

# Package ‘nipalsMCIA’

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**Title** Multiple Co-Inertia Analysis via the NIPALS Method

**Version** 1.0.0

**Description** Computes Multiple Co-Inertia Analysis (MCIA), a dimensionality reduction (jDR) algorithm, for a multi-block dataset using a modification to the Nonlinear Iterative Partial Least Squares method (NIPALS) proposed in (Hanafi et. al, 2010). Allows multiple options for row- and table-level preprocessing, and speeds up computation of variance explained. Vignettes detail application to bulk- and single cell- multi-omics studies.

**License** GPL-3

**URL** <https://github.com/Muunraker/nipalsMCIA>

**BugReports** <https://github.com/Muunraker/nipalsMCIA/issues>

**Depends** R (>= 4.3.0)

**Imports** ComplexHeatmap, dplyr, fgsea, ggplot2 (>= 3.0.0), graphics, grid, methods, MultiAssayExperiment, SummarizedExperiment, pracma, rlang, RSpectra, scales, stats

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## Description

Computes Multiple Co-Inertia Analysis (MCIA), a dimensionality reduction (jDR) algorithm, for a multi-block dataset using a modification to the Nonlinear Iterative Partial Least Squares method (NIPALS) proposed in (Hanafi et. al, 2010). Allows multiple options for row- and table-level preprocessing, and speeds up computation of variance explained. Vignettes detail application to bulk- and single cell- multi-omics studies.

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## See Also

Useful links:

- <https://github.com/Muunraker/nipalsMCIA>
- Report bugs at <https://github.com/Muunraker/nipalsMCIA/issues>

## Description

A function that normalizes an input dataset (data block) according to a variety of options. Intended to be used after column/row-level normalization.

## Usage

```
block_preproc(df, block_preproc_method)
```

**Arguments**

- `df` dataset to preprocess (must be in data matrix form)
- `block_preproc_method` method which is used to normalize blocks, with options:
- `'unit_var'` FOR CENTERED MATRICES ONLY - divides each block by the square root of its variance
  - `'num_cols'` divides each block by the number of variables in the block.
  - `'largest_sv'` divides each block by its largest singular value.
  - `'none'` performs no preprocessing

**Value**

the preprocessed dataset

**Examples**

```
df <- matrix(rbinom(15, 1, prob = 0.3), ncol = 3)
preprocessed_dataframe <- block_preproc(df, "unit_var")
```

---

block\_weights\_heatmap *block\_weights\_heatmap*

---

**Description**

Function to plot heatmap of block score weights

**Usage**

```
block_weights_heatmap(mcia_results)
```

**Arguments**

`mcia_results` MCIA results object returned from `'nipals_multiblock'`

**Details**

Plotting function for heatmap of block score weights

**Value**

heatmap object containing the block weights as a heatmap

**Examples**

```
data(NCI60)
data_blocks_mae <- simple_mae(data_blocks, row_format="sample",
                             colData=metadata_NCI60)
mcia_results <- nipals_multiblock(data_blocks_mae, num_PCs = 10,
                                 plots = "none", tol = 1e-12)
block_weights_heatmap(mcia_results)
```

---

cc\_preproc

*Centered Column Profile Pre-processing*

---

**Description**

Converts data blocks into centered column profiles where each block has unit variance. Mimics the pre-processing in the Omicade4 package (Meng et al. 2014)

**Usage**

```
cc_preproc(df)
```

**Arguments**

df                    the data frame to apply pre-processing to, in "sample" x "variable" format

**Details**

Performs the following steps on a given data frame:

- Offsets data to make whole matrix non-negative
- Divides each column by its sum
- Subtracts (row sum/total sum) from each row
- Multiplies each column by  $\sqrt{\text{column sum/total sum}}$
- Divides the whole data frame by its total variance (the sqrt of the sum of singular values)

**Value**

the processed data frame

**Examples**

```
df <- matrix(rbinom(15, 1, prob = 0.3), ncol = 3)
preprocessed_dataframe <- cc_preproc(df)
```

---

`col_preproc`*Centered Column Profile Pre-processing*

---

### Description

Converts data blocks into centered column profiles where each block has unit variance. Mimics the pre-processing in the Omicade4 package (Meng et al. 2014)

### Usage

```
col_preproc(df, col_preproc_method)
```

### Arguments

`df` the data frame to apply pre-processing to, in "sample" x "variable" format

`col_preproc_method`

denotes the type of column-centered preprocessing. Options are:

- 'colprofile' Performs the following steps on a given data frame:
  - Offsets data to make whole matrix non-negative
  - Divides each column by its sum
  - Subtracts (row sum/total sum) from each row
  - Multiplies each column by  $\sqrt{\text{column sum/total sum}}$
- 'standardized' centers each column and divides by its standard deviation.
- 'centered\_only' ONLY centers data

### Details

Performs preprocessing on a sample/variable (row/column) level according to the parameter given.

### Value

the processed data frame

### Examples

```
df <- matrix(rbinom(15, 1, prob = 0.3), ncol = 3)
preprocessed_dataframe <- col_preproc(df, col_preproc_method = 'colprofile')
```

---

data_blocks	<i>NCI-60 Multi-Omics Data</i>
-------------	--------------------------------

---

**Description**

A dataset of measurements of 12,895 mRNA, 537 miRNA, and 7,016 protein variables (columns) on 21 cancer cell lines (rows) from the NCI-60 cancer cell line database.

**Value**

Large list with 3 elements (one for each omic)

**Source**

Meng et. al, 2016 supplementary materials <https://doi.org/10.1093/bib/bbv108>

**References**

<https://github.com/aedin/NCI60Example>

---

deflate_block_bl	<i>Deflation via block loadings</i>
------------------	-------------------------------------

---

**Description**

Removes data from a data frame in the direction of a given block loadings vector.

**Usage**

```
deflate_block_bl(df, bl)
```

**Arguments**

df	a data frame in "sample" x "variable" format
bl	a block loadings vector in variable space

**Details**

Subtracts the component of each row in the direction of a given block loadings vector to yield a 'deflated' data matrix.

**Value**

the deflated data frame

## Examples

```
df <- matrix(rbinom(15, 1, prob = 0.3), ncol = 3)
block_loading <- rbinom(3, 1, prob = 0.3)
deflated_data <- deflate_block_bl(df, block_loading)
```

---

deflate\_block\_gs      *Deflation via global scores*

---

## Description

Removes data from a data frame in the direction of a given global scores vector.

## Usage

```
deflate_block_gs(df, gs)
```

## Arguments

df                    a data frame in "sample" x "variable" format  
gs                    a global scores vector in sample space

## Details

Subtracts the component of each column in the direction of a given global scores vector to yield a 'deflated' data matrix.

## Value

the deflated data frame

## Examples

```
df <- matrix(rbinom(15, 1, prob = 0.3), ncol = 3)
global_score <- rbinom(5, 1, prob = 0.3)
deflated_data <- deflate_block_gs(df, global_score)
```



---

extract_from_mae	<i>Extract a list of harmonized data matrices from an MAE object</i>
------------------	--

---

**Description**

Extract a list of harmonized data matrices for input into `nipals_multiblock()` from an MAE object

**Usage**

```
extract_from_mae(MAE_object, subset_data = "all")
```

**Arguments**

MAE_object	an MAE object containing experiment data for extraction <code>colData</code> field optional experiments should either be <code>SummarizedExperiment</code> , <code>SingleCellExperiment</code> , or <code>RangedSummarizedExperiment</code> classes
subset_data	<ul style="list-style-type: none"><li>• 'all' use all experiments in MAE object</li><li>• 'c(omic1,omic2,...)' list of omics from <code>names(MAE_object)</code></li></ul>

**Value**

List of harmonized data matrices for input into `nipals_multiblock()`

**Examples**

```
data(NCI60)
data_blocks_mae <- simple_mae(data_blocks,row_format="sample",
                             colData=metadata_NCI60)
NCI60_input = extract_from_mae(data_blocks_mae,subset='all')
```

---

get_colors	<i>Assigning colors to different omics</i>
------------	--

---

**Description**

Creates a list of omics and associated colors for plotting. The default palette was chosen to be color-blindness friendly.

**Usage**

```
get_colors(
  mcia_results,
  color_pal = scales::viridis_pal,
  color_pal_params = list()
)
```

**Arguments**

**mcia\_results**    object returned from nipals\_multiblock() function  
**color\_pal**        a function which returns color palettes (e.g. scales)  
**color\_pal\_params**  
                     list of parameters for the corresponding function

**Value**

List of omics with assigned colors

**Examples**

```

data(NCI60)
data_blocks_mae <- simple_mae(data_blocks, row_format="sample",
                             colData=metadata_NCI60)
mcia_results <- nipals_multiblock(data_blocks_mae, num_PCs = 10,
                                 plots = "none", tol = 1e-12)
colors_omics <- get_colors(mcia_results)
  
```

---

get\_metadata\_colors    *Assigning colors to different values of a metadata column*

---

**Description**

Creates a list of metadata columns and associated colors for plotting. The default palette was chosen to be color-blindness friendly.

**Usage**

```

get_metadata_colors(
  mcia_results,
  color_col,
  color_pal = scales::viridis_pal,
  color_pal_params = list()
)
  
```

**Arguments**

**mcia\_results**    object returned from nipals\_multiblock() function  
**color\_col**        an integer or string specifying the column that will be used for color\_col  
**color\_pal**        a function which returns color palettes (e.g. scales)  
**color\_pal\_params**  
                     list of parameters for the corresponding function

**Value**

List of metadata columns with assigned colors

**Examples**

```
data(NCI60)
data_blocks_mae <- simple_mae(data_blocks, row_format="sample",
                             colData=metadata_NCI60)
mcia_results <- nipals_multiblock(data_blocks_mae, num_PCs = 10,
                                 plots = "none", tol = 1e-12)
colors_omics <- get_metadata_colors(mcia_results, "cancerType",
                                   color_pal_params = list(option = "E"))
```

---

`get_tv`*Computes the total variance of a multi-omics dataset*

---

**Description**

Computes the total variances of all data blocks in a multi-omics dataset, intended for datasets that do not use ‘CCpreproc’

**Usage**

```
get_tv(ds)
```

**Arguments**

`ds` a list of multi-omics dataframes/matrices in "sample x variable" format

**Value**

the total variance of the dataset (i.e. sum of block variances)

**Examples**

```
data(NCI60)
tot_var <- get_tv(data_blocks)
```

---

`global_scores_eigenvalues_plot`*global\_scores\_eigenvalues\_plot*

---

**Description**

Function to plot eigenvalues of scores up to `num_PCs`

**Usage**

```
global_scores_eigenvalues_plot(mcia_results)
```

**Arguments**

`mcia_results` MICA results object returned from ‘`nipals_multiblock`’

**Details**

Plotting function for eigenvalues of scores up to `num_PCs`

**Value**

Displays the contribution plot using eigenvalues

**Examples**

```
data(NCI60)
data_blocks_mae <- simple_mae(data_blocks, row_format="sample",
                             colData=metadata_NCI60)
mcia_results <- nipals_multiblock(data_blocks_mae, num_PCs = 10,
                                plots = "none", tol=1e-12)
global_scores_eigenvalues_plot(mcia_results)
```

---

`global_scores_heatmap` *Plotting a heatmap of global factors scores (sample v. factors)*

---

**Description**

Plots a heatmap of MICA global scores

**Usage**

```
global_scores_heatmap(
  mcia_results,
  color_col = NULL,
  color_pal = scales::viridis_pal,
  color_pal_params = list(option = "D")
)
```

**Arguments**

`mcia_results` the mca object matrix after running MICA, must also contain metadata with columns corresponding to `color_col`

`color_col` an integer or string specifying the column that will be used for `color_col`

`color_pal` a list of colors or function which returns a list of colors

`color_pal_params` a list of parameters for the color function

**Value**

ComplexHeatmap object

---

gsea_report	<i>Perform biological annotation-based comparison</i>
-------------	---

---

**Description**

Runs fgsea for the input gene vector

**Usage**

```
gsea_report(
  metagenes,
  path.database,
  factors = NULL,
  pval.thr = 0.05,
  nproc = 4
)
```

**Arguments**

metagenes	Vector of gene scores where the row names are HUGO symbols
path.database	path to a GMT annotation file
factors	vector of factors which should be analyzed
pval.thr	p-value threshold (default to 0.05)
nproc	number of processors to utilize

**Value**

data frame with the most significant p-value number of significant pathways  
the selectivity scores across the given factors

---

metadata_NCI60	<i>NCI-60 Multi-Omics Metadata</i>
----------------	------------------------------------

---

**Description**

Metadata for the included multi-omics dataset, denoting the cancer type associated with each of the 21 cell lines.

**Value**

List with 21 elements

**Source**

Meng et. al, 2016 supplementary materials <https://doi.org/10.1093/bib/bbv108>

**References**

<https://github.com/aedin/NCI60Example>

---

NipalsResult-class      *An S4 class to contain results computed with ‘nipals\_multiblock()’*

---

**Description**

An S4 class to contain results computed with ‘nipals\_multiblock()’

**Value**

A NipalsResult object.

**Slots**

global\_scores A matrix containing global scores as columns.

global\_loadings A matrix containing global loadings as columns.

block\_score\_weights A matrix containing block weights as columns.

block\_scores A list of matrices. Each matrix contains the scores as columns for a given block.

block\_loadings A list of matrices. Each matrix contains the loadings as columns for a given block.

eigvals A list of singular values of the data matrix at each deflation step.

col\_preproc\_method character for the column-level preprocessing method used. See ‘col\_preproc()’.

block\_preproc\_method character for the block-level preprocessing method used. See ‘block\_preproc()’.

block\_variances A list of variances for each block.

metadata A data frame of metadata originally passed into ‘nipals\_multiblock()’.

---

nipals\_iter                      *NIPALS Iteration*

---

**Description**

Applies one iteration stage/loop of the NIPALS algorithm.

**Usage**

```
nipals_iter(ds, tol = 1e-12, maxIter = 1000, isCentered = FALSE)
```

**Arguments**

<code>ds</code>	a list of data matrices, each in "sample" x "variable" format
<code>tol</code>	a number for the tolerance on the stopping criterion for NIPALS
<code>maxIter</code>	a number for the maximum number of times NIPALS should iterate
<code>isCentered</code>	TRUE if data blocks have feature mean zero, FALSE otherwise

**Details**

Follows the NIPALS algorithm as described by Hanafi et. al. (2010). Starts with a random vector in sample space and repeatedly projects it onto the variable vectors and block scores to generate block and global loadings/scores/weights. The loop stops when either the stopping criterion is low enough, or the maximum number of iterations is reached. Intended as a utility function for ‘nipals\_multiblock’ to be used between deflation steps.

**Value**

a list containing the global/block scores, loadings and weights for a given order

**Examples**

```
data(NCI60)
data_blocks <- lapply(data_blocks, as.matrix)
nipals_results <- nipals_iter(data_blocks, tol = 1e-7, maxIter = 1000)
```

---

`nipals_multiblock`      *Main NIPALS computation loop*

---

**Description**

Applies the full adjusted NIPALS algorithm to generate block and global scores/loadings with the desired deflation method.

**Usage**

```
nipals_multiblock(
  data_blocks_mae,
  col_preproc_method = "colprofile",
  block_preproc_method = "unit_var",
  num_PCs = 10,
  tol = 1e-09,
  max_iter = 1000,
  color_col = NULL,
  deflationMethod = "block",
  plots = "all"
)
```

**Arguments**

<code>data_blocks_mae</code>	a <code>MultiAssayExperiment</code> class object (with sample metadata as a dataframe in the <code>colData</code> attribute).
<code>col_preproc_method</code>	an option for the desired column-level data pre-processing, either: <ul style="list-style-type: none"> <li>• <code>'colprofile'</code> applies column-centering, row and column weighting by contribution to variance.</li> <li>• <code>'standardized'</code> centers each column and divides by its standard deviation.</li> <li>• <code>'centered_only'</code> ONLY centers data</li> </ul>
<code>block_preproc_method</code>	an option for the desired block-level data pre-processing, either: <ul style="list-style-type: none"> <li>• <code>'unit_var'</code> FOR CENTERED MATRICES ONLY - divides each block by the square root of its variance</li> <li>• <code>'num_cols'</code> divides each block by the number of variables in the block.</li> <li>• <code>'largest_sv'</code> divides each block by its largest singular value.</li> <li>• <code>'none'</code> performs no preprocessing</li> </ul>
<code>num_PCs</code>	the maximum order of scores/loadings
<code>tol</code>	a number for the tolerance on the stopping criterion for NIPALS
<code>max_iter</code>	a number for the maximum number of times NIPALS should iterate
<code>color_col</code>	Optional argument with the column name of the <code>'metadata'</code> data frame used to define plotting colors
<code>deflationMethod</code>	an option for the desired deflation method, either: <ul style="list-style-type: none"> <li>• <code>'block'</code> deflation via block loadings (for MCIA, default)</li> <li>• <code>'global'</code> deflation via global scores (for CPCA)</li> </ul>
<code>plots</code>	an option to display various plots of results: <ul style="list-style-type: none"> <li>• <code>'all'</code> displays plots of block scores, global scores, and eigenvalue scree plot</li> <li>• <code>'global'</code> displays only global score projections and eigenvalue scree plot</li> <li>• <code>'none'</code> does not display plots</li> </ul>

**Details**

Follows the NIPALS algorithm as described by Hanafi et. al. (2010). For each order of scores/loadings, the vectors are computed via the `'nipals_iter'` function, then used to deflate the data matrix according to the desired deflation method. This process is repeated up to the desired maximum order of scores/loadings.

**Value**

a `'nipalsResult'` object with the following fields:

- `'global_scores'` a matrix containing global scores as columns (NOT normalized to unit variance)



- ‘global\_loadings’ a matrix containing global loadings as columns
- ‘global\_score\_weights’ a matrix of weights to express global scores as a combination of block scores. Has dimensions "num\_Blocks" by "num\_PCs"
- ‘eigvals’ a matrix containing the eigenvalue for each computed global score.
- ‘block scores’ a list of matrices, each contains the scores for one block
- ‘block loadings’ a list of matrices, each contains the loadings for one block (w/ unit length)
- ‘block score weights’ a matrix containing weights for each block score of each order used to construct the global scores.
- ‘col\_preproc\_method’ the column preprocessing method used on the data.
- ‘block\_variances’ a list of variances of each block AFTER NORMALIZATION OPTION APPLIED
- ‘metadata’ the metadata dataframe supplied with the ‘metadata’ argument. Note: overrides metadata present in any MAE class object.

### Examples

```
data(NCI60)
data_blocks_mae <- simple_mae(data_blocks,row_format="sample",
                             colData=metadata_NCI60)
NIPALS_results <- nipals_multiblock(data_blocks_mae, num_PCs = 10,
                                   tol = 1e-12, max_iter = 1000,
                                   col_preproc_method = "colprofile",
                                   deflationMethod = "block")
MCIA_results <- nipals_multiblock(data_blocks_mae, num_PCs = 4)
CPCA_results <- nipals_multiblock(data_blocks_mae, num_PCs = 4,
                                  deflationMethod = 'global')
```

---

nmb\_get\_bl

*Accessor function for block loadings*


---

### Description

Retrieves the block loadings as a list of matrices from a ‘NipalsResult’ object, typically output from ‘nipals\_multiblock()’.

### Usage

```
nmb_get_bl(nmb_object)
```

### Arguments

nmb\_object      A ‘NipalsResult’ object.

### Value

a list of matrices containing block loadings.

**Examples**

```
data("NCI60")
data_blocks_mae <- simple_mae(data_blocks, row_format="sample",
                              colData=metadata_NCI60)
mcia_out <- nipals_multiblock(data_blocks_mae, num_PCs = 10)
block_loadings<- nmb_get_bl(mcia_out)
```

---

**nmb\_get\_bs***Accessor function for block scores*

---

**Description**

Retrieves the block scores as a list of matrices from a ‘NipalsResult’ object, typically output from ‘nipals\_multiblock()’.

**Usage**

```
nmb_get_bs(nmb_object)
```

**Arguments**

nmb\_object      A ‘NipalsResult’ object.

**Value**

a list of matrices containing block scores.

**Examples**

```
data("NCI60")
data_blocks_mae <- simple_mae(data_blocks, row_format="sample",
                              colData=metadata_NCI60)
mcia_out <- nipals_multiblock(data_blocks_mae, num_PCs = 10)
block_scores <- nmb_get_bs(mcia_out)
```

---

**nmb\_get\_bs\_weights***Accessor function for block score weights*

---

**Description**

Retrieves the block score weights from a ‘NipalsResult’ object, typically output from ‘nipals\_multiblock()’.

**Usage**

```
nmb_get_bs_weights(nmb_object)
```

**Arguments**

nmb\_object      A 'NipalsResult' object.

**Value**

a matrix containing the block score weights.

**Examples**

```
data("NCI60")
data_blocks_mae <- simple_mae(data_blocks, row_format="sample",
                             colData=metadata_NCI60)
mcia_out <- nipals_multiblock(data_blocks_mae, num_PCs = 10)
block_score_weights <- nmb_get_bs_weights(mcia_out)
```

---

nmb\_get\_eigs                      *Accessor function for eigenvalues*

---

**Description**

Retrieves the eigenvalues from a 'NipalsResult' object, typically output from 'nipals\_multiblock()'.

**Usage**

```
nmb_get_eigs(nmb_object)
```

**Arguments**

nmb\_object      A 'NipalsResult' object.

**Value**

a matrix containing the eigenvalues for all global scores.

**Examples**

```
data("NCI60")
data_blocks_mae <- simple_mae(data_blocks, row_format="sample",
                             colData=metadata_NCI60)
mcia_out <- nipals_multiblock(data_blocks_mae, num_PCs = 10)
nipals_eigvals <- nmb_get_eigs(mcia_out)
```

---

nmb\_get\_gl                      *Accessor function for global loadings*

---

**Description**

Retrieves the global loadings as a matrix from a ‘NipalsResult’ object, typically output from ‘nipals\_multiblock()’.

**Usage**

```
nmb_get_gl(nmb_object)
```

**Arguments**

nmb\_object        A ‘NipalsResult’ object.

**Value**

a matrix containing global loadings.

**Examples**

```
data("NCI60")
data_blocks_mae <- simple_mae(data_blocks, row_format="sample",
                             colData=metadata_NCI60)
mcia_out <- nipals_multiblock(data_blocks_mae, num_PCs = 10)
global_loadings <- nmb_get_gl(mcia_out)
```

---

nmb\_get\_gs                      *Accessor function for global scores*

---

**Description**

Retrieves the global scores as a matrix from a ‘NipalsResult’ object, typically output from ‘nipals\_multiblock()’.

**Usage**

```
nmb_get_gs(nmb_object)
```

**Arguments**

nmb\_object        A ‘NipalsResult’ object.

**Value**

a matrix containing global scores.

**Examples**

```

data("NCI60")
data_blocks_mae <- simple_mae(data_blocks, row_format="sample",
                             colData=metadata_NCI60)
mcia_out <- nipals_multiblock(data_blocks_mae, num_PCs = 10)
global_scores <- nmb_get_gs(mcia_out)

```

---

nmb\_get\_metadata      *Accessor function for metadata*

---

**Description**

Retrieves the metadata from a 'NipalsResult' object, typically output from 'nipals\_multiblock()'.

**Usage**

```
nmb_get_metadata(nmb_object)
```

**Arguments**

nmb\_object      A 'NipalsResult' object.

**Value**

a dataframe containing metadata associated with the 'NipalsResult' object.

**Examples**

```

data("NCI60")
data_blocks_mae <- simple_mae(data_blocks, row_format="sample",
                             colData=metadata_NCI60)
mcia_out <- nipals_multiblock(data_blocks_mae, num_PCs = 10)
nipals_metadata <- nmb_get_metadata(mcia_out)

```

---

ord\_loadings      *Ranked global loadings dataframe*

---

**Description**

Creates a dataframe with ranked loadings for a given factor

**Usage**

```
ord_loadings(
  mcia_out,
  omic = "all",
  absolute = FALSE,
  descending = TRUE,
  factor = 1
)
```

**Arguments**

mcia_out	object returned from nipals_multiblock() function
omic	choose an omic to rank, or choose 'all' for all, ((omic = "all", omic = "miRNA", etc.))
absolute	whether to rank by absolute value
descending	whether to rank in descending or ascending order
factor	choose a factor (numeric value from 1 to number of factors in mcia_out)

**Value**

ranked dataframe

**Examples**

```
data(NCI60)
data_blocks_mae <- simple_mae(data_blocks, row_format="sample",
                             colData=metadata_NCI60)
mcia_results <- nipals_multiblock(data_blocks_mae, num_PCs = 10,
                                 plots = "none", tol = 1e-12)
all_pos_1 <- ord_loadings(mcia_out = mcia_results, omic = "all",
                         absolute = FALSE, descending = TRUE, factor = 1)
```

---

predict\_gs

*Prediction of new global scores based on block loadings and weights*

---

**Description**

Uses previously-computed block scores and weights to compute a global score for new data.

**Usage**

```
predict_gs(mcia_results, test_data)
```

**Arguments**

- `mcia_results` an mcia object output by `nipals_multiblock()` containing block scores, weights, and pre-processing identifier.
- `test_data` an MAE object with the same block types and features as the training dataset. Feature and omic order must match 'bl'.

**Details**

Projects the new observations onto each block loadings vector, then weights the projection according to the corresponding block weights.

**Value**

a matrix of predicted global scores for the training data

**Examples**

```
data(NCI60)
data_blocks_mae <- simple_mae(data_blocks, row_format="sample",
                             colData=metadata_NCI60)
mcia_results <- nipals_multiblock(data_blocks_mae, num_PCs = 2)
new_data <- data_blocks_mae # should update with a truly new dataset
preds <- predict_gs(mcia_results, new_data)
```

---

`projection_plot`      *projection\_plot*

---

**Description**

Function to generate a projection plot of MCIA results.

**Usage**

```
projection_plot(
  mcia_results,
  projection,
  orders = c(1, 2),
  block_name = NULL,
  color_col = NULL,
  color_pal = scales::viridis_pal,
  color_pal_params = list(option = "E"),
  legend_loc = "bottomleft",
  color_override = NULL,
  cex = 0.5
)
```

**Arguments**

mcia_results	MCIA results object returned from 'nipals_multiblock'
projection	of plot, with the following options <ul style="list-style-type: none"> <li>• 'all' - scatter plot of two orders of global and block scores (aka factors).</li> <li>• 'global' - scatter plot of two orders of global scores only (aka factors).</li> <li>• 'block' - scatter plot of two orders of block scores only (aka factors) for given block.</li> </ul>
orders	Option to select orders of factors to plot against each other (for projection plots)
block_name	Name of the block to be plotted (if 'projection = block' argument used).
color_col	an integer or string specifying the column that will be used for color_col
color_pal	a list of colors or function which returns a list of colors
color_pal_params	a list of parameters for the color function
legend_loc	Option for legend location, or "none" for no legend.
color_override	Option to override colors when necessary, helpful for projection = "global" or "block"
cex	Resizing parameter for drawing the points

**Details**

Plotting function for a projection plot.

**Value**

Displays the desired plots

**Examples**

```
data(NCI60)
data_blocks_mae <- simple_mae(data_blocks, row_format="sample",
                             colData=metadata_NCI60)
mcia_results <- nipals_multiblock(data_blocks_mae, num_PCs = 10,
                                 plots = "none", tol = 1e-12)
projection_plot(mcia_results, projection = "all", orders = c(1,2),
               color_col = "cancerType", legend_loc = "bottomright")
```

---

simple\_mae

*Create an MAE object from a list of data matrices and column data*

---

**Description**

Create an MAE object from a set of data matrices and column data.



**Usage**

```
simple_mae(matrix_list, row_format = "feature", colData_input = NULL)
```

**Arguments**

`matrix_list`      named list of data matrices

`row_format`        for lists of data frames, indicates whether rows of datasets denote ‘feature’ (default) or ‘sample’.

`colData_input`    a data frame containing sample metadata; sample names in the rownames should correspond to samples names in ‘matrix\_list’

**Details**

Requires that sample names match across experiments and are identical to primary names, will only convert data matrices to SummarizedExperiment class. If the data is more complex, please follow the guidelines for creating an MAE object outlined in ‘help(MultiAssayExperiment)’

**Value**

List of harmonized data matrices for input into `nipals_multiblock()`

**Examples**

```
data(NCI60)
data_blocks_mae <- simple_mae(data_blocks, row_format = "sample",
                              colData = metadata_NCI60)
```

---

<code>vis_load_ord</code>	<i>Visualize ranked loadings</i>
---------------------------	----------------------------------

---

**Description**

Visualize a scree plot of loadings recovered from `nipalsMCIA()` output loadings matrix ranked using the `ord_loadings()` functions

**Usage**

```
vis_load_ord(gl_f_ord, omic_name, colors_omics, n_feat = 15)
```

**Arguments**

`gl_f_ord`            Ranked loading dataframe output from `ord_loadings()` function

`omic_name`          name of the given omic dataset

`colors_omics`      named list of colors associated with omics, output of `get_colors()` function

`n_feat`              number of features to visualize

**Value**

Plot in features for a factor by rank

**Examples**

```
data(NCI60)
data_blocks_mae <- simple_mae(data_blocks, row_format="sample",
                              colData=metadata_NCI60)
mcia_results <- nipals_multiblock(data_blocks_mae, num_PCs = 10,
                                 plots = "none", tol = 1e-12)
all_pos_1 <- ord_loadings(mcia_out = mcia_results, omic = "all",
                          absolute = FALSE, descending = TRUE, factor = 1)
colors_omics <- get_colors(mcia_results)
vis_load_ord(all_pos_1, colors_omics = colors_omics)
```

---

vis\_load\_plot

*Visualize all loadings on two factor axes*

---

**Description**

Visualize all loadings recovered from nipalsMCIA() output loadings matrix ranked using across two factor axes

**Usage**

```
vis_load_plot(mcia_out, axes = c(1, 2), colors_omics)
```

**Arguments**

mcia_out	object returned from nipals_multiblock() function
axes	list of two numbers associated with two factors to visualize
colors_omics	named list of colors associated with omics, output of get_colors() function

**Value**

Plot of MCIA feature loadings for chosen axes

**Examples**

```
data(NCI60)
data_blocks_mae <- simple_mae(data_blocks, row_format="sample",
                              colData=metadata_NCI60)
mcia_results <- nipals_multiblock(data_blocks_mae, num_PCs = 10,
                                 plots = "none", tol = 1e-12)
colors_omics <- get_colors(mcia_results)
vis_load_plot(mcia_results, axes = c(1, 4), colors_omics = colors_omics)
```

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