

# Package ‘nipalsMCIA’

February 21, 2025

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

**Version** 1.5.4

**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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nipalsMCIA-package	<i>nipalsMCIA: Multiple Co-Inertia Analysis via the NIPALS Method</i>
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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>

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block_preproc	<i>Block-level preprocessing</i>
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---

## 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`*NCI-60 Multi-Omics Data*

---

**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`*Deflation via block loadings*

---

**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", harmonize = TRUE)
```

**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>
harmonize	<p>A boolean whether samples should be checked for duplicates</p> <ul style="list-style-type: none"> <li>• 'TRUE' (default) merges duplicate samples via the '<code>MultiAssayExperiment::mergeReplicates</code>' function</li> <li>• 'FALSE' skips sample duplicate check - USE THIS FOR LARGE-SAMPLE DATASETS.</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    MCIA 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 MCIA 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 mcia object matrix after running MCIA, 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	<i>An S4 class to contain results computed with ‘nipals_multiblock()’</i>
--------------------	---

---

**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)
```

**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

**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",
  harmonize = TRUE
)
```

**Arguments**

`data_blocks_mae` a MultiAssayExperiment class object (with sample metadata as a dataframe in the `colData` attribute).

`col_preproc_method` an option for the desired column-level data pre-processing, either:

- ‘colprofile’ applies column-centering, row and column weighting by contribution to variance.
- ‘standardized’ centers each column and divides by its standard deviation.
- ‘centered\_only’ ONLY centers data

`block_preproc_method` an option for the desired block-level data pre-processing, either:

- ‘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

`num_PCs` the maximum order of scores/loadings

`tol` a number for the tolerance on the stopping criterion for NIPALS

`max_iter` a number for the maximum number of times NIPALS should iterate

`color_col` Optional argument with the column name of the ‘metadata’ data frame used to define plotting colors

`deflationMethod` an option for the desired deflation method, either:

- ‘block’ deflation via block loadings (for MCIA, default)
- ‘global’ deflation via global scores (for CPCA)

`plots` an option to display various plots of results:

- ‘all’ displays plots of block scores, global scores, and eigenvalue scree plot
- ‘global’ displays only global score projections and eigenvalue scree plot



---

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	<i>Accessor function for global scores</i>
------------	--

---

**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	<i>Accessor function for metadata</i>
------------------	---------------------------------------

---

**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	<i>Ranked global loadings dataframe</i>
--------------	---

---

**Description**

Creates a dataframe with ranked loadings for a given factor

**Usage**

```

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

```

**Arguments**

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

**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_results = mcia_results, omic = "all",
                        absolute = FALSE, descending = TRUE, factor = 1)

```

---

predict_gs	<i>Prediction of new global scores based on block loadings and weights</i>
------------	--

---

## Description

Uses previously-computed block scores and weights to compute a global score for new data. Only validated for MCIA results, as CPCA loadings aren't compatible with un-deflated data.

## Usage

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

## Arguments

mcia_results	an mcia object output by <code>nipals_multiblock()</code> 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.



---

vis_load_ord	<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(
  mcia_results,
  omic,
  factor = 1,
  n_feat = 15,
  absolute = TRUE,
  descending = TRUE,
  color_pal = scales::viridis_pal,
  color_pal_params = list()
)
```

**Arguments**

mcia_results	object returned from nipals_multiblock() function
omic	name of the given omic dataset
factor	choose a factor (numeric value from 1 to number of factors in mcia_results)
n_feat	number of features to visualize
absolute	whether to rank by absolute value
descending	whether to rank in descending or ascending order
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**

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)
vis_load_ord(mcia_results, omic="mrna")
```

---

vis_load_plot	<i>Visualize all loadings on two factor axes</i>
---------------	--

---

**Description**

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

**Usage**

```
vis_load_plot(  
  mcia_results,  
  axes = c(1, 2),  
  color_pal = scales::viridis_pal,  
  color_pal_params = list()  
)
```

**Arguments**

mcia_results	object returned from nipals_multiblock() function
axes	list of two numbers associated with two factors to visualize
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**

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)  
vis_load_plot(mcia_results, axes = c(1, 4))
```

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