vectorize Fac object</i>
-------------	-----------------------------

Description

Vectorize Fac object

Usage

```
fac_to_vect(Fac)
```

Arguments

Fac Fac object output of [parafac](#).

Value

Vectorized Fac object

Examples

```
set.seed(123)
A = array(rnorm(108*2), c(108, 2))
B = array(rnorm(100*2), c(100, 2))
C = array(rnorm(10*2), c(10, 2))
Fac = list(A, B, C)
v = fac_to_vect(Fac)
```

flipLoadings	<i>Sign flip the loadings of many randomly initialized models to make consistent overview plots.</i>
--------------	--

Description

Sign flip the loadings of many randomly initialized models to make consistent overview plots.

Usage

```
flipLoadings(models, X)
```

Arguments

models Output of [parafac](#).
X Input dataset of parafac modelling procedure.

Value

models with sign flipped components where applicable.

Examples

```
A = array(rnorm(108*2), c(108,2))
B = array(rnorm(100*2), c(100,2))
C = array(rnorm(10*2), c(10,2))
X = reinflateTensor(A, B, C)
models = parafac(X, 2, nstart=10, output="all", sortComponents=TRUE)
flippedModels = flipLoadings(models, X)
```

Fujita2023

Fujita2023 longitudinal microbiome data

Description

The Fujita2023 longitudinal microbiome dataset as a three-dimensional array, with replicates in mode 1, microbial abundances in mode 2 and time in mode 3.

Usage

```
Fujita2023
```

Format

Fujita2023:

A list object with three elements:

data Array object of the data cube

mode1 Dataframe with all the subject metadata, ordered the same as the rows in the data cube.

mode2 Taxonomic classification of the microbiota, ordered the same as the columns in the data cube.

mode3 Dataframe with the time metadata, ordered the same as the third dimension in the array.

...

Source

[doi:10.1186/s40168023014745](https://doi.org/10.1186/s40168023014745)

importPhyloseq *Import Phyloseq object for PARAFAC modelling*

Description

Import Phyloseq object for PARAFAC modelling

Usage

```
importPhyloseq(phyloseqObject, subjectIDs, thirdMode)
```

Arguments

phyloseqObject	Phyloseq object containing at least an otu table and sample data, preferably also taxonomic information.
subjectIDs	Column name in sam_data corresponding to the subject IDs.
thirdMode	Column name in sam_data corresponding to the study design aspect to put in the third mode of the data cube.

Value

List object containing:

- 'data': data cube
- 'mode1': metadata of the subject mode
- 'mode2': taxonomy information
- 'mode3': metadata of the third mode

Examples

```
library(phyloseq)
data(GlobalPatterns)
GP = GlobalPatterns

# Add custom subject IDs to the sample data to make this example work
alteredSampleData = sample_data(GP)
alteredSampleData$subjectID = c(1,2,3,1,2,1,2,3,1,2,1,2,1,2,3,1,2,3,1,2,3,4,5,1,2,3)
df = phyloseq(otu_table(GP), tax_table(GP), alteredSampleData)

# Make a data cube with SampleType (soil, feces, etc.) as the third mode.
result = importPhyloseq(df, subjectIDs = "subjectID", thirdMode="SampleType")
```

```
importTreeSummarizedExperiment
  Import TreeSummarizedExperiment object for PARAFAC modelling
```

Description

Import TreeSummarizedExperiment object for PARAFAC modelling

Usage

```
importTreeSummarizedExperiment(
  treeObject,
  subjectIDs,
  thirdMode,
  taxa_are_rows
)
```

Arguments

treeObject	TreeSummarizedExperiment object containing at least an OTU table and sample information, preferably also taxonomic information.
subjectIDs	Column name in the sample information corresponding to the subject IDs.
thirdMode	Column name in the sample information corresponding to the study design aspect to put in the third mode of the data cube.
taxa_are_rows	Boolean specifying if the taxa are in the rows of the OTU table (TRUE) or not (FALSE).

Value

List object containing:

- 'data': data cube
- 'mode1': metadata of the subject mode
- 'mode2': taxonomy information
- 'mode3': metadata of the third mode

Examples

```
library(TreeSummarizedExperiment)

fakeOTU = t(rTensor::k_unfold(rTensor::as.tensor(Fujita2023$data), 2)@data)
fakeTaxa = as.matrix(Fujita2023$mode2)
fakeSam = as.data.frame(cbind(rep(1:8, 110), rep(1:110, each=8)))
colnames(fakeSam) = c("replicate.id", "timepoint")

fakeTreeObj = TreeSummarizedExperiment(assays = list(Count = fakeOTU),
```

```

                                rowData = fakeSam,
                                colData = fakeTaxa)
dataset = importTreeSummarizedExperiment(fakeTreeObj,
                                         subjectIDs="replicate.id",
                                         thirdMode="timepoint",
                                         taxa_are_rows=FALSE)

```

initializePARAFAC *Initialize PARAFAC algorithm input vectors*

Description

Initialize PARAFAC algorithm input vectors

Usage

```
initializePARAFAC(Tensor, nfac, initialization = "random", output = "Fac")
```

Arguments

Tensor	Input dataset matrix or tensor
nfac	Number of components to initialize.
initialization	Either "random" for random initialization or "svd" for svd based.
output	Output the initialized components as a Fac object ("Fac", default) or as a vector ("vect").

Value

Fac or vector with initialized components.

Examples

```

A = array(rnorm(108,2), c(108,2))
B = array(rnorm(100,2), c(100,2))
C = array(rnorm(10,2), c(10,2))
Tensor = reinflateTensor(A, B, C, returnAsTensor=TRUE)
init = initializePARAFAC(Tensor, 2)

```

multiwayCenter	<i>Center a multi-way array</i>
----------------	---------------------------------

Description

Center a multi-way array

Usage

```
multiwayCenter(X, mode = 1)
```

Arguments

X	Multi-way array
mode	Mode to center across (default 1).

Value

Centered multi-way array

Examples

```
cube_cnt = multiwayCenter(Fujita2023$data)
```

multiwayCLR	<i>Perform a centered log-ratio transform over a multi-way array</i>
-------------	--

Description

Note: Propagates NAs corresponding to missing samples.

Usage

```
multiwayCLR(X, pseudocount = 1)
```

Arguments

X	Multi-way array of counts
pseudocount	Pseudocount value to use (default 1).

Value

CLRed cube

Examples

```
cubeCLR = multiwayCLR(Fujita2023$data)
```

multiwayScale	<i>Scale a multi-way array</i>
---------------	--------------------------------

Description

Scale a multi-way array

Usage

```
multiwayScale(X, mode = 2)
```

Arguments

X	Multi-way array
mode	Mode to scale within: 1=subjects,2=features,3=time (default 2).

Value

Scaled multi-way array

Examples

```
cube_scl = multiwayCenter(Fujita2023$data)
```

parafac	<i>Parallel Factor Analysis</i>
---------	---------------------------------

Description

Parallel Factor Analysis

Usage

```
parafac(  
  Tensor,  
  nfac,  
  nstart = 1,  
  maxit = 500,  
  ctol = 1e-04,  
  initialization = "random",  
  output = "best",  
  sortComponents = FALSE  
)
```

Arguments

Tensor	3-way matrix of numeric data
nfac	Number of factors (components) to fit.
nstart	Number of models to randomly initialize (default 1).
maxit	Maximum number of iterations allowed without convergence (default 500).
ctol	Relative change in loss tolerated to call the algorithm converged in the ALS case (default 1e-4).
initialization	"Random" for randomly initialized input vectors or "nvec" for svd-based best guess.
output	String ("best"/"all") Return only the best model of the nstart models ("best") or return all of them in a list object ("all").
sortComponents	Boolean to sort the components based on their variance explained (default FALSE)

Value

List object of the PARAFAC model or models.

Examples

```
X = array(rnorm(108*100*10), c(108,100,10))
model = parafac(X, 2)
```

parafac_core_als *Internal PARAFAC alternating least-squares (ALS) core algorithm*

Description

Internal PARAFAC alternating least-squares (ALS) core algorithm

Usage

```
parafac_core_als(Tensor, nfac, init, maxit = 500, ctol = 1e-04)
```

Arguments

Tensor	Tensor data object
nfac	Number of components to compute
init	Initialization from initializePARAFAC .
maxit	Maximum number of iterations to run (default 500).
ctol	Loss function tolerance for convergence (default 1e-4)

Value

List containing a Fac object and the loss per iteration

Examples

```

A = array(rnorm(108*2), c(108,2))
B = array(rnorm(100*2), c(100,2))
C = array(rnorm(10*2), c(10,2))
Tensor = reinflateTensor(A, B, C)
init = initializePARAFAC(Tensor, 2)
model = parafac_core_als(Tensor, 2, init)

```

parafac_fun	<i>PARAFAC loss function calculation</i>
-------------	--

Description

PARAFAC loss function calculation

Usage

```
parafac_fun(x, Tensor, lambdas = NULL)
```

Arguments

x	Vector of fitted loadings generated by the PARAFAC algorithm, can also be a Fac object
Tensor	input data
lambdas	If lambdas (from the kruskal tensor case) are generated to make the Fac norm 1, they can be supplied.

Value

Scalar value of the loss function

Examples

```

A = array(rnorm(108*2), c(108,2))
B = array(rnorm(100*2), c(100,2))
C = array(rnorm(10*2), c(10,2))
X = reinflateTensor(A, B, C)
model = parafac(X, 2)
f = parafac_fun(model$Fac, X)

```

plotModelMetric *Plot diagnostics of many initialized PARAFAC models.*

Description

Plot diagnostics of many initialized PARAFAC models.

Usage

```
plotModelMetric(
  metric,
  plottingMode = "box",
  ylabel = "metric",
  titleString = ""
)
```

Arguments

metric	Matrix of metrics per initialized model (number of models x number of components).
plottingMode	Plot the metrics as a box plot ("box", default) or as a bar plot ("bar").
ylabel	String of the y axis label (default "metric").
titleString	String of the plot title (default "").

Value

A plot of the metrics

Examples

```
varExp = array(runif(100*2, min=50, max=100), c(100,2))
plotModelMetric(varExp, plottingMode="box", ylabel="Variation explained (%)")
```

plotModelStability *Plot a summary of the loadings of many initialized parafac models.*

Description

Plot a summary of the loadings of many initialized parafac models.

Usage

```
plotModelStability(
  models,
  dataset,
  colourCols = NULL,
  legendTitles = NULL,
  xLabels = NULL,
  legendColNums = NULL,
  arrangeModes = NULL,
  continuousModes = NULL,
  overallTitle = ""
)
```

Arguments

models	Models list output from <code>parafac()</code> using <code>output="all"</code> .
dataset	A longitudinal microbiome dataset, ideally processed with <code>processDataCube()</code> , formatted as follows: data Array object of the data cube mode1 Dataframe with all the subject metadata, ordered the same as the rows in the data cube. mode2 Taxonomic classification of the microbiota, ordered the same as the columns in the data cube. mode3 Dataframe with the time metadata, ordered the same as the third dimension in the array.
colourCols	Vector of strings stating which column names should be factorized for colours per mode.
legendTitles	Vector of strings stating the legend title per mode.
xLabels	Vector of strings stating the x-axis labels per mode.
legendColNums	Vector of integers stating the desired number of columns for the legends per mode.
arrangeModes	Vector of boolean values per mode, stating if the loadings should be arranged according to <code>colourCols</code> (TRUE) or not (FALSE).
continuousModes	Vector of boolean values per mode, stating if the loadings should be plotted as a line plot (TRUE) or a bar plot (FALSE).
overallTitle	Overall title of the plot.

Value

Plot of loadings with error bars

Examples

```
processedFujita = processDataCube(Fujita2023, sparsityThreshold=0.99, centerMode=1, scaleMode=2)
models = parafac(processedFujita$data, 2, nstart=10, output="all")
plotModelStability(models, processedFujita)
```

plotModelTCCs *Plots Tucker Congruence Coefficients of randomly initialized models.*

Description

Plots Tucker Congruence Coefficients of randomly initialized models.

Usage

```
plotModelTCCs(models)
```

Arguments

models Models list output of `parafac()` using `output="all"`.

Value

Plot of TCCs

Examples

```
processedFujita = processDataCube(Fujita2023, sparsityThreshold=0.99, centerMode=1, scaleMode=2)
models = parafac(processedFujita$data, 3, nstart=10, output="all")
plotModelTCCs(models)
```

plotPARAFACmodel *Plot a PARAFAC model*

Description

Plot a PARAFAC model

Usage

```
plotPARAFACmodel(
  model,
  dataset,
  numComponents,
  colourCols = NULL,
  legendTitles = NULL,
  xLabels = NULL,
  legendColNums = NULL,
  arrangeModes = NULL,
  continuousModes = NULL,
  overallTitle = ""
)
```

Arguments

model	Model output from <code>parafac()</code> .
dataset	A longitudinal microbiome dataset, ideally processed with <code>processDataCube()</code> , formatted as follows: data Array object of the data cube mode1 Dataframe with all the subject metadata, ordered the same as the rows in the data cube. mode2 Taxonomic classification of the microbiota, ordered the same as the columns in the data cube. mode3 Dataframe with the time metadata, ordered the same as the third dimension in the array.
numComponents	Number of PARAFAC components in the model.
colourCols	Vector of strings stating which column names should be factorized for colours per mode.
legendTitles	Vector of strings stating the legend title per mode.
xLabels	Vector of strings stating the x-axis labels per mode.
legendColNums	Vector of integers stating the desired number of columns for the legends per mode.
arrangeModes	Vector of boolean values per mode, stating if the loadings should be arranged according to colourCols (TRUE) or not (FALSE).
continuousModes	Vector of boolean values per mode, stating if the loadings should be plotted as a line plot (TRUE) or a bar plot (FALSE).
overallTitle	Overall title of the plot.

Value

Plot object

Examples

```
library(multiway)
library(dplyr)
library(ggplot2)
set.seed(0)

# Process the data
processedFujita = processDataCube(Fujita2023, sparsityThreshold=0.9, centerMode=1, scaleMode=2)

# Make PARAFAC model
model = parafac(processedFujita$data, nfac=2, nstart=10, verbose=FALSE)

# Make plot
plotPARAFACmodel(model, processedFujita,
  numComponents = 2,
  colourCols = c("", "Genus", ""))
```

```

legendTitles = c("", "Genus", ""),
xLabels = c("Replicate", "Feature index", "Time point"),
legendColNums = c(0,5,0),
arrangeModes = c(FALSE, TRUE, FALSE),
continuousModes = c(FALSE,FALSE,TRUE),
overallTitle = "Fujita PARAFAC model")

```

processDataCube	<i>Process a multi-way array of count data.</i>
-----------------	---

Description

Process a multi-way array of count data.

Usage

```

processDataCube(
  dataset,
  sparsityThreshold = 1,
  considerGroups = FALSE,
  groupVariable = "",
  CLR = TRUE,
  centerMode = 0,
  scaleMode = 0
)

```

Arguments

dataset	A longitudinal microbiome dataset, formatted as follows: data Array object of the data cube filled with counts mode1 Dataframe with all the subject metadata, ordered the same as the rows in the data cube. mode2 Taxonomic classification of the microbiota, ordered the same as the columns in the data cube. mode3 Dataframe with the time metadata, ordered the same as the third dimension in the array. See Fujita2023 , Shao2019 or vanderPloeg2024 for more information.
sparsityThreshold	Maximum sparsity for a feature to be selected (default=1, i.e. do not select features).
considerGroups	Consider groups when calculating sparsity (default=FALSE).
groupVariable	Column name in dataset\$mode1 that should be used to consider groups (default="").
CLR	Perform a centered log-ratio transformation of the count data (default=TRUE).

centerMode	Mode to center across: 1=subjects,2=features,3=time (default 0, i.e. do not center). See multiwayCenter() for more information.
scaleMode	Mode to scale within: 1=subjects,2=features,3=time (default 0, i.e. do not scale). See multiwayScale() for more information.

Value

CLRed, centered and scaled cube

Examples

```
processedCube = processDataCube(Fujita2023)
```

reinflateFac	<i>Calculate Xhat from a model Fac object</i>
--------------	---

Description

Calculate Xhat from a model Fac object

Usage

```
reinflateFac(Fac, X, returnAsTensor = FALSE)
```

Arguments

Fac	Fac object from parafac
X	Input data X
returnAsTensor	Boolean to return Xhat as rTensor tensor (TRUE) or matrix (default, FALSE).

Value

Xhat

Examples

```
processedFujita = processDataCube(Fujita2023, sparsityThreshold=0.99, centerMode=1, scaleMode=2)
model = parafac(processedFujita$data, nfac=1, nstart=1)
Xhat = reinflateFac(model$Fac, processedFujita$data)
```

reinflateTensor	<i>Create a tensor out of a set of matrices similar to a component model.</i>
-----------------	---

Description

Create a tensor out of a set of matrices similar to a component model.

Usage

```
reinflateTensor(A, B, C, returnAsTensor = FALSE)
```

Arguments

A	I x N matrix corresponding to loadings in the first mode for N components.
B	J x N matrix corresponding to loadings in the second mode for N components.
C	K x N matrix corresponding to loadings in the third mode for N components.
returnAsTensor	Boolean return as rTensor S4 tensor object (default FALSE).

Value

M, an I x J x K tensor.

Examples

```
A = rnorm(108)
B = rnorm(100)
C = rnorm(10)
M = reinflateTensor(A,B,C)
```

reshapeData	<i>Reorganize longitudinal microbiome into a data cube ready for PARAFAC modelling.</i>
-------------	---

Description

Reorganize longitudinal microbiome into a data cube ready for PARAFAC modelling.

Usage

```
reshapeData(
  Xlong,
  subjectMetadata,
  featureMetadata,
  timepointMetadata,
  timepointOrder = sort(unique(timepointMetadata))
)
```


Arguments

Xlong	Longitudinal microbiome count data in matrix (long) format.
subjectMetadata	Vector containing the subjects corresponding to the measurements in Xlong.
featureMetadata	Taxonomic classification of the microbiota, ordered the same as the columns in Xlong.
timepointMetadata	Vector containing the time points corresponding to the measurements in Xlong.
timepointOrder	Vector containing the required order of the timepoints in timepointMetadata (default: <code>sort(unique(timepointMetadata))</code>).

Value

#' A list object containing

data Array object of the data cube

mode1 Dataframe with the subjects, ordered the same as the rows in the data cube.

mode2 Taxonomic classification of the microbiota, ordered the same as the columns in the data cube.

mode3 Dataframe with the time metadata, ordered the same as the third dimension in the data cube.

...

Examples

```
library(dplyr)

Xlong = array(rnorm(108*5*10), c(108*5, 10))
subjects = rep(1:108, 5)
features = rep(1:10)
timepoints = rep(1:5, each=108)

dataset = reshapeData(Xlong, subjects, features, timepoints)
```

Shao2019

Shao2019 longitudinal microbiome data

Description

The Shao2019 longitudinal microbiome dataset as a three-dimensional array, with subjects in mode 1, microbial abundances in mode 2 and time in mode 3. Note: only time points 4, 7, 21 and Infancy are used. Note: all-zero microbial abundances have been removed to save disk space.

Usage

Shao2019

Format

Shao2019:

A list object with three elements:

data Array object of the data cube

mode1 Dataframe with all the subject metadata, ordered the same as the rows in the data cube.

mode2 Taxonomic classification of the microbiota, ordered the same as the columns in the data cube.

mode3 Dataframe with the time metadata, ordered the same as the third dimension in the array.

...

Source

[doi:10.1038/s4158601915601](https://doi.org/10.1038/s4158601915601)

sortComponents	<i>Sort PARAFAC components based on variance explained per component.</i>
----------------	---

Description

Sort PARAFAC components based on variance explained per component.

Usage

```
sortComponents(Fac, X)
```

Arguments

Fac	Fac object output of a parafac model
X	Input data

Value

Fac object of sorted components

Examples

```
X = array(rnorm(108*100*10), c(108,100,10))
model = parafac(X, 2)
sortedFac = sortComponents(model$Fac, X)
```

`transformPARAFACloadings`

Transform PARAFAC loadings to an orthonormal basis. Note: this function only works for 3-way PARAFAC models.

Description

Transform PARAFAC loadings to an orthonormal basis. Note: this function only works for 3-way PARAFAC models.

Usage

```
transformPARAFACloadings(Fac, modeToCorrect, moreOutput = FALSE)
```

Arguments

<code>Fac</code>	Fac object from a PARAFAC object, see parafac() .
<code>modeToCorrect</code>	Correct the subject (1), feature (2) or time mode (3).
<code>moreOutput</code>	Give orthonormal basis and transformation matrices as part of output (default FALSE).

Value

Corrected loadings of the specified mode.

Examples

```
processedFujita = processDataCube(Fujita2023, sparsityThreshold=0.99, centerMode=1, scaleMode=2)
model = parafac(processedFujita$data, nfac=2, nstart=1)
transformedA = transformPARAFACloadings(model$Fac, 1)
```

`vanderPloeg2024`

vanderPloeg2024 longitudinal multi-omics dataset

Description

The vanderPloeg2024 longitudinal multi-omics dataset containing six oral microbiome niches, as well as salivary metabolomics and oral health measurements.

Usage

```
vanderPloeg2024
```

Format

vanderPloeg2024:

Each measured dataset contains three elements:

data Array object of the data cube

mode1 Dataframe with all the subject metadata, ordered the same as the rows in the data cube.

mode2 Taxonomic classification of the microbiota, ordered the same as the columns in the data cube.

mode3 Dataframe with the time metadata, ordered the same as the third dimension in the array.

...

Source

[doi:10.1101/2024.03.18.585469](https://doi.org/10.1101/2024.03.18.585469)

vect_to_fac	<i>Convert vectorized output of PARAFAC to a Fac list object with all loadings per mode.</i>
-------------	--

Description

Convert vectorized output of PARAFAC to a Fac list object with all loadings per mode.

Usage

```
vect_to_fac(vect, X, sortComponents = FALSE)
```

Arguments

vect Vectorized output of PARAFAC modelling

X Input data

sortComponents Sort the order of the components by variation explained (default FALSE).

Value

Fac: list object with all loadings in all components per mode, ordered the same way as Z\$modes.

Examples

```
set.seed(123)
A = array(rnorm(108*2), c(108, 2))
B = array(rnorm(100*2), c(100, 2))
C = array(rnorm(10*2), c(10, 2))

X = reinflateTensor(A, B, C)
result = initializePARAFAC(X, 2, initialization="random", output="vect")
Fac = vect_to_fac(result, X)
```

Index

* datasets

Fujita2023, [10](#)
Shao2019, [25](#)
vanderPloeg2024, [27](#)

assessModelQuality, [3](#)
assessModelStability, [4](#)

calculateFMS, [5](#)
calculateSparsity, [6](#)
calculateVarExp, [7](#)
calcVarExpPerComponent, [7](#)
corcondia, [8](#)

fac_to_vect, [9](#)
flipLoadings, [9](#)
Fujita2023, [4](#), [6](#), [10](#), [22](#)

importPhyloseq, [11](#)
importTreeSummarizedExperiment, [12](#)
initializePARAFAC, [13](#), [16](#)

multiwayCenter, [14](#)
multiwayCenter(), [23](#)
multiwayCLR, [14](#)
multiwayScale, [15](#)
multiwayScale(), [23](#)

parafac, [9](#), [15](#), [26](#)
parafac(), [6](#), [7](#), [19–21](#), [27](#)
parafac_core_als, [16](#)
parafac_fun, [17](#)
plotModelMetric, [18](#)
plotModelStability, [18](#)
plotModelTCCs, [20](#)
plotPARAFACmodel, [20](#)
processDataCube, [22](#)
processDataCube(), [19](#), [21](#)

reinflateFac, [23](#)
reinflateTensor, [24](#)

reshapeData, [24](#)

Shao2019, [4](#), [6](#), [22](#), [25](#)
sortComponents, [26](#)

transformPARAFACloadings, [27](#)

vanderPloeg2024, [4](#), [6](#), [22](#), [27](#)
vect_to_fac, [28](#)