

# Package: ggbiplot (via r-universe)

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**Type** Package

**Title** A ggplot2 based biplot

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**Description** A ggplot2 based biplot. It provides a drop-in replacement for biplot.princomp(). It implements a biplot and scree plot using ggplot2.

**Depends** ggplot2, plyr, scales, grid

**License** GPL-2

**URL** <http://github.com/vqv/ggbiplot>

**Collate** 'ggbiplot.r' 'ggscreeplot.r'

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

**RemoteUrl** <https://github.com/vqv/ggbiplot>

**RemoteRef** HEAD

**RemoteSha** f7ea76da44ee68cc0ab68c35202e1dab06aaa027

## Contents

ggbiplot . . . . .	2
ggscreeplot . . . . .	3
wine . . . . .	3

<b>Index</b>	<b>5</b>
--------------	----------

ggbiplot

*Biplot for Principal Components using ggplot2***Description**

Biplot for Principal Components using ggplot2

**Usage**

```
ggbiplot(pcoobj, choices = 1:2, scale = 1, pc.biplot =
TRUE, obs.scale = 1 - scale, var.scale = scale, groups =
NULL, ellipse = FALSE, ellipse.prob = 0.68, labels =
NULL, labels.size = 3, alpha = 1, var.axes = TRUE, circle
= FALSE, circle.prob = 0.69, varname.size = 3,
varname.adjust = 1.5, varname.abbrev = FALSE, ...)
```

**Arguments**

pcobj	an object returned by pcomp() or princomp()
choices	which PCs to plot
scale	covariance biplot (scale = 1), form biplot (scale = 0). When scale = 1, the inner product between the variables approximates the covariance and the distance between the points approximates the Mahalanobis distance.
obs.scale	scale factor to apply to observations
var.scale	scale factor to apply to variables
pc.biplot	for compatibility with biplot.princomp()
groups	optional factor variable indicating the groups that the observations belong to. If provided the points will be colored according to groups
ellipse	draw a normal data ellipse for each group?
ellipse.prob	size of the ellipse in Normal probability
labels	optional vector of labels for the observations
labels.size	size of the text used for the labels
alpha	alpha transparency value for the points (0 = TRUEransparent, 1 = opaque)
circle	draw a correlation circle? (only applies when pcomp was called with scale = TRUE and when var.scale = 1)
var.axes	draw arrows for the variables?
varname.size	size of the text for variable names
varname.adjust	adjustment factor the placement of the variable names, >= 1 means farther from the arrow
varname.abbrev	whether or not to abbreviate the variable names

**Value**

a ggplot2 plot

**Examples**

```
data(wine)
wine.pca <- prcomp(wine, scale. = TRUE)
print(ggbiplot(wine.pca, obs.scale = 1, var.scale = 1, groups = wine.class, ellipse = TRUE, circle = TRUE))
```

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ggscreeplot

*Screepplot for Principal Components*

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**Description**

Screepplot for Principal Components

**Usage**

```
ggscreeplot(pcobj, type = c("pev", "cev"))
```

**Arguments**

pcobj	an object returned by prcomp() or princomp()
type	the type of scree plot. 'pev' corresponds proportion of explained variance, i.e. the eigenvalues divided by the trace. 'cev' corresponds to the cumulative proportion of explained variance, i.e. the partial sum of the first k eigenvalues divided by the trace.

**Examples**

```
data(wine)
wine.pca <- prcomp(wine, scale. = TRUE)
print(ggscreeplot(wine.pca))
```

---

wine

*Chemical composition of three cultivars of wine*

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**Description**

Chemical constituents of wines from three different cultivars grown in the same region in Italy. The cultivars, 'barolo', 'barbera', and 'grignolino', are indicated in wine.class.

**Usage**

```
data(wine)
```

**Format**

The format is: chr "wine"

**Source**

<http://archive.ics.uci.edu/ml/datasets/Wine>

**Examples**

```
data(wine)
wine.pca <- prcomp(wine, scale. = TRUE)
print(ggscreplot(wine.pca))
print(ggbiplot(wine.pca, obs.scale = 1, var.scale = 1, groups = wine.class, ellipse = TRUE, circle = TRUE))
```

# Index

\* **datasets**

wine, 3

ggbiplot, 2

ggscreeplot, 3

wine, 3