Package ‘EnhancedVolcano’

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Type Package

Title Publication-ready volcano plots with enhanced colouring and labeling

Version 1.22.0

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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 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

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Sharmila Rana [aut],
Emir Turkes [ctb],
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EnhancedVolcano

Publication-ready volcano plots with enhanced colouring and label-
ing.

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,
pontSize = 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),
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

topleft 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.

lab A column name in toptable containing variable names. Can be rownames(toptable).
x A column name in toptable containing log2 fold changes.
y A column name in toptable containing nominal or adjusted p-values.
selectLab A vector containing a subset of lab.
xlim Limits of the x-axis.
ylim Limits of the y-axis.
lab Label for x-axis.
ylab Label for y-axis.
axisLabSize Size of x- and y-axis labels.
title Plot title.
subtitle Plot subtitle.
caption Plot caption.
titleLabSize Size of plot title.
subtitleLabSize Size of plot subtitle.
captionLabSize Size of plot caption.
pCutoff Cut-off for statistical significance. A horizontal line will be drawn at -log10(pCutoff).
pCutoffCol 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 'y', but adjusted p-values as pCutoffCol. In this way, a plot is generated via -log10(unadjusted p-value), but cut-offs based on adjusted p-values.

FCcutoff Cut-off for absolute log2 fold-change. Vertical lines will be drawn at the negative and positive values of log2FCcutoff.
cutoffLineType Line type for FCcutoff and pCutoff ('blank', 'solid', 'dashed', 'dotted', 'dotdash', 'longdash', 'twodash').
cutoffLineColor Line colour for FCcutoff and pCutoff.
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 continuous 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 ggalt.

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.
<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>shade</td>
<td>A vector of variable names to shade.</td>
</tr>
<tr>
<td>shadeFill</td>
<td>Colour of shaded regions.</td>
</tr>
<tr>
<td>shadeAlpha</td>
<td>Alpha for purposes of controlling colour transparency of shaded region.</td>
</tr>
<tr>
<td>shadeSize</td>
<td>Size of the shade contour lines.</td>
</tr>
<tr>
<td>shadeBins</td>
<td>Number of bins for the density of the shade.</td>
</tr>
<tr>
<td>drawConnectors</td>
<td>Logical, indicating whether or not to connect plot labels to their corresponding points by line connectors.</td>
</tr>
<tr>
<td>widthConnectors</td>
<td>Line width of connectors.</td>
</tr>
<tr>
<td>typeConnectors</td>
<td>Have the arrow head open ('open') or filled ('closed')?</td>
</tr>
<tr>
<td>endsConnectors</td>
<td>Which end of connectors to draw arrow head? ('last', 'first', 'both').</td>
</tr>
<tr>
<td>lengthConnectors</td>
<td>Length (size) of the connector arrowheads.</td>
</tr>
<tr>
<td>colConnectors</td>
<td>Line colour of connectors and line segments.</td>
</tr>
<tr>
<td>max.overlaps</td>
<td>Equivalent of max.overlaps in ggrepel. Set to 'Inf' to always display all labels when drawConnectors = TRUE.</td>
</tr>
<tr>
<td>maxoverlapsConnectors</td>
<td>See max.overlaps.</td>
</tr>
<tr>
<td>min.segment.length</td>
<td>When drawConnectors = TRUE, specifies the minimum length of the connector line segments.</td>
</tr>
<tr>
<td>directionConnectors</td>
<td>direction in which to draw connectors. 'both', 'x', or 'y'.</td>
</tr>
<tr>
<td>arrowheads</td>
<td>Logical, indicating whether or not to draw arrow heads or or just have straight lines.</td>
</tr>
<tr>
<td>hline</td>
<td>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., c(60,90).</td>
</tr>
<tr>
<td>hlineType</td>
<td>Line type for hline ('blank', 'solid', 'dashed', 'dotted', 'dotdash', 'longdash', 'twodash').</td>
</tr>
<tr>
<td>hlineCol</td>
<td>Colour of hline.</td>
</tr>
<tr>
<td>hlineWidth</td>
<td>Width of hline.</td>
</tr>
<tr>
<td>vline</td>
<td>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., c(60,90).</td>
</tr>
<tr>
<td>vlineType</td>
<td>Line type for vline ('blank', 'solid', 'dashed', 'dotted', 'dotdash', 'longdash', 'twodash').</td>
</tr>
<tr>
<td>vlineCol</td>
<td>Colour of vline.</td>
</tr>
<tr>
<td>vlineWidth</td>
<td>Width of vline.</td>
</tr>
<tr>
<td>gridlines.major</td>
<td>Logical, indicating whether or not to draw major gridlines.</td>
</tr>
</tbody>
</table>
**EnhancedVolcano**

- `gridlines.minor` Logical, indicating whether or not to draw minor gridlines.
- `border` Add a border for just the x and y axes (‘partial’) or the entire plot grid (‘full’)?
- `borderWidth` Width of the border on the x and y axes.
- `borderColour` Colour of the border on the x and y axes.
- `raster` Logical, indicating whether to rasterize the geom_point layer. Requires installation of `ggrastr`.

**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)**

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**Examples**

```r
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)
cnts <- 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','

cnts <- 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 = 1e-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)
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