

Package ‘GAPR’

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Title Generalized Association Plots

Version 0.1.5

Description Provides a comprehensive framework for visualizing associations and interaction structures in matrix-formatted data using Generalized Association Plots (GAP). The package implements multiple proximity computation methods (e.g., correlation, distance metrics), ordering techniques including hierarchical clustering (HCT) and Rank-2-Ellipse (R2E) seriation, and optional flipping strategies to enhance visual symmetry. It supports a variety of covariate-based color annotations, allows flexible customization of layout and output, and is suitable for analyzing multivariate data across domains such as social sciences, genomics, and medical research. The method is based on Generalized Association Plots introduced by Chen (2002) <<https://www3.stat.sinica.edu.tw/statistica/J12N1/J12N11/J12N11.html>> and further extended by Wu, Tien, and Chen (2010) <[doi:10.1016/j.csda.2008.09.029](https://doi.org/10.1016/j.csda.2008.09.029)>.

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LinkingTo Rcpp

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Contents

AR	2
--------------	---

computeProximity	2
ellipse_sort	4
GAP	4
GAP_Blue_White_Red	11
GAP_d	12
GAP_Rainbow	12
GAR	12
grayscale_palette	13
hctree_sort	13
RGAR	14
Index	16

AR	<i>Compute the Anti-Robinson (AR) score</i>
----	---

Description

Calculates the total number of Anti-Robinson violations over all triplets in the matrix using the specified ordering. This is equivalent to GAR with a full window.

Usage

AR(mat_sorted)

Arguments

mat_sorted A numeric, symmetric sorted distance matrix.

Value

The AR score (the total number of structural violations).
Please refer to [GAP](#) for complete usage examples.

computeProximity	<i>Compute Proximity Matrix</i>
------------------	---------------------------------

Description

This function takes a numeric matrix and computes a square proximity matrix (similarity or distance) based on a specified method.

Usage

computeProximity(data, proxType, side, isContainMissingValue)

Arguments

data	A numeric matrix with n rows and p columns. Each row typically represents an observation.
proxType	An integer specifying the type of proximity measure to use.
side	An integer indicating the direction for computing proximity.
isContainMissingValue	An integer indicating whether the input data contains missing values.

Details**proxType**

Available proxType options include:

- 0: Euclidean
- 1: Pearson correlation
- 2: Kendall correlation
- 3: Spearman correlation
- 4: Adjusted tangent correlation (atancorr)
- 5: City-block (Manhattan) distance
- 6: Absolute Pearson correlation
- 7: Uncentered correlation
- 8: Absolute uncentered correlation
- 20: Hamman similarity (binary)
- 21: Jaccard index (binary)
- 22: Phi coefficient (binary)
- 23: Rao coefficient (binary)
- 24: Rogers-Tanimoto similarity (binary)
- 25: Simple matching coefficient (binary)
- 26: Sneath coefficient (binary)
- 27: Yule's Q (binary)

Ensure the data type matches the selected method. For example, binary methods should only be used on binary (0/1) data.

side

Use 0 for row-wise proximity and 1 for column-wise proximity.

isContainMissingValue

Set to 1 if the input data includes missing values; otherwise, use 0.

Value

A square matrix representing the proximity between rows or columns, depending on the selected side.

ellipse_sort	<i>Ellipse Sort</i>
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Description

This function applies an Rank-2-Ellipse seriation method to reorder a proximity matrix.

Usage

```
ellipse_sort(data)
```

Arguments

data	A square numeric proximity matrix (either $n \times n$ or $p \times p$), representing pairwise distances or similarities between items.
------	--

Value

An integer vector representing the reordered indices of the matrix rows.

GAP	<i>Generalized Association Plots (GAP)</i>
-----	--

Description

Generates a generalized association plot for the given matrix or data frame, with optional proximity computation, ordering, flipping, coloring, and export options.

Usage

```
GAP(
  data,
  isProximityMatrix = FALSE,
  XdNum = NULL,
  XcNum = NULL,
  YdNum = NULL,
  YcNum = NULL,
  row.name = NULL,
  Xd.name = NULL,
  Xc.name = NULL,
  row.prox = NULL,
  col.prox = NULL,
  show.row.prox = TRUE,
  show.col.prox = TRUE,
  row.order = NULL,
  col.order = NULL,
```

```

    row.flip = NULL,
    col.flip = NULL,
    row.externalOrder = NULL,
    col.externalOrder = NULL,
    original.color = NULL,
    row.color = NULL,
    col.color = NULL,
    Xd.color = NULL,
    Xc.color = NULL,
    Yd.color = NULL,
    Yc.color = NULL,
    row.label.size = NULL,
    col.label.size = NULL,
    Xd.label.size = NULL,
    Xc.label.size = NULL,
    Yd.label.size = NULL,
    Yc.label.size = NULL,
    colorbar.margin = 1.5,
    border = FALSE,
    border.width = 1,
    isContainMissingValue = 0,
    MissingValue.color = "gray",
    exp.row_order = FALSE,
    exp.column_order = FALSE,
    exp.row_names = FALSE,
    exp.column_names = FALSE,
    exp.Xc = FALSE,
    exp.Yc = FALSE,
    exp.Xd = FALSE,
    exp.Yd = FALSE,
    exp.Xd_codebook = FALSE,
    exp.Yd_codebook = FALSE,
    exp.originalmatrix = FALSE,
    exp.row_prox = FALSE,
    exp.col_prox = FALSE,
    PNGfilename = NULL,
    PNGwidth = 1800,
    PNGheight = 1200,
    PNGres = 150,
    show.plot = FALSE
  )

```

Arguments

data A data frame to be visualized.

isProximityMatrix Logical. Whether the input data is already a proximity matrix.

XdNum, XcNum, YdNum, YcNum Integer vectors specifying discrete/continuous covariates on X and Y axes.

`row.name` Either a character vector, or an integer vector to be used as row names.
`Xd.name, Xc.name` Either A string, or a character vector to be used as `Xc.name/Xd.name`.
`row.prox, col.prox` A string indicating the method used to compute row/column proximity.
`show.row.prox, show.col.prox` Logical. Whether to show row/column proximity matrices.
`row.order, col.order` A string specifying the method used to order rows/columns.
`row.flip, col.flip` A string specifying the row/column flipping method.
`row.externalOrder, col.externalOrder` Integer vectors used as external references for flipping.
`original.color` Color palette for the original data matrix.
`row.color, col.color` Color palettes for the row/column proximity matrices.
`Xd.color, Xc.color, Yd.color, Yc.color` Color palettes for covariate matrices.
`row.label.size, col.label.size` Numeric values controlling the font size of row and column labels.
`Xd.label.size, Xc.label.size, Yd.label.size, Yc.label.size` Numeric values controlling the font size of covariate labels for X and Y axes.
`colorbar.margin` Numeric. The margin space between the colorbar and the main plot area.
`border` Logical. Whether to draw borders around each matrix.
`border.width` Numeric value specifying border width.
`isContainMissingValue` Integer. Set to 1 if the input data contains missing values; otherwise, use 0.
`MissingValue.color` Color to represent missing values in the matrix. Default is "gray".
`exp.row_order, exp.column_order` Logical. Whether to export row/column order.
`exp.row_names, exp.column_names` Logical. Whether to export sorted row/column names.
`exp.Xc, exp.Yc, exp.Xd, exp.Yd` Logical. Whether to export sorted covariate matrices.
`exp.Xd_codebook, exp.Yd_codebook` Logical. Whether to export codebooks for discrete covariates.
`exp.originalmatrix` Logical. Whether to export the reordered original matrix.
`exp.row_prox, exp.col_prox` Logical. Whether to export computed proximity matrices (after ordering).
`PNGfilename` A string specifying the output filename for the PNG image.

PNGwidth, PNGheight	Width/height of the PNG image in pixels.
PNGres	Resolution of the PNG image in DPI.
show.plot	Logical. Whether to display the plot in the R graphics window after generation.

Details

isProximityMatrix

If `isProximityMatrix = TRUE`, you may directly provide a proximity matrix as the input data. In this case, the provided proximity matrix is treated as the “original matrix” for visualization; therefore `original.color` and `exp.originalmatrix` control the display of the input matrix (i.e., the proximity matrix). Accordingly, only row-based settings will be applied, such as `row.order`, `row.flip`, `row.externalOrder`, `row.name`, `row.label.size`, `exp.row_order`, and `exp.row_names`. Note that correlation matrices (e.g., “pearson”) must be converted to distance matrices before being used, and the selected color scheme must also be one of the supported diverging palettes (e.g., “GAP_Blue_White_Red”, “BrBG”, “PiYG”, “PRGn”, “PuOr”, “RdBu”, “RdGy”).

XdNum, XcNum, YdNum, YcNum

These parameters are used to specify which columns in data should be treated as covariates on the X or Y axes. Provide the column indices (e.g., `XdNum = c(3, 5)`) of discrete or continuous variables. Discrete covariates (Xd and Yd) are used as provided in the input data and treated as categorical labels.

Xd.name, Xc.name

If not provided, the default labels will be a sequence of numbers based on the number of selected variables (e.g., “1”, “2”, ..., up to the length of `XdNum` or `XcNum`).

row.name

This parameter can be:

- A character vector providing custom row names.
- An integer (column index) indicating a column in data to be used as row names.
- If `row.name = NULL`, the row names will be automatically generated as `1:nrow(data)`.

row.prox, col.prox

Available proximity methods for `row.prox` and `col.prox` include:

- “euclidean”
- “pearson”
- “kendall”
- “spearman”
- “atancorr” (adjusted tangent correlation)
- “city-block” (Manhattan distance)
- “abs_pearson”
- “uncenteredcorr”
- “abs_uncenteredcorr”

- "maximum"
- "canberra"

For binary data, the following methods are supported:

- "hamman"
- "jaccard"
- "phi"
- "rao"
- "rogers"
- "simple"
- "sneath"
- "yule"

show.row.prox, show.col.prox

If set to TRUE, the corresponding proximity matrix will be visualized. If set to FALSE, the proximity matrix will not be shown, but the associated proximity and ordering methods will still be applied. In such cases, the dendrogram (tree structure) will appear alongside the original plot, reflecting the proximity-based ordering.

row.order, col.order

The ordering method determines how the rows or columns are reordered. Supported options include:

- "original" — Use the original data order.
- "random" — Randomly permute the order.
- "reverse" — Reverse the original order.
- "r2e" — Rank-two ellipse ordering.
- "single" — Single-linkage hierarchical clustering.
- "complete" — Complete-linkage hierarchical clustering.
- "average" — Average-linkage hierarchical clustering (UPGMA).
- *any method name from the seriation package* — such as "TSP", "Spectral", "ARSA", etc.

If the ordering method is "original", "random", or "reverse", then proximity matrices are not required, and the parameters `row.prox` or `col.prox` may be left unset.

For all other ordering methods, a proximity matrix must be computed first. Therefore, `row.prox` or `col.prox` must be specified accordingly.

Note: it is necessary to explicitly specify one of the valid ordering options; the function does not assume a default.

row.flip, col.flip

Supported flipping methods include:

- "r2e" — Flip using the rank-two ellipse (R2E) method.
- "uncle" — Apply uncle-flipping based on tree structure.

- "grandpa" — Apply grandpa-flipping based on tree structure.

Usage restrictions:

1. Flipping is only applicable when a hierarchical clustering tree is generated. Therefore, if `row.order` or `col.order` is set to "original", "random", "reverse", "r2e", or a seriation method, tree structures are not built and flipping cannot be applied.
2. When using "r2e" as the ordering method, only "r2e" flipping is allowed. "uncle" or "grandpa" flipping will be ignored.
3. **Do not specify both `externalOrder` and `flip` at the same time.** These options are mutually exclusive. If both are provided, the function will throw an error.

`row.externalOrder`, `col.externalOrder`

External orders are used as references when flipping the hierarchical clustering tree. If a tree is available, the external order guides the flipping of the dendrogram's leaf nodes to better match a predefined sequence.

Important: Do not use `externalOrder` together with `flip`; they are mutually exclusive.

Color settings

The function supports a variety of color palette options for visualizing the original matrix, proximity matrices, and covariate matrices.

Supported built-in palettes include:

- "GAP_Rainbow"
- "GAP_Blue_White_Red"
- "GAP_d"
- "grayscale_palette" (for Binary data)

You may also specify any palette name from the RColorBrewer package. However, note that some palettes—such as those under the "Qualitative" category—are not suitable for visualizing continuous data like proximity matrices. For gray-scale representations of continuous matrices, the "Greys" palette from RColorBrewer can be used.

All palette names must be passed as character strings (e.g., "GAP_Rainbow", "Set1").

original.color: The system will automatically determine the appropriate default color palette based on data type. If the input data is binary, the default is a grayscale palette; otherwise, it defaults to "GAP_Rainbow".

row.color, col.color: The system chooses a default palette based on the proximity method used. For distance-based methods (e.g., "euclidean", "city-block"), the default is "GAP_Rainbow". For correlation-based methods (e.g., "pearson", "spearman"), the default is "GAP_Blue_White_Red".

Xd.color, Yd.color (discrete covariates): The default color palette is "GAP_d", which supports up to 16 distinct categories. If there are more than 16 unique levels, a custom palette should be provided by the user.

Label size settings

Font sizes for axis labels and covariate matrices can be customized individually. Default values are:

- `row.label.size`: 2

- `col.label.size`: 8
- `Xd.label.size`, `Xc.label.size`, `Yd.label.size`, `Yc.label.size`, `Xc.label.size`: 8

You may increase or decrease these values to improve readability depending on figure size and resolution.

Export-related options (exp.*)

When any of the `exp.*` parameters are set to `TRUE`, the corresponding data will be stored in a list and returned by the function. This allows users to programmatically retrieve the order, reordered matrix, proximity matrices, covariate data, or codebooks after plotting.

PNG output settings

The following parameters control the export of the PNG image:

- `PNGfilename`: The name of the PNG file to be saved.
 - The file extension `.png` must be included manually (e.g., `"myplot.png"`).
 - If no file path is specified, the image will be saved in a system-generated temporary directory (via `tempdir()`) using the default filename `"output_plot.png"`.
 - To save the image to a specific location, provide the full path (e.g., `"C:/.../myplot.png"`).
- `PNGwidth`: Width of the output image in pixels. Default = 1800.
- `PNGheight`: Height of the output image in pixels. Default = 1200.
- `PNGres`: Resolution (dots per inch, DPI). Default = 150.

Value

A composite plot (e.g., heatmap with annotations) is saved or displayed. Additional information may be exported based on the settings.

If one or more export-related options (`exp.*`) are set to `TRUE`, the function returns a list containing the requested components. Each element in the list corresponds to an exportable data object,

Examples

```
# Example using the crabs dataset from the MASS package
if (requireNamespace("MASS", quietly = TRUE)) {
  df_crabs <- MASS::crabs
  CRAB_result <- GAP(
    data = df_crabs,
    YdNum = c(1,2),      # First two columns as Y discrete covariates
    YcNum = 3,           # Third column as Y continuous covariate
    row.name = c(1,2,3), # Use First three columns as row names
    row.prox = "euclidean",
    col.prox = "euclidean",
    row.order = "average",
    col.order = "average",
    row.flip = "r2e",
    col.flip = "r2e",
    border = TRUE,
    border.width = 1,
    exp.row_order = TRUE,
```

```

    exp.column_order = TRUE,
    exp.row_names = TRUE,
    exp.column_names = TRUE,
    exp.Yd_codebook = TRUE,
    exp.Yd = TRUE,
    exp.Yc = TRUE,
    exp.originalmatrix = TRUE,
    exp.row_prox = TRUE,
    exp.col_prox = TRUE,
    PNGfilename = file.path(tempdir(), "output_plot.png"),
    show.plot = TRUE
  )

  # Access exported results:
  CRAB_result$row_order      # Row order after ordering
  CRAB_result$column_order  # Column order after ordering
  CRAB_result$row_names     # Row names after ordering
  CRAB_result$column_names  # Column names after ordering
  CRAB_result$Yd_codebook   # Codebook for Y discrete covariates
  CRAB_result$Yd            # Y discrete covariates after ordering
  CRAB_result$Yc            # Y continuous covariates after ordering
  CRAB_result$originalmatrix # Original matrix (after ordering)
  CRAB_result$row_prox      # Row proximity matrix (after ordering)
  CRAB_result$col_prox      # Column proximity matrix (after ordering)

  # Evaluate row ordering quality
  AR(CRAB_result$row_prox)
  GAR(CRAB_result$row_prox, w = 10)
  RGAR(CRAB_result$row_prox, w = 10)
}

```

GAP_Blue_White_Red	<i>Color palette: GAP_Blue_White_Red</i>
--------------------	--

Description

A diverging color palette from blue to white to red, suitable for visualizing correlations.

Usage

```
GAP_Blue_White_Red
```

Format

An object of class character of length 20.

GAP_d	<i>Color palette: GAP_d</i>
-------	-----------------------------

Description

A 16-category discrete color palette.

Usage

GAP_d

Format

An object of class character of length 16.

GAP_Rainbow	<i>Color palette: GAP_Rainbow</i>
-------------	-----------------------------------

Description

A color palette with 13 colors in rainbow used for continuous data.

Usage

GAP_Rainbow

Format

An object of class character of length 13.

GAR	<i>Compute the Generalized Anti-Robinson (GAR) score</i>
-----	--

Description

Calculates the number of Anti-Robinson violations within a specified window *w*, allowing evaluation of local structural consistency in the reordered matrix.

Usage

GAR(mat_sorted, w = NULL)

Arguments

- mat_sorted A numeric, symmetric sorted distance matrix.
- w Window size (integer). If NULL, uses global comparisons (equivalent to AR).

Value

The GAR score (the total number of violations).
Please refer to [GAP](#) for complete usage examples.

grayscale_palette	<i>Color palette: grayscale_palette</i>
-------------------	---

Description

A simple two-color grayscale palette from white to black, often used for binary data visualization.

Usage

grayscale_palette

Format

An object of class character of length 2.

hctree_sort	<i>HCTree Sort</i>
-------------	--------------------

Description

This function applies a hierarchical clustering tree (HCT) sorting algorithm to reorder rows of a proximity matrix. It supports external ordering constraints, different linkage-based order types, and optional flipping for optimal layout.

Usage

hctree_sort(distance_matrix, externalOrder = NULL, orderType, flipType)

Arguments

- distance_matrix A square numeric proximity matrix (either $n \times n$ or $p \times p$) representing pairwise distances between items.
- externalOrder An integer vector specifying an initial or external ordering of the items (can be empty or NULL if not used).
- orderType An integer indicating the type of hierarchical clustering order to apply.
- flipType An integer indicating the flipping methods.

Details

distance_matrix

The input matrix must represent pairwise distances between items. If you start with a similarity matrix (e.g., a correlation matrix), you must convert it to a dissimilarity matrix before use. For example, for correlation-based similarities, use `as.matrix(as.dist(1 - cor_matrix))` or other appropriate transformations to convert it to a proper distance matrix. The matrix should also be symmetric and non-negative.

orderType

Specifies the linkage method used for hierarchical clustering:

- 0: Single-linkage
- 1: Complete-linkage
- 2: Average-linkage (UPGMA)

flipType

Controls how the branches of the clustering tree are flipped:

- 1: Flip based on externalOrder This option should be used only when externalOrder is provided.
- 2: Uncle-flipping
- 3: Grandpa-flipping

Important: Do not specify both `flipType = 1` and a `NULL` or missing `externalOrder`. When using `flipType = 1`, `externalOrder` must be a valid integer vector.

Value

A list representing a dendrogram tree structure, containing: `left`, `right`, and `height` for tree construction, and `order` for the optimal leaf order.

RGAR

Compute the Relative Generalized Anti-Robinson (RGAR) score

Description

This function returns the relative GAR score, representing the proportion of Anti-Robinson violations over the total number of evaluated triplets.

Usage

```
RGAR(mat_sorted, w = NULL)
```

Arguments

<code>mat_sorted</code>	A numeric, symmetric sorted distance matrix.
<code>w</code>	Window size (integer). If <code>NULL</code> , uses global comparisons (equivalent to AR normalized).

Value

The RGAR score (between 0 and 1).

Please refer to [GAP](#) for complete usage examples.

Index

* datasets

GAP_Blue_White_Red, [11](#)

GAP_d, [12](#)

GAP_Rainbow, [12](#)

grayscale_palette, [13](#)

AR, [2](#)

computeProximity, [2](#)

ellipse_sort, [4](#)

GAP, [2](#), [4](#), [13](#), [15](#)

GAP_Blue_White_Red, [11](#)

GAP_d, [12](#)

GAP_Rainbow, [12](#)

GAR, [12](#)

grayscale_palette, [13](#)

hctree_sort, [13](#)

RGAR, [14](#)