

# Package ‘EnhancedVolcano’

July 9, 2025

**Type** Package

**Title** Publication-ready volcano plots with enhanced colouring and labeling

**Version** 1.26.0

**Maintainer** Kevin Blighe <kevin@clinicalbioinformatics.co.uk>

**Description** Volcano plots represent a useful way to visualise the results of differential expression analyses. Here, we present a highly-configurable function that produces publication-ready volcano plots. EnhancedVolcano will attempt to fit as many point labels in the plot window as possible, thus avoiding 'clogging' up the plot with labels that could not otherwise have been read. Other functionality allows the user to identify up to 4 different types of attributes in the same plot space via colour, shape, size, and shade parameter configurations.

**License** GPL-3

**Depends** ggplot2, ggrepel

**Imports** methods

**Suggests** ggalt, ggrastr, RUnit, BiocGenerics, knitr, DESeq2, pasilla, airway, org.Hs.eg.db, gridExtra, magrittr, rmarkdown

**URL** <https://github.com/kevinblighe/EnhancedVolcano>

**biocViews** RNASeq, GeneExpression, Transcription, DifferentialExpression, ImmunoOncology

**VignetteBuilder** knitr

**RoxygenNote** 7.1.2

**git\_url** <https://git.bioconductor.org/packages/EnhancedVolcano>

**git\_branch** RELEASE\_3\_21

**git\_last\_commit** e2756f5

**git\_last\_commit\_date** 2025-04-15

**Repository** Bioconductor 3.21

**Date/Publication** 2025-07-09

**Author** Kevin Blighe [aut, cre],  
Sharmila Rana [aut],  
Emir Turkes [ctb],

Benjamin Ostendorf [ctb],  
 Andrea Grioni [ctb],  
 Myles Lewis [aut]

## Contents

EnhancedVolcano . . . . .	2
<b>Index</b>	<b>9</b>

---

EnhancedVolcano	<i>Publication-ready volcano plots with enhanced colouring and labeling.</i>
-----------------	------------------------------------------------------------------------------

---

## Description

Volcano plots represent a useful way to visualise the results of differential expression analyses. Here, we present a highly-configurable function that produces publication-ready volcano plots [`@EnhancedVolcano`]. `EnhancedVolcano` will attempt to fit as many variable names in the plot window as possible, thus avoiding 'clogging' up the plot with labels that could not otherwise have been read.

## Usage

```
EnhancedVolcano(
  toptable,
  lab,
  x,
  y,
  selectLab = NULL,
  xlim = c(min(toptable[[x]], na.rm = TRUE) - 1.5, max(toptable[[x]], na.rm = TRUE) +
    1.5),
  ylim = c(0, max(-log10(toptable[[y]]), na.rm = TRUE) + 5),
  xlab = bquote(~Log[2] ~ "fold change"),
  ylab = bquote(~-Log[10] ~ italic(P)),
  axisLabSize = 18,
  title = "Volcano plot",
  subtitle = bquote(italic(EnhancedVolcano)),
  caption = paste0("total = ", nrow(toptable), " variables"),
  titleLabSize = 18,
  subtitleLabSize = 14,
  captionLabSize = 14,
  pCutoff = 1e-05,
  pCutoffCol = y,
  FCcutoff = 1,
  cutoffLineType = "longdash",
  cutoffLineCol = "black",
```

```
cutoffLineWidth = 0.4,
pointSize = 2,
labSize = 5,
labCol = "black",
labFace = "plain",
boxedLabels = FALSE,
parseLabels = FALSE,
shape = 19,
shapeCustom = NULL,
col = c("grey30", "forestgreen", "royalblue", "red2"),
colCustom = NULL,
colAlpha = 1/2,
colGradient = NULL,
colGradientBreaks = c(pCutoff, 1),
colGradientLabels = c("0", "1.0"),
colGradientLimits = c(0, 1),
legendLabels = c("NS", expression(Log[2] ~ FC), "p-value", expression(p - value ~ and
  ~ log[2] ~ FC)),
legendPosition = "top",
legendLabSize = 14,
legendIconSize = 5,
legendDroplevels = TRUE,
encircle = NULL,
encircleCol = "black",
encircleFill = "pink",
encircleAlpha = 3/4,
encircleSize = 2.5,
shade = NULL,
shadeFill = "grey",
shadeAlpha = 1/2,
shadeSize = 0.01,
shadeBins = 2,
drawConnectors = FALSE,
widthConnectors = 0.5,
typeConnectors = "closed",
endsConnectors = "first",
lengthConnectors = unit(0.01, "npc"),
colConnectors = "grey10",
max.overlaps = 15,
maxoverlapsConnectors = NULL,
min.segment.length = 0,
directionConnectors = "both",
arrowheads = TRUE,
hline = NULL,
hlineType = "longdash",
hlineCol = "black",
hlineWidth = 0.4,
vline = NULL,
```

```

vlineType = "longdash",
vlineCol = "black",
vlineWidth = 0.4,
gridlines.major = TRUE,
gridlines.minor = TRUE,
border = "partial",
borderWidth = 0.8,
borderColour = "black",
raster = FALSE
)

```

### Arguments

<code>toptable</code>	A data-frame of test statistics (if not, a data frame, an attempt will be made to convert it to one). Requires at least the following: column for variable names (can be rownames); a column for log2 fold changes; a column for nominal or adjusted p-value.
<code>lab</code>	A column name in <code>toptable</code> containing variable names. Can be <code>rownames(toptable)</code> .
<code>x</code>	A column name in <code>toptable</code> containing log2 fold changes.
<code>y</code>	A column name in <code>toptable</code> containing nominal or adjusted p-values.
<code>selectLab</code>	A vector containing a subset of <code>lab</code> .
<code>xlim</code>	Limits of the x-axis.
<code>ylim</code>	Limits of the y-axis.
<code>xlab</code>	Label for x-axis.
<code>ylab</code>	Label for y-axis.
<code>axisLabSize</code>	Size of x- and y-axis labels.
<code>title</code>	Plot title.
<code>subtitle</code>	Plot subtitle.
<code>caption</code>	Plot caption.
<code>titleLabSize</code>	Size of plot title.
<code>subtitleLabSize</code>	Size of plot subtitle.
<code>captionLabSize</code>	Size of plot caption.
<code>pCutoff</code>	Cut-off for statistical significance. A horizontal line will be drawn at $-\log_{10}(\text{pCutoff})$ .
<code>pCutoffCol</code>	Column name of statistical significance values to be used as the cut-off. A typical usage situation would be to pass nominal [un-adjusted] p-values as <code>'y'</code> , but adjusted p-values as <code>pCutoffCol</code> . In this way, a plot is generated via $-\log_{10}(\text{unadjusted p-value})$ , but cut-offs based on adjusted p-values.
<code>FCcutoff</code>	Cut-off for absolute log2 fold-change. Vertical lines will be drawn at the negative and positive values of $\log_2 \text{FCcutoff}$ .
<code>cutoffLineType</code>	Line type for <code>FCcutoff</code> and <code>pCutoff</code> ('blank', 'solid', 'dashed', 'dotted', 'dot-dash', 'longdash', 'twodash').
<code>cutoffLineCol</code>	Line colour for <code>FCcutoff</code> and <code>pCutoff</code> .

cutoffLineWidth	Line width for FCcutoff and pCutoff.
pointSize	Size of plotted points for each variable. Can be a single value or a vector of sizes.
labSize	Size of labels for each variable.
labCol	Colour of labels for each variable.
labFace	Font face of labels for each variable.
boxedLabels	Logical, indicating whether or not to draw labels in boxes.
parseLabels	Logical, indicating whether or not to parse expressions in labels
shape	Shape of the plotted points. Either a single value for all points, or 4 values corresponding to the default 4 legend labels specified by legendLabels.
shapeCustom	Named vector / key-value pairs that will over-ride the default shape scheme. The order must match that of toptable. Names / keys relate to groups / categories; values relate to shape encodings.
col	Colour shading for plotted points, corresponding to the default 4 legend labels specified by legendLabels.
colCustom	Named vector / key-value pairs that will over-ride the default colour scheme. The order must match that of toptable. Names / keys relate to groups / categories; values relate to colour.
colAlpha	Alpha for purposes of controlling colour transparency of variable points.
colGradient	If activated, over-rides the default discrete colour scheme and replaces it with a continous scheme that shades based on nominal or adjusted p-value specified by y. For example, c('red2', 'blue2').
colGradientBreaks	Break-points for the two colours specified by colGradient.
colGradientLabels	Labels for the break-points specified by colGradientBreaks.
colGradientLimits	Limits of the colour scheme specified by colGradient, i.e., max and min possible p-values.
legendLabels	Plot legend text labels.
legendPosition	Position of legend ('top', 'bottom', 'left', 'right').
legendLabSize	Size of plot legend text.
legendIconSize	Size of plot legend icons / symbols.
legendDropLevels	Logical, drop unused factor levels from legend.
encircle	A vector of variable names to encircle. Requires installation of package <a href="#">ggalt</a> .
encircleCol	Colour of the encircled line.
encircleFill	Colour fill of the encircled region.
encircleAlpha	Alpha for purposes of controlling colour transparency of encircled region.
encircleSize	Line width of the encircled line.

<code>shade</code>	A vector of variable names to shade.
<code>shadeFill</code>	Colour of shaded regions.
<code>shadeAlpha</code>	Alpha for purposes of controlling colour transparency of shaded region.
<code>shadeSize</code>	Size of the shade contour lines.
<code>shadeBins</code>	Number of bins for the density of the shade.
<code>drawConnectors</code>	Logical, indicating whether or not to connect plot labels to their corresponding points by line connectors.
<code>widthConnectors</code>	Line width of connectors.
<code>typeConnectors</code>	Have the arrow head open ('open') or filled ('closed')?
<code>endsConnectors</code>	Which end of connectors to draw arrow head? ('last', 'first', 'both').
<code>lengthConnectors</code>	Length (size) of the connector arrowheads.
<code>colConnectors</code>	Line colour of connectors and line segments.
<code>max.overlaps</code>	Equivalent of <code>max.overlaps</code> in <code>ggrepel</code> . Set to 'Inf' to always display all labels when <code>drawConnectors = TRUE</code> .
<code>maxoverlapsConnectors</code>	See <code>max.overlaps</code> .
<code>min.segment.length</code>	When <code>drawConnectors = TRUE</code> , specifies the minimum length of the connector line segments.
<code>directionConnectors</code>	direction in which to draw connectors. 'both', 'x', or 'y'.
<code>arrowheads</code>	Logical, indicating whether or not to draw arrow heads or or just have straight lines.
<code>hline</code>	Draw one or more horizontal lines passing through this/these values on y-axis. For single values, only a single numerical value is necessary. For multiple lines, pass these as a vector, e.g., <code>c(60,90)</code> .
<code>hlineType</code>	Line type for <code>hline</code> ('blank', 'solid', 'dashed', 'dotted', 'dotdash', 'longdash', 'twodash').
<code>hlineCol</code>	Colour of <code>hline</code> .
<code>hlineWidth</code>	Width of <code>hline</code> .
<code>vline</code>	Draw one or more vertical lines passing through this/these values on x-axis. For single values, only a single numerical value is necessary. For multiple lines, pass these as a vector, e.g., <code>c(60,90)</code> .
<code>vlineType</code>	Line type for <code>vline</code> ('blank', 'solid', 'dashed', 'dotted', 'dotdash', 'longdash', 'twodash').
<code>vlineCol</code>	Colour of <code>vline</code> .
<code>vlineWidth</code>	Width of <code>vline</code> .
<code>gridlines.major</code>	Logical, indicating whether or not to draw major gridlines.

<code>gridlines.minor</code>	Logical, indicating whether or not to draw minor gridlines.
<code>border</code>	Add a border for just the x and y axes ('partial') or the entire plot grid ('full')?
<code>borderWidth</code>	Width of the border on the x and y axes.
<code>borderColour</code>	Colour of the border on the x and y axes.
<code>raster</code>	Logical, indicating whether to rasterize the <code>geom_point</code> layer. Requires installation of <a href="#">ggtrastr</a> .

## Details

Volcano plots represent a useful way to visualise the results of differential expression analyses. Here, we present a highly-configurable function that produces publication-ready volcano plots [[@EnhancedVolcano](#)]. `EnhancedVolcano` will attempt to fit as many variable names in the plot window as possible, thus avoiding 'clogging' up the plot with labels that could not otherwise have been read.

## Value

A [ggplot2](#) object.

## Author(s)

Kevin Blighe <[kevin@clinicalbioinformatics.co.uk](mailto:kevin@clinicalbioinformatics.co.uk)>

## Examples

```
library('pasilla')
pasCts <- system.file('extdata', 'pasilla_gene_counts.tsv',
  package='pasilla', mustWork=TRUE)
pasAnno <- system.file('extdata', 'pasilla_sample_annotation.csv',
  package='pasilla', mustWork=TRUE)
cts <- as.matrix(read.csv(pasCts, sep='\t', row.names='gene_id'))
coldata <- read.csv(pasAnno, row.names=1)
coldata <- coldata[,c('condition', 'type')]
rownames(coldata) <- sub('fb', '', rownames(coldata))
cts <- cts[, rownames(coldata)]
library('DESeq2')
dds <- DESeqDataSetFromMatrix(countData = cts,
  colData = coldata,
  design = ~ condition)

featureData <- data.frame(gene=rownames(cts))
mcols(dds) <- DataFrame(mcols(dds), featureData)
dds <- DESeq(dds)
res <- results(dds)

EnhancedVolcano(res,
  lab = rownames(res),
  x = 'log2FoldChange',
  y = 'pvalue',
```

```
pCutoff = 10e-4,  
FCcutoff = 1.333,  
xlim = c(-5.5, 5.5),  
ylim = c(0, -log10(10e-12)),  
pointSize = 1.5,  
labSize = 2.5,  
title = 'DESeq2 results',  
subtitle = 'Differential expression',  
caption = 'FC cutoff, 1.333; p-value cutoff, 10e-4',  
legendPosition = "right",  
legendLabSize = 14,  
col = c('grey30', 'forestgreen', 'royalblue', 'red2'),  
colAlpha = 0.9,  
drawConnectors = TRUE,  
hline = c(10e-8),  
widthConnectors = 0.5)
```



# Index

EnhancedVolcano, [2](#)

ggalt, [5](#)

ggplot2, [7](#)

ggrastr, [7](#)