

# Package: GPAbin (via r-universe)

May 12, 2026

**Title** Unifying Multiple Biplot Visualisations into a Single Display

**Version** 1.1.1

**Description** Aligning multiple visualisations by utilising generalised orthogonal Procrustes analysis (GPA) before combining coordinates into a single biplot display as described in Nienkemper-Swanepoel, le Roux and Lubbe (2023)<[doi:10.1080/03610918.2021.1914089](https://doi.org/10.1080/03610918.2021.1914089)>. This is mainly suitable to combine visualisations constructed from multiple imputations, however, it can be generalised to combine variations of visualisations from the same datasets (i.e. resamples).

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**Imports** ca, jomo, mi, mice, missMDA, mitools, stringr

**Suggests** testthat, knitr

**Config/Needs/website** rmarkdown

**BugReports** <https://github.com/jnienk/GPAbin/issues>

**URL** <https://jnienk.github.io/GPAbin/>

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**Repository** <https://jnienk.r-universe.dev>

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biplFig	<i>Biplot function</i>
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### Description

Creates a multiple correspondence analysis (MCA) biplot

### Usage

```
biplFig(
  missbp,
  Z.col = "#61223b",
  CLP.col = "#b79962",
  Z.pch = 19,
  CLP.pch = 15,
  Z.cex = 1.5,
  CLP.cex = 1.7,
  title = ""
)
```

### Arguments

missbp	An object of class <code>missbp</code> obtained from preceding function <code>missmi()</code>
Z.col	Colour of sample coordinates
CLP.col	Colour of category level point coordinates
Z.pch	Plotting character of sample coordinates
CLP.pch	Plotting character of category level point coordinates
Z.cex	Size of plotting character for sample points

CLP.cex	Size of plotting character for category level point points
title	Title of the plot

**Value**

- If `compdat = NULL` in `evalMeas`, only a GPABin biplot will be constructed.
- If a complete data set (`compdat`) was specified in `evalMeas`, two biplots will be constructed: (1) Complete MCA biplot and (2) GPABin biplot.

**Examples**

```
data(implist)
missbp <- missmi(implist)|> DRT() |> GPABin() |> biplFig()
```

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CLPpred	<i>Category level prediction</i>
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**Description**

Predicts category levels from an MCA based biplot using the distances between coordinates

**Usage**

```
CLPpred(CLPs = CLPs, Zs = Zs, p = p, n = n, lvls = lvls, datIN = datIN)
```

**Arguments**

CLPs	Category level point coordinates
Zs	Sample coordinates
p	Number of variables
n	Number of samples
lvls	Names of category levels
datIN	Input data from which CLPs and Zs are obtained

**Value**

predCL	Final predicted categorical data set
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compdat

*Complete data example*

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**Description**

Simulated data example

**Format**

A data frame with 1000 rows and 5 columns.

**Details**

V1 Variable 1

V1 Variable 2

V1 Variable 3

V1 Variable 4

V1 Variable 5

**Source**

Simulated data from a uniform distribution that is categorised into levels.

---

DRT

*Dimension reduction*

---

**Description**

Multiple correspondence analysis is performed on the multiple imputed datasets

**Usage**

```
DRT(missbp, method = c("MCA"))
```

**Arguments**

missbp An object of class `missbp` obtained from preceding function `missmi()`

method Select a dimension reduction technique. In the current version MCA is available.

**Value**

The `missbp` object is appended with the following objects:

<code>Z</code>	List of sample coordinates
<code>CLP</code>	List of category level point coordinates
<code>lvls</code>	List of category level names
<code>m</code>	Number of multiple imputations

See also [missmi](#) and [impute](#).

**Examples**

```
data(implist)
missbp <- missmi(implist) |> DRT()
```

---

evalMeas

*Evaluation measures when complete data is available*

---

**Description**

Calculates measures of comparison based on distances between two configurations in two dimensions.

**Usage**

```
evalMeas(missbp, compdat = NULL)
```

**Arguments**

<code>missbp</code>	An object of class <code>missbp</code> obtained from preceding function <code>missmi()</code> .
<code>compdat</code>	Complete data matrix representing the input data of <code>missmi()</code>

**Value**

The `missbp` object is appended with the following objects:

<code>eval</code>	Returns a data table with five evaluation measures: Procrustes Statistic (PS), Similarity Proportion (SP), Response Profile Recovery (RPR), Absolute Mean Bias (AMB), Root Mean Squared Bias (RMSB)
<code>GPAPred</code>	A dataframe representing predicted categorical responses from the GPABin biplot.
<code>compPred</code>	A dataframe representing predicted categorical responses from the complete MCA biplot.
<code>compZs</code>	Sample coordinates for the MCA biplot of the complete data.
<code>compCLPs</code>	CLPs for the MCA biplot of the complete data.

`complvls` Names of the CLPs for the MCA biplot of the complete data.

See also `missmi`, `impute`, `DRT` and `GPABin`.

For more detail, refer to Nienkemper-Swanepoel, J., le Roux, N. J., & Gardner-Lubbe, S. (2021). GPABin: unifying visualizations of multiple imputations for missing values. *Communications in Statistics - Simulation and Computation*, 52(6), 2666–2685. <https://doi.org/10.1080/03610918.2021.1914089>.

## Examples

```
data(compdat)
data(implist)
missbp <- missmi(implist) |> DRT() |> GPABin() |> evalMeas(compdat=compdat)
```

---

`ggbiplFig`

*ggBiplot function*

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## Description

Creates a multiple correspondence analysis (MCA) biplot in `ggplot`.

## Usage

```
ggbiplFig(
  missbp,
  Z.col = "#61223b",
  CLP.col = "#b79962",
  Z.pch = 19,
  CLP.pch = 15
)
```

## Arguments

<code>missbp</code>	An object of class <code>missbp</code> obtained from preceding function <code>missmi()</code>
<code>Z.col</code>	Colour of sample coordinates
<code>CLP.col</code>	Colour of category level point coordinates
<code>Z.pch</code>	Plotting character of sample coordinates
<code>CLP.pch</code>	Plotting character of category level point coordinates

## Value

- `plot` Returns a GPABin `ggplot` biplot.
- `plotC` Returns an MCA `ggplot` biplot of the complete data set, if provided.

**Examples**

```

data(implist)
data(compdat)
missbp <- missmi(implist)|> DRT() |> GPAbin() |>
evalMeas(compdat = compdat) |> ggbiplFig()

### GPAbin biplot

missbp$plot

### MCA biplot

missbp$plotC

```

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GPA

*Generalised Orthogonal Procrustes Analysis*


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**Description**

This function contains the OPA function to compare two configurations and the GPA function for multiple configuration comparisons

**Usage**

```
GPA(Xk, G.target = NULL, iter = 500, eps = 0.001)
```

**Arguments**

Xk	list containing the testee configurations which is updated on #each iteration
G.target	Target configuration. If not specified the centroid configuration will be used as the target
iter	Number of iterations allowed before convergence
eps	Threshold value for convergence of the alogrithm

**Value**

Xk.F	List containing the updated testee configurations
sk.F	Vector containing the final scaling factors
Qk.F	List containing the final rotation matrices
Gmat	Final target configuration
sum.sq	Final minimised sum of squared distance

---

GPABin

*Function to unify coordinates of multiple configurations*

---

### Description

Combines multiple configurations from dimension reduction solutions applied to multiple imputed data sets

### Usage

```
GPABin(missbp, G.target = NULL)
```

### Arguments

<code>missbp</code>	An object of class <code>missmi</code> obtained from preceding function <code>missmi()</code>
<code>G.target</code>	Target configuration. If not specified the centroid configuration will be used as the target.

### Value

The `missbp` object is appended with the following objects:

<code>Z.GPA.list</code>	List containing the sample coordinates for each MI after GPA
<code>CLP.GPA.list</code>	List containing the CLPs for each MI after GPA
<code>G.target</code>	Target configuration
<code>Z.GPABin</code>	Sample coordinates for the GPABin biplot
<code>CLP.GPABin</code>	CLPs for the GPABin biplot

See also [missmi](#), [impute](#) and [DRT](#).

For more detail, refer to Nienkemper-Swanepoel, J., le Roux, N. J., & Gardner-Lubbe, S. (2021). GPABin: unifying visualizations of multiple imputations for missing values. *Communications in Statistics - Simulation and Computation*, 52(6), 2666–2685. <https://doi.org/10.1080/03610918.2021.1914089>.

### Examples

```
data(implist)
missbp <- missmi(implist) |> DRT() |> GPABin()
```

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implist	<i>List of multiple imputed data sets</i>
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---

**Description**

Five multiple imputations of `missdat`

**Format**

List containing five multiple imputations of `missdat`. Each list item a data frame with 1000 rows and 5 columns.

**Details**

**V1** Variable 1

**V1** Variable 2

**V1** Variable 3

**V1** Variable 4

**V1** Variable 5

**Source**

simulated example data imputed with `mice::mice(missdat, m=5, method="polyreg", maxit=10, remove.collinear=FALSE, printFlag = FALSE)`

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impute	<i>Multiple imputation</i>
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**Description**

Choose between four available multiple imputation strategies in R.

**Usage**

```
impute(missbp, imp.method = c("MIMCA", "jomo", "DPMPM", "mice"), m = 5)
```

**Arguments**

<code>missbp</code>	An object of class <code>missmi</code> obtained from preceding function <code>missmi()</code> .
<code>imp.method</code>	Select one of four imputation methods: <code>MIMCA</code> , <code>jomo</code> , <code>DPMPM</code> , <code>mice</code>
<code>m</code>	Number of multiple imputations

**Value**

The `missbp` object is appended with the following object:

`dataimp`            List of imputed data

See also [MIMCA](#), [jomo1cat](#), [mi](#) and [mice](#).

**Examples**

```
data(missdat)
missbp <- missmi(missdat) |> impute(imp.method="DPMPM", m=5)
```

---

<code>missdat</code>	<i>Missing data example</i>
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**Description**

`compdat` containing approximately 35% simulated missing values according to a missing at random (MAR) missing data mechanism

**Format**

A data frame with 1000 rows and 5 columns.

**Details**

**V1** Variable 1

**V1** Variable 2

**V1** Variable 3

**V1** Variable 4

**V1** Variable 5

**Source**

Simulated data from a uniform distribution that is categorised into levels.

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missmi	<i>First step before constructing unified biplots</i>
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**Description**

This function produces a list of elements to be used when producing a GPABin biplot.

**Usage**

```
missmi(data)
```

**Arguments**

data	input data frame or list
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**Value**

X	The processed data
m	Number of multiple imputations applied
n	The number of samples
p	The number of variables
miss_pct	Percentage of missing values

**Examples**

```
data(missdat)
missbp <- missmi(missdat)
data(implist)
missbp <- missmi(implist)
```

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OPA	<i>Orthogonal Procrustes Analysis</i>
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**Description**

This function performs Orthogonal Procrustes Analysis on centred data

**Usage**

```
OPA(missbp, compdat, centring = TRUE, dim = "2D")
```

**Arguments**

missbp	An object of class <code>missmi</code> obtained from preceding function <code>missmi()</code>
compdat	Complete data set, only available for simulated data examples.
centring	Logical argument to apply centering, default is TRUE.
dim	Number of dimensions to use in final solutions (2D or All available dimensions.)

**Value**

ProcStat	Procrustes Statistic
compZ	Sample coordinates representing the complete data set
compCLP	Category level point coordinates representing the complete data set
complvls	Category levels
compdat	Complete data set, only available for simulated data examples

---

`print.missmi`                      *Generic print function for objects of class `missmi`*

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**Description**

This function is used to print output when the `missmi` biplot object is created.

**Usage**

```
## S3 method for class 'missmi'
print(x, ...)
```

**Arguments**

<code>x</code>	an object of class <code>missmi</code> .
<code>...</code>	additional arguments.

**Value**

This function will not produce a return value, it is called for side effects.

**Examples**

```
data(missdat)
missbp <- missmi(missdat)
data(implist)
missbp <- missmi(implist)
print(missbp)
```

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