Package: parafac4microbiome (via r-universe)

February 24, 2025

Title Parallel Factor Analysis Modelling of Longitudinal Microbiome Data

Version 1.0.3

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 Caroll and Chang (1970) <doi:10.1007/BF02310791> and Harshman (1970) <https://www.psychology.uwo.ca/faculty/harshman/wpppfac0.pdf>.

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Encoding UTF-8

Roxygen list(markdown = TRUE)

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Depends R (>= 2.10)

LazyData true

Suggests knitr, MicrobiotaProcess, phyloseq, rmarkdown, SummarizedExperiment, testthat (>= 3.0.0), TreeSummarizedExperiment, withr

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VignetteBuilder knitr

URL https://grvanderploeg.github.io/parafac4microbiome/, https://github.com/GRvanderPloeg/parafac4microbiome

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Repository https://grvanderploeg.r-universe.dev

RemoteUrl https://github.com/grvanderploeg/parafac4microbiome

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Contents

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

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,
  method = "als",
  ctol = 1e-06,
  maxit = 2500,
  max_fn = 10000,
  rel_tol = 1e-08,
  abs_tol = 1e-08,
  grad_tol = 1e-08,
  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).
`method`	Use ALS algorithm ("als", default) or use all-at-once optimization ("opt"). The all-at-once optimization is based on a nonlinear conjugate gradient method with Hestenes-Stiefel updates and the More-Thuente line search algorithm.
`ctol`	Change in SSQ needed for model to be converged (default 1e-6).
`maxit`	Maximum number of iterations (default 2500).
`max_fn`	Maximum number of function evaluations allowed without convergence in the OPT case (default 10000).
`rel_tol`	Relative change in loss tolerated to call the algorithm converged in the OPT case (default 1e-8).
`abs_tol`	Absolute loss tolerated to call the algorithm converged in the OPT case (default 1e-8).

grad_tol	Tolerance on the two-norm of the gradient divided over the number of elements in the gradient in the OPT case (default 1e-8).
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,
                                ctol=1e-4,
                                maxit=250)
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,
  method = "als",
  ctol = 1e-06,
  maxit = 2500,
  max_fn = 10000,
  rel_tol = 1e-08,
  abs_tol = 1e-08,
  grad_tol = 1e-08,
  numCores = 1
)
```

Arguments

dataset	See Fujita2023, Shao2019 or vanderPloeg2024.
minNumComponents	Minimum number of components (default 1).
maxNumComponents	Maximum number of components (default 5).
numFolds	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).
method	Use ALS algorithm ("als", default) or use all-at-once optimization ("opt"). The all-at-once optimization is based on a nonlinear conjugate gradient method with Hestenes-Stiefel updates and the More-Thuente line search algorithm.
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 in the ALS case (default 500).
max_fn	Maximum number of function evaluations allowed without convergence in the OPT case (default 10000).
rel_tol	Relative change in loss tolerated to call the algorithm converged in the OPT case (default 1e-8).
abs_tol	Absolute loss tolerated to call the algorithm converged in the OPT case (default 1e-8).

grad_tol	Tolerance on the two-norm of the gradient divided over the number of elements in the gradient in the OPT case (default 1e-8).
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,
                                      ctol=1e-4,
                                      maxit=250)
```

---

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 x 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 *Calculate the variation explained by a PARAFAC model.*

Description

Calculate the variation explained by a PARAFAC model.

Usage

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

Arguments

Fac	Fac object output from the parafac() 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$data
model = parafac(X, nfac=1, nstart=1, verbose=FALSE)
calculateVarExp(model$Fac, X)
```

calcVarExpPerComponent *Calculate the variance explained of a PARAFAC model, per component*

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 *Vectorize Fac object*

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

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

`importMicrobiotaProcess` *Import MicrobiotaProcess object for PARAFAC modelling*

Description

Import MicrobiotaProcess object for PARAFAC modelling

Usage

```
importMicrobiotaProcess(MPobject, subjectIDs, thirdMode, taxa_are_rows = TRUE)
```

Arguments

MPobject	MicrobiotaProcess 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(MicrobiotaProcess)

# Generate synthetic data
sample_info = data.frame(Sample = factor(c("S1", "S2", "S3", "S4", "S5")),
                         time = factor(c("T1", "T2", "T1", "T2", "T1")))
otu_table = matrix(runif(25, min = 0, max = 100), nrow = 5, ncol = 5,
                   dimnames = list(paste0("OTU", 1:5), sample_info$Sample))

taxonomy_table = data.frame(OTU = paste0("OTU", 1:5),
                            Kingdom = rep("King", 5),
                            Phylum = rep("Phy", 5),
                            Class = rep("Cla", 5),
                            Order = rep("Ord", 5),
                            Family = rep("Fam", 5),
                            Genus = rep("Gen", 5))

# Create Summarized Experiment
synthetic_SE = SummarizedExperiment::SummarizedExperiment(
               assays = list(otu = otu_table),
               colData = sample_info,
               rowData = taxonomy_table)

# Convert to MicrobiotaProcess object
synthetic_MPSE = as.MPSE(synthetic_SE)

dataset = importMicrobiotaProcess(synthetic_MPSE,
                                  subjectIDs = "Sample",
                                  thirdMode = "time",
```

```
                                    taxa_are_rows = TRUE)
```

`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` *Center a multi-way array*

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` *Perform a centered log-ratio transform over a multi-way array*

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 *Scale a multi-way array*

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 *Parallel Factor Analysis*

Description

Parallel Factor Analysis

Usage

```
parafac(
  Tensor,
  nfac,
  nstart = 1,
  maxit = 500,
  max_fn = 10000,
  ctol = 1e-04,
  rel_tol = 1e-08,
  abs_tol = 1e-08,
  grad_tol = 1e-08,
  initialization = "random",
  method = "als",
  verbose = FALSE,
```

```
  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 in the ALS case (default 500).
max_fn	Maximum number of function evaluations allowed without convergence in the OPT case (default 10000).
ctol	Relative change in loss tolerated to call the algorithm converged in the ALS case (default 1e-4).
rel_tol	Relative change in loss tolerated to call the algorithm converged in the OPT case (default 1e-8).
abs_tol	Absolute loss tolerated to call the algorithm converged in the OPT case (default 1e-8).
grad_tol	Tolerance on the two-norm of the gradient divided over the number of elements in the gradient in the OPT case (default 1e-8).
initialization	"Random" for randomly initialized input vectors or "nvec" for svd-based best guess.
method	Use ALS algorithm ("als", default) or use all-at-once optimization ("opt"). The all-at-once optimization is based on a nonlinear conjugate gradient method with Hestenes-Stiefel updates and the More-Thuente line search algorithm.
verbose	**[Deprecated]** verbose output
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 *PARAFAC loss function calculation*

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)
```

---

parafac_gradient *Calculate gradient of PARAFAC model.*

Description

Calculate gradient of PARAFAC model.

Usage

```
parafac_gradient(x, Tensor)
```

Arguments

x	Vector of fitted loadings generated by the PARAFAC algorithm, can also be a Fac object
Tensor	input data

Value

Gradient of the PARAFAC model.

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)
init = initializePARAFAC(X, 2)
g = parafac_gradient(init, 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 parafac() using output="all".
dataset	A longitudinal microbiome dataset, ideally processed with processDataCube(), 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 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 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 parafac().
dataset	A longitudinal microbiome dataset, ideally processed with processDataCube(), 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` *Process a multi-way array of count data.*

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 *Calculate Xhat from a model Fac object*

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$data, nfac=1, nstart=1, verbose=FALSE)
Xhat = reinflateFac(model$Fac, processedFujita$data)
```

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

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)
```

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/s41586019156O1

`sortComponents` *Sort PARAFAC components based on variance explained per component.*

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

Fac	Fac object from a PARAFAC object, see parafac().
modeToCorrect	Correct the subject (1), feature (2) or time mode (3).
moreOutput	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$data, nfac=2, nstart=1, verbose=FALSE)
transformedA = transformPARAFACloadings(model$Fac, 1)
```

vanderPloeg2024 *vanderPloeg2024 longitudinal microbiome data*

Description

The vanderPloeg2024 longitudinal microbiome dataset as a three-dimensional array, with subjects in mode 1, microbial abundances in mode 2, and time in mode 3. Note: all-zero microbial abundances have been removed to save disk space.

Usage

```
vanderPloeg2024
```

Format

`vanderPloeg2024`**:**

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:10.1101/2024.03.18.585469

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

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)
```

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