

# Package ‘aplotExtra’

August 4, 2026

**Title** Creating Composite Plots using 'aplot'

**Version** 0.0.6

**Description** Many complex plots are actually composite plots, such as 'oncoplot', 'funkyheatmap', 'upsetplot', etc. We can produce subplots using 'ggplot2' and combine them to create composite plots using 'aplot'. In this way, it is easy to customize these complex plots, by adding, deleting or modifying subplots in the final plot. This package provides a set of utilities to help users to create subplots and complex plots.

**Depends** R (>= 4.1.0)

**Imports** aplot (>= 0.2.3), dplyr, forcats, ggfun (>= 0.1.1), ggplot2, grid, maftools, purrr, rlang, stats, tibble, tidyr, utils, ggstar, yulab.utils (>= 0.0.8)

**Suggests** ggtree, data.table, RColorBrewer, R.utils, testthat (>= 3.0.0)

**URL** <https://github.com/YuLab-SMU/aplotExtra>

**License** Artistic-2.0

**Encoding** UTF-8

**Config/testthat/edition** 3

**Config/roxygen2/version** 8.0.0

**NeedsCompilation** no

**Author** Guangchuang Yu [aut, cre] (ORCID: <<https://orcid.org/0000-0002-6485-8781>>),  
Shuangbin Xu [ctb] (ORCID: <<https://orcid.org/0000-0003-3513-5362>>),  
Chun-Hui Gao [ctb] (ORCID: <<https://orcid.org/0000-0002-1445-7939>>),  
Shensuo Li [ctb] (ORCID: <<https://orcid.org/0009-0006-3229-3700>>)

**Maintainer** Guangchuang Yu <guangchuangyu@gmail.com>

**Repository** CRAN

**Date/Publication** 2026-08-04 15:00:02 UTC

Contents

|                               |          |
|-------------------------------|----------|
| funky_bar . . . . .           | 2        |
| funky_heatmap . . . . .       | 3        |
| funky_point . . . . .         | 3        |
| funky_text . . . . .          | 4        |
| get_all_subsets . . . . .     | 4        |
| oncoplot . . . . .            | 5        |
| oncoplot_components . . . . . | 6        |
| upset_plot . . . . .          | 6        |
| <b>Index</b>                  | <b>8</b> |

---

|           |                  |
|-----------|------------------|
| funky_bar | <i>funky_bar</i> |
|-----------|------------------|

---

Description

create bar plot for funkyheatmap

Usage

funky\_bar(data, cols)

Arguments

|      |                  |
|------|------------------|
| data | data frame       |
| cols | selected columns |

Value

ggplot object

Author(s)

Guangchuang Yu

---

|               |                      |
|---------------|----------------------|
| funky_heatmap | <i>funky_heatmap</i> |
|---------------|----------------------|

---

**Description**

create a funkyheatmap

**Usage**

```
funky_heatmap(..., data = NULL, widths = NULL, options = NULL)
```

**Arguments**

|         |                                                                                               |
|---------|-----------------------------------------------------------------------------------------------|
| ...     | funky plots (e.g., outputs of <code>funky_point</code> , <code>funky_bar</code> , etc.)       |
| data    | If data is provided, create a funkyheatmap from it. Otherwise, create composite plot from ... |
| widths  | relative widths of the plots                                                                  |
| options | any ggplot component that can be added to the plots                                           |

**Value**

gglist object

**Author(s)**

Guangchuang Yu

---

|             |                    |
|-------------|--------------------|
| funky_point | <i>funky_point</i> |
|-------------|--------------------|

---

**Description**

create dot plot for funkyheatmap

**Usage**

```
funky_point(data, cols, cols2 = NULL, ...)
```

**Arguments**

|       |                                                             |
|-------|-------------------------------------------------------------|
| data  | data frame                                                  |
| cols  | selected columns                                            |
| cols2 | selected columns to keep names                              |
| ...   | additional parameters, passing to <a href="#">geom_star</a> |

**Value**

ggplot object

**Author(s)**

Guangchuang Yu

---

|            |                   |
|------------|-------------------|
| funky_text | <i>funky_text</i> |
|------------|-------------------|

---

**Description**

create text plot (i.e., rownames) for funkyheatmap

**Usage**

```
funky_text(data, cols = 1, hjust = 0)
```

**Arguments**

|       |                           |
|-------|---------------------------|
| data  | data frame                |
| cols  | selected column           |
| hjust | text alignment adjustment |

**Value**

ggplot object

**Author(s)**

Guangchuang Yu

---

|                 |                                                             |
|-----------------|-------------------------------------------------------------|
| get_all_subsets | <i>Get the items/names/ids of subsets from a named list</i> |
|-----------------|-------------------------------------------------------------|

---

**Description**

Get the items/names/ids of subsets from a named list

**Usage**

```
get_all_subsets(list, name_separator = "/")
```

**Arguments**

`list`                    a named list  
`name_separator`    default is /

**Value**

a tibble

**Examples**

```
list = list(A = sample(LETTERS, 20),
            B = sample(LETTERS, 22),
            C = sample(LETTERS, 24),
            D = sample(LETTERS, 30, replace = TRUE))
get_all_subsets(list)
```

---

|          |                                    |
|----------|------------------------------------|
| oncoplot | <i>ploting oncoplot with aplot</i> |
|----------|------------------------------------|

---

**Description**

ploting oncoplot with aplot

**Usage**

```
oncoplot(maf, genes = 20)
```

**Arguments**

`maf`                    MAF object.  
`genes`                  the gene names or the number, default is 20.

**Value**

oncoplot object, which is also a aplot object

**Examples**

```
laml.maf <- system.file("extdata", "tcga_laml.maf.gz", package = "maftools")
laml.clin <- system.file('extdata', 'tcga_laml_annot.tsv', package = 'maftools')
laml <- maftools::read.maf(maf = laml.maf, clinicalData = laml.clin)
oncoplot(maf = laml, genes = 20)
```

---

|                     |                                         |
|---------------------|-----------------------------------------|
| oncoplot_components | <i>Get reusable oncoplot components</i> |
|---------------------|-----------------------------------------|

---

### Description

Build the reusable panels and tidy data used by `oncoplot()`. This function is intended for downstream packages that want to assemble an oncoplot with additional tracks while reusing the aplo-  
tExtra mutation matrix, sample burden, gene burden, and mutation color mapping.

### Usage

```
oncoplot_components(maf, genes = 20)
```

### Arguments

|                    |                                                |
|--------------------|------------------------------------------------|
| <code>maf</code>   | A MAF object.                                  |
| <code>genes</code> | The gene names or number of top mutated genes. |

### Value

A list with components:

**data** Tidy oncoplot matrix.

**main** Main mutation tile plot.

**sample** Sample-level top annotation plot.

**gene** Gene-level side annotation plot.

**colors** Named mutation-class color vector.

---

|            |                   |
|------------|-------------------|
| upset_plot | <i>upset_plot</i> |
|------------|-------------------|

---

### Description

Plot a upset plot

### Usage

```
upset_plot(
  list,
  nintersects = NULL,
  order.intersect.by = c("size", "name"),
  order.set.by = c("size", "name"),
  color.intersect.by = "none",
  color.set.by = "none",
  remove_empty_intersects = TRUE
)
```

**Arguments**

`list` a list of sets

`nintersects` number of intersects. If NULL, all intersections will show.

`order.intersect.by` one of 'size' or 'name'

`order.set.by` one of 'size' or 'name'

`color.intersect.by` color scheme for 'intersect' bars (e.g., "Set2"), default is "none"

`color.set.by` color scheme for 'set' bars (e.g., "Set3"), default is "none"

`remove_empty_intersects` remove the intersects which have zero elements. Default is TRUE.

**Details**

This function generate a upset plot by creating a composite plot which contains subplots generated by ggplot2.

**Value**

an upset plot

**Examples**

```
list = list(A = sample(LETTERS, 20),
            B = sample(LETTERS, 22),
            C = sample(LETTERS, 14),
            D = sample(LETTERS, 30, replace = TRUE))
upset_plot(list)
upset_plot(list, remove_empty_intersects = TRUE)
upset_plot(list, order.intersect.by = "name")
upset_plot(list, order.set.by = "name")
upset_plot(list, nintersects = 6)
```

# Index

funky\_bar, [2](#)  
funky\_heatmap, [3](#)  
funky\_point, [3](#)  
funky\_text, [4](#)  
  
geom\_star, [3](#)  
get\_all\_subsets, [4](#)  
  
oncoplot, [5](#)  
oncoplot(), [6](#)  
oncoplot\_components, [6](#)  
  
upset\_plot, [6](#)