# Package: bipl5 (via r-universe)

October 15, 2024

**Title** Construct Reactive Calibrated Axes Biplots

**Version** 1.0.2

**Description** A modern view on the principal component analysis biplot with calibrated axes. Create principal component analysis biplots rendered in HTML with significant reactivity embedded within the plot. Furthermore, the traditional biplot view is enhanced by translated axes with inter-class kernel densities superimposed. For more information on biplots, see Gower, J.C., Lubbe, S. and le Roux, N.J. (2011, ISBN: 978-0-470-01255-0).

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**Depends** R (>= 2.10)

**URL** `https://cran.r-project.org/web/packages/bipl5/index.html`

**BugReports** `https://github.com/RuanBuys/bipl5/issues`

**Suggests** testthat (>= 3.0.0)

**Config/testthat/edition** 3

**Repository** https://ruanbuys.r-universe.dev

**RemoteUrl** https://github.com/ruanbuys/bipl5

**RemoteRef** HEAD

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# Contents

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## `bipl5` *bipl5: Constructing Reactive Calibrated Axes Biplots*

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### Description

A modern view on PCA biplot with calibrated axes. Create PCA biplots rendered in HTML with significant reactivity embedded on the plot. Furthermore, the traditional biplot view is enhanced by translated axes with interclass kernel densities superimposed.

### Details

| | |
|---|---|
| Package: | bipl5 |
| Type: | Package |
| Version: | 0.0.0.9400 |
| Date: | 16-10-2023 |
| License: | MIT |
| LazyLoad: | TRUE |

### Author(s)

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### Core Functions

- PCAbiplot
- TDAbiplot
- FMbiplot
- predict.bipl5
- print.bipl5

### Code Availability

The newest version of the package can be obtained on GitHub: `https://github.com/RuanBuys/bipl5`

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## `colorpal` *bipl5 default color scales*

---

### Description

bipl5 default color scales

### Usage

```
colorpal(number = 16)
```

### Arguments

| | |
|---|---|
| `number` | Integer - number of distinct colors to return. Ranges from 1 to 16. |

### Value

Character vector of default colors in `bipl5`. There are sixteen unique colors defined.

### Examples

```
colorpal(number=7)
```

---

## `FMbiplot` *Determine various measures of fit for the PCA biplot*

---

### Description

Print various measures of fit of the biplot display to the console

### Usage

```
FMbiplot(x)
```

### Arguments

| | |
|---|---|
| `x` | An object of class `bipl5` |

## Value

A list returned invisibly containing the following fit measures:

- Cumulative Predictivity
- Marginal Predictivity for the first three principal components
- Marginal Adequacy for the first three principal components
- Overall quality of display

## Examples

```
x<-PCAbiplot(iris[,-5])
FMbiplot(x)
```

---

# `PCAbiplot` *Construct a rank-2 PCA biplot*

## Description

Rank-2 PCA biplots are constructed based on a combination of the first three principal components.

## Usage

```
PCAbiplot(
  x,
  group = NULL,
  scale = TRUE,
  basis = 1:2,
  symbol = "circle",
  color = NULL,
  build_plot = TRUE
)
```

## Arguments

| | |
|---|---|
| `x` | A numeric matrix or data frame of size n x p |
| `group` | Vector of size n representing the class of each observation in x |
| `scale` | Boolean: indicating whether the data matrix should be standardized before SVD is performed. Similar to the `cor` argument in `princomp` |
| `basis` | A vector specifying which eigenvectors serve as basis for the plot. Currently only a biplot of rank 2 is supported. |
| `symbol` | Plotting symbol to be used per class group |
| `color` | Colors to be utilized per class group |
| `build_plot` | Boolean, indicating whether the biplot should be drawn or not. Mostly used in internal function calls serve as basis for the biplot. Currently only a biplot of rank 2 is supported. |

## Details

The method performs Principal Component Analysis (PCA) on the input data and constructs both a traditional biplot using vector representation and with calibrated axes. The data is clustered together on the display by the `group` parameter. The `scale` parameter determines if SVD is performed on the covariance matrix or correlation of `x`. It is highly recommended to set `scale=TRUE` as the rendered display is sensitive to the scaling in `x`.

By default three sets of principal components are used for the scaffolding axes, namely: 1 and 2, 1 and 3, and 2 and 3. The function constructs these biplots in the `plot_ly` graphing library with reactivity embedded on the display. The following features are available on the display:

- A dropdown menu to change the principal components used to construct the display. Currently only the first three pairwise are supported.
- A button to give fit statistics of the biplot. Once clicked, a table is added to give the adequacy and predictivity of each axis for the display.
- A button that inserts a graph depicting the cumulative predictivity of each axis against the dimension of the biplot. See FMbiplot for the coordinates.
- A button that changes the display from vector representation of the variables, to calibrated axes in their original scale. The vector representation includes a unit circle around the origin.
- Prediction lines are inserted onto the display if an observation is clicked. The prediction lines can be removed by clicking on the legend entry.

## Value

A named list of class `bipl5` with the following attributes

| | |
|---|---|
| `x` | A data frame which is the original input data |
| `Z` | A matrix of n x 2 representing the coordinates of each observation on the biplot |
| `rank` | The rank of the approximated data |
| `scale` | Whether the data is standardized prior to performing dimension reduction |
| `group` | The grouping vector of the data |
| `mu` | The vector of column means of the input data |
| `stddev` | Vector of column standard deviations if the scale parameter is set to TRUE. |
| `PCA` | The singular value decomposition of the covariance/correlation matrix, see `svd` |
| `bipl` | The plotly graph displaying the biplot, see `plot_ly` |
| `Adequacy` | The adequacy of each axis displayed for each set of principal components |
| `Predictivity` | The predictivity of each axis displayed for each set of principal components |

## See Also

`print.bipl5` to display the biplot graph and further see `TDAbiplot` to draw a biplot with calibrated density axes. Fit measures can be obtained by `FMbiplot`

### Examples

```
## Consruct a biplot with
x<-PCAbiplot(iris[,1:4],group=iris[,5])
#alternatively
print(x)

## Construct a biplot that preserves the correlation structure among the
## variables
y<-PCAbiplot(iris[,-5],group=iris[,5],scale=TRUE)
```

---

## `plot.bipl5` *Plot an object of class* `bipl5`

### Description

Plot an object of class `bipl5`

### Usage

```
## S3 method for class 'bipl5'
plot(x, y = NULL, ...)
```

### Arguments

| | |
|---|---|
| `x` | An object of class `bipl5` |
| `y` | Unsupported |
| `...` | Unsupported |

### Value

A `plot_ly` graph containing the biplot

### Examples

```
x<-PCAbiplot(iris[,-5])
plot(x)
```

---

## `predict.bipl5` *Method to obtain the predicted or fitted values of the biplot*

---

### Description

Extract the fitted values of the biplot display

### Usage

```
## S3 method for class 'bipl5'
predict(object, ..., kable.args = NULL)
```

### Arguments

| | |
|---|---|
| `object` | An object of class `bipl5` from which predicted values are to be obtained |
| `...` | Not used |
| `kable.args` | Additional arguments to be passes to the `kable` function, |

### Value

The function invisibly returns the predicted values of the biplot display, and outputs the predicted values via the `kable` function

### Examples

```
kable.args<-list()
kable.args$format<-"pipe"
x<-PCAbiplot(iris[,-5])
predict(x,kable.args)
```

---

## `print.bipl5` *Default print method for an object of class* `bipl5`

---

### Description

Default print method for an object of class `bipl5`

### Usage

```
## S3 method for class 'bipl5'
print(x, ..., plot = TRUE)
```

### Arguments

| | |
|---|---|
| `x` | Object of class `bipl5` |
| `...` | Additional parameters |
| `plot` | Boolean. Whether or not to display the plot |

### Value

The object is returned invisibly

### Examples

```
x<-PCAbiplot(iris[,1:4],group=iris[,5])
print.bipl5(x)
```

---

## `Symbol_List` *Retrieve all valid plotting symbols for the* `plotly` *library*

### Description

Retrieve all valid plotting symbols for the `plotly` library

### Usage

```
Symbol_List()
```

### Value

A vector of all the valid plotting symbols used in the `plot_ly` library.

### Examples

```
Symbol_List()
```

---

## `TDAbiplot` *Construct PCA biplots with translated calibrated density axes*

### Description

Construct various rank-2 PCA biplots with translated axes based on a combination of the first three principal components.

### Usage

```
TDAbiplot(
  x,
  dist = NULL,
  inflate = 1,
  alpha = 0.95,
  alpha_Elip = NULL,
  swop = FALSE,
  density.args = NULL,
  color = NULL,
```

```
  symbol = "circle"
)

## S3 method for class 'bipl5'
TDAbiplot(
  x,
  dist = NULL,
  inflate = 1,
  alpha = 0.95,
  alpha_Elip = NULL,
  swop = FALSE,
  density.args = NULL,
  color = NULL,
  symbol = "circle"
)
```

## Arguments

| | |
|---|---|
| `x` | An object of class `bipl5`. See `PCAbiplot` in this regard. |
| `dist` | Minimum distance between each axis. Default is roughly 12.5% of the plot diameter |
| `inflate` | Density inflation factor |
| `alpha` | Argument passes to `alpha_Elip` |
| `alpha_Elip` | A function taking two arguments, Z and alpha. The output of the function should be a two-column matrix of coordinates which will be used to construct an alpha-ellipse. See details below. |
| `swop` | Swop the direction which to which each axis is translated |
| `density.args` | Arguments to be passed to the density function |
| `color` | Colors to be utilized per class group |
| `symbol` | Plotting symbol to be used per class group |

## Details

This function produces a PCA biplot with translated calibrated axes. The function constructs this biplot in the `plot_ly` graphing library with reactivity embedded on the display. The following features are available on the display:

- A dropdown menu to change the principal components used to construct the display. Currently only the first three pairwise are supported.
- A button to give fit statistics of the biplot. Once clicked, a table is added to give the adequacy and predictivity of each axis for the display.
- A button that inserts a graph depicting the cumulative predictivity of each axis against the dimension of the biplot.
- Prediction lines are inserted onto the display if an observation is clicked. The prediction lines can be removed by clicking on the legend entry.

The `alpha_Elip` argument is used to subset the biplot plotting coordinates (Z) to remove the effect of outliers in the data. A common suggestion is to use an alphabag or on Convex hull peeling algorithm to strip away extreme points. The alpha-ellipse will be constructed around this data, and will impact the lengths of the calibrated axes.

## Value

A named list of class `bipl5`, see `PCAbiplot`, with the following attributes:

| | |
|---|---|
| `x` | A data frame which is the original input data |
| `Z` | A matrix of n x 2 representing the coordinates of each observation on the biplot |
| `rank` | The rank of the approximated data |
| `scale` | Whether the data is standardized prior to performing dimension reduction |
| `group` | The grouping vector of the data |
| `mu` | The vector of column means of the input data |
| `stddev` | Vector of column standard deviations if the scale parameter is set to TRUE. |
| `PCA` | The singular value decomposition of the covariance/correlation matrix, see `svd` |
| `plot` | The plotly graph displaying the biplot, see `plot_ly` |
| `Adequacy` | The adequacy of each axis displayed for each set of principal components |
| `Predictivity` | The predictivity of each axis displayed for each set of principal components |

## See Also

PCAbiplot FMbiplot

## Examples

```
## Simple illustration of a calibrated density axis biplot
x<-PCAbiplot(iris[,-5],group=iris[,5])
TDAbiplot(x,dist=1,inflate=1)

## Change the plotting characters of class-groups:
y<- x |> TDAbiplot(dist=1,inflate=1,symbol=c("circle","diamond","square"))

## Custom kernel densities can be drawn on the axes:
density.args<-list()
density.args$kernel <- "optcosine"
density.args$bw <- "sj"

y<- x |> TDAbiplot(dist=1,inflate=1,density.args=density.args)

## To lessen the effects of outliers, a smaller alpha-ellipse can be
## used to determine axis lengths. Define a function that strips away
## outliers, for example a convex hull peeling algorithm:

HullPeeling <- function(x,alpha) {
  n<-nrow(x)
  propinside<-1
```

```
    target<-1-alpha
    x2<-x
    while (propinside>target) {
      hull<-grDevices::chull(x2)
      x2old<-x2
      x2<-x2[-hull,]
      propinside<-nrow(x2)/n
    }
      return(x2[grDevices::chull(x2),])
  }

  y<- x |> TDAbiplot(dist=1,inflate=1, alpha_Elip=HullPeeling, alpha=0.4)
```

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