

# Package: ggcompoplot (via r-universe)

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**Type** Package

**Title** Plot Posterior Assignment Values From a 'DAPC' Analysis

**Version** 0.1.0

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**Description** The package 'adegenet' calculates posterior population assignments, which can be plotted as a stacked bar chart. This package creates a 'ggplot2' version of this bar chart, faceted by population.

**Imports** ggplot2, reshape2, grDevices, adegenet

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 5.0.1

**Config/pak/sysreqs** libglpk-dev make libicu-dev libxml2-dev zlib1g-dev

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

**RemoteUrl** <https://github.com/zkamvar/ggcompoplot>

**RemoteRef** HEAD

**RemoteSha** bcf007d1ffd4d39afd9ac347213d2416163f380c

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char2pal *Creates a named color palette.*

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**Description**

This is useful for defining a color palette that can be used by population factors.

**Usage**

```
char2pal(x, pal = rainbow)
```

**Arguments**

x a vector of identifiers to be used for colors.  
pal a color palette. Default is [rainbow](#)

**Value**

a named character vector of hexadecimal colors.

**Examples**

```
char2pal(LETTERS)
```

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ggcompoplot *Plot posterior values from DAPC analysis in adegenet*

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**Description**

Plot posterior values from DAPC analysis in adegenet

**Usage**

```
ggcompoplot(da.object, gid, pal = rainbow, cols = 1)
```

**Arguments**

da.object an object of class "dapc"  
gid an object of class "genind"  
pal a color palette  
cols the number of columns to display

**Value**

a ggplot object with each population stacked on top of each other.

**Examples**

```
library('adegenet')
library('ggcompoplot')
library('ggplot2')
data(microbov)
strata(microbov) <- data.frame(other(microbov))
dapc1 <- dapc(microbov, n.pca=20, n.da=15)
setPop(microbov) <- ~breed
compoplot(dapc1, lab="") # Adegenet compoplot
# Showing per breed
ggcompoplot(dapc1, microbov) + theme(axis.text.x = element_blank())
## Not run:

# 3 columns
ggcompoplot(dapc1, microbov, col = 3) + theme(axis.text.x = element_blank())

# Different color palette
ggcompoplot(dapc1, microbov, col = 3, pal = funky) + theme(axis.text.x = element_blank())

# Per Country
setPop(microbov) <- ~coun
ggcompoplot(dapc1, microbov) + theme(axis.text.x = element_blank())

## End(Not run)
```

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