

Package ‘EnhancedVolcano’

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Type Package

Title Publication-ready volcano plots with enhanced colouring and labeling

Version 1.0.1

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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 transcript names in the plot window as possible, thus avoiding 'clogging' up the plot with labels that could not otherwise have been read.

License GPL-3

Depends R (>= 3.5.0), ggplot2, ggrepel

Imports

Suggests RUnit, BiocGenerics, knitr, DESeq2, pasilla, airway, gridExtra, magrittr

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

biocViews ImmunoOncology, RNASeq, GeneExpression, Transcription, DifferentialExpression

VignetteBuilder knitr

git_url <https://git.bioconductor.org/packages/EnhancedVolcano>

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R topics documented:

EnhancedVolcano-package	2
EnhancedVolcano	2

Index	6
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EnhancedVolcano-package

EnhancedVolcano: Publication-ready volcano plots with enhanced colouring and labeling.

Description

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EnhancedVolcano

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Usage

```
EnhancedVolcano(
  toptable,
  lab,
  x,
  y,
  selectLab = NULL,
  xlim = c(min(toptable[,x], na.rm=TRUE), max(toptable[,x], na.rm=TRUE)),
  ylim = c(0, max(-log10(toptable[,y]), na.rm=TRUE) + 5),
  xlab = bquote(~Log[2]~ "fold change"),
  ylab = bquote(~-Log[10]~italic(P)),
  axisLabSize = 16,
  pCutoff = 0.05,
  pLabellingCutoff = pCutoff,
  FCcutoff = 2.0,
  title = "",
  titleLabSize = 16,
  transcriptPointSize = 0.8,
  transcriptLabSize = 3.0,
  col = c("grey30", "forestgreen", "royalblue", "red2"),
  colOverride = NULL,
  colAlpha = 1/2,
  legend = c("NS", "Log2 FC", "P", "P & Log2 FC"),
  legendPosition = "top",
  legendLabSize = 10,
```

```

legendIconSize = 3.0,
DrawConnectors = FALSE,
widthConnectors = 0.5,
colConnectors = "black",
cutoffLineType = "longdash",
cutoffLineCol = "black",
cutoffLineWidth = 0.4,
gridlines.major = TRUE,
gridlines.minor = TRUE,
border = "partial",
borderWidth = 0.8,
borderColour = "black")

```

Arguments

toptable	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 transcript names (can be rownames); a column for log2 fold changes; a column for nominal or adjusted p-value. REQUIRED.
lab	A column name in toptable containing transcript names. Can be rownames(toptable). REQUIRED.
x	A column name in toptable containing log2 fold changes. REQUIRED.
y	A column name in toptable containing nominal or adjusted p-values. REQUIRED.
selectLab	A vector containing a subset of lab. Only values in selectLab that pass FCcut-off and pCutoff thresholds will be labelled in the plot. DEFAULT = NULL. OPTIONAL.
xlim	Limits of the x-axis. DEFAULT = c(min(toptable[,x], na.rm=TRUE), max(toptable[,x], na.rm=TRUE)). OPTIONAL.
ylim	Limits of the y-axis. DEFAULT = c(0, max(-log10(toptable[,y]), na.rm=TRUE) + 5). OPTIONAL.
xlab	Label for x-axis. DEFAULT = bquote(~Log[2]~ "fold change"). OPTIONAL.
ylab	Label for y-axis. DEFAULT = bquote(~-Log[10]~italic(P)). OPTIONAL.
axisLabSize	Size of x- and y-axis labels. DEFAULT = 16. OPTIONAL.
pCutoff	Cut-off for statistical significance. A horizontal line will be drawn at -log10(pCutoff). DEFAULT = 0.05. OPTIONAL.
pLabellingCutoff	Labelling cut-off for statistical significance. DEFAULT = pCutoff. OPTIONAL.
FCcutoff	Cut-off for absolute log2 fold-change. Vertical lines will be drawn at the negative and positive values of FCCutoff. DEFAULT = 2.0. OPTIONAL.
title	Plot title. DEFAULT = "". OPTIONAL.
titleLabSize	Size of plot title. DEFAULT = 16. OPTIONAL.
transcriptPointSize	Size of plotted points for each transcript. DEFAULT = 0.8. OPTIONAL.
transcriptLabSize	Size of labels for each transcript. DEFAULT = 3.0. OPTIONAL.
col	Colour shading for plotted points, corresponding to < abs(FCcutoff) && > pCutoff, > abs(FCcutoff), < pCutoff, > abs(FCcutoff) && < pCutoff. DEFAULT = c("grey30", "forestgreen", "royalblue", "red2"). OPTIONAL.

<code>colOverride</code>	Named vector / key-value pairs that will over-ride the default colour scheme. The order must match that of <code>toptable</code> . Names / keys relate to groups / categories; values relate to colour. DEFAULT = NULL. OPTIONAL.
<code>colAlpha</code>	Alpha for purposes of controlling colour transparency of transcript points. DEFAULT = 0.5. OPTIONAL.
<code>legend</code>	Plot legend text. DEFAULT = <code>c("NS", "Log2 FC", "P", "P & Log2 FC")</code> . OPTIONAL.
<code>legendPosition</code>	Position of legend ("top", "bottom", "left", "right"). DEFAULT = "top". OPTIONAL.
<code>legendLabSize</code>	Size of plot legend text. DEFAULT = 10. OPTIONAL.
<code>legendIconSize</code>	Size of plot legend icons / symbols. DEFAULT = 3.0. OPTIONAL.
<code>DrawConnectors</code>	Fit labels onto plot and connect to their respective points by lines (TRUE/FALSE). DEFAULT = FALSE. OPTIONAL.
<code>widthConnectors</code>	Line width of connectors to plot points. DEFAULT = 0.5. OPTIONAL.
<code>colConnectors</code>	Line colour of connectors to plot points. DEFAULT = "black". OPTIONAL.
<code>cutoffLineType</code>	Line type for FCcutoff and pCutoff ("blank", "solid", "dashed", "dotted", "dot-dash", "longdash", "twodash"). DEFAULT = "longdash". OPTIONAL.
<code>cutoffLineCol</code>	Line colour for FCcutoff and pCutoff. DEFAULT = "black". OPTIONAL.
<code>cutoffLineWidth</code>	Line width for FCcutoff and pCutoff. DEFAULT = 0.4. OPTIONAL.
<code>gridlines.major</code>	Draw major gridlines? (TRUE/FALSE). DEFAULT = TRUE. OPTIONAL
<code>gridlines.minor</code>	Draw minor gridlines? (TRUE/FALSE). DEFAULT = TRUE. OPTIONAL
<code>border</code>	Add a border for just the x and y axes ('partial') or the entire plot grid ('full')? DEFAULT = 'partial'. OPTIONAL.
<code>borderWidth</code>	Width of the border on the x and y axes. DEFAULT = 0.8. OPTIONAL.
<code>borderColour</code>	Colour of the border on the x and y axes. DEFAULT = "black". OPTIONAL.

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 transcript 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>

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 = "padj",
  ylab = bquote(~-Log[10]~adjusted~italic(P)),
  pCutoff = 10e-4,
  FCcutoff = 1.333,
  xlim=c(-5.5, 5.5),
  ylim=c(0, -log10(10e-12)),
  transcriptLabSize = 3.5,
  title = "DESeq2 results",
  legendPosition = "right",
  legendLabSize = 14,
  col = c("grey30", "forestgreen", "royalblue", "red2"),
  colAlpha=0.9,
  DrawConnectors = TRUE,
  widthConnectors=0.2)
```

Index

EnhancedVolcano, [2](#)
EnhancedVolcano-package, [2](#)
ggplot2, [4](#)