Package 'BioVenn'

January 20, 2025

Title Create Area-Proportional Venn Diagrams from Biological Lists

Version 1.1.3

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Description Creates an area-proportional Venn diagram of 2 or 3 circles. 'BioVenn' is the only R package that can automatically generate an accurate area-proportional Venn diagram by having only lists of (biological) identifiers as input. Also offers the option to map Entrez and/or Affymetrix IDs to Ensembl IDs. In SVG mode, text and numbers can be dragged and dropped. Based on the BioVenn web interface available at <https://www.biovenn.nl>. Hulsen (2021) <doi:10.3233/DS-210032>.

License GPL-3

Imports biomaRt, graphics, grDevices, plotrix, svglite

Suggests knitr, rmarkdown

VignetteBuilder knitr

Encoding UTF-8

RoxygenNote 7.1.1

NeedsCompilation no

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Repository CRAN

Date/Publication 2021-06-19 08:10:02 UTC

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draw.venn   *Draw an area-proportional Venn diagram of 2 or 3 circles*

Description

This function creates an area-proportional Venn diagram of 2 or 3 circles, based on lists of (biological) identifiers. It requires three parameters: input lists X, Y and Z. For a 2-circle Venn diagram, one of these lists should be left empty. Duplicate identifiers are removed automatically, and a mapping from Entrez and/or Affymetrix to Ensembl IDs is available. BioVenn is case-sensitive. In SVG mode, text and numbers can be dragged and dropped.

Usage

```
draw.venn(
  list_x,
  list_y,
  list_z,
  title = "BioVenn",
  t_f = "serif",
  t_fb = 2,
  t_s = 1.5,
  t_c = "black",
  subtitle = "(C) 2007-2020 Tim Hulsen",
  st_f = "serif",
  st_fb = 2,
  st_s = 1.2,
  st_c = "black",
  xtitle = "ID Set X",
  xt_f = "serif",
  xt_fb = 2,
  xt_s = 1,
  xt_c = "black",
  ytitle = "ID Set Y",
  yt_f = "serif",
  yt_fb = 2,
  yt_s = 1,
  yt_c = "black",
  ztitle = "ID Set Z",
  zt_f = "serif",
  zt_fb = 2,
  zt_s = 1,
  zt_c = "black",
  nrtype = "abs",
  nr_f = "serif",
  nr_fb = 2,
  nr_s = 1,
  nr_c = "black",
```

```
    x_c = "red",
    y_c = "green",
    z_c = "blue",
    bg_c = "white",
    width = 1000,
    height = 1000,
    output = "screen",
    filename = NULL,
    map2ens = FALSE
)
```

Arguments

list_x	(Required) List with IDs from dataset X
list_y	(Required) List with IDs from dataset Y
list_z	(Required) List with IDs from dataset Z
title	(Optional) The title of the Venn diagram (default is "BioVenn")
t_f	(Optional) The font of the main title (default is "serif")
t_fb	(Optional) The font "face" of the main title (1=plain, 2=bold, 3=italic, 4=bold-italic; default is 2)
t_s	(Optional) The size of the main title (cex; relative to the standard size; default is 1.5)
t_c	(Optional) The colour of the main title (default is "black")
subtitle	(Optional) The subtitle of the Venn diagram (default is "(C) 2007-2020 Tim Hulsen")
st_f	(Optional) The font of the subtitle (default is "serif")
st_fb	(Optional) The font "face" of the subtitle (1=plain, 2=bold, 3=italic, 4=bold-italic; default is 2)
st_s	(Optional) The size of the subtitle (cex; relative to the standard size; default is 1.2)
st_c	(Optional) The colour of the subtitle (default is "black")
xtitle	(Optional) The X title of the Venn diagram (default is "ID set X")
xt_f	(Optional) The font of the X title (default is "serif")
xt_fb	(Optional) The font "face" of the X title (1=plain, 2=bold, 3=italic, 4=bold-italic; default is 2)
xt_s	(Optional) The size of the X title (cex; relative to the standard size; default is 1)
xt_c	(Optional) The colour of the X title (default is "black")
ytitle	(Optional) The Y title of the Venn diagram (default is "ID set Y")
yt_f	(Optional) The font of the Y title (default is "serif")
yt_fb	(Optional) The font "face" of the Y title (1=plain, 2=bold, 3=italic, 4=bold-italic; default is 2)
yt_s	(Optional) The size of the Y title (cex; relative to the standard size; default is 1)

yt_c	(Optional) The colour of the Y title (default is "black")
ztitle	(Optional) The Z title of the Venn diagram (default is "ID set Z")
zt_f	(Optional) The font of the Z title (default is "serif")
zt_fb	(Optional) The font "face" of the Z title (1=plain, 2=bold, 3=italic, 4=bold-italic; default is 2)
zt_s	(Optional) The size of the Z title (cex; relative to the standard size; default is 1)
zt_c	(Optional) The colour of the Z title (default is "black")
nrtype	(Optional) The type of the numbers to be displayed: absolute (abs) numbers or percentages (pct) (default is "abs")
nr_f	(Optional) The font of the numbers (default is "serif")
nr_fb	(Optional) The font "face" of the numbers (1=plain, 2=bold, 3=italic, 4=bold-italic; default is 2)
nr_s	(Optional) The size of the numbers (cex; relative to the standard size; default is 1)
nr_c	(Optional) The colour of the numbers (default is "black")
x_c	(Optional) The colour of the X circle (default is "red")
y_c	(Optional) The colour of the X circle (default is "green")
z_c	(Optional) The colour of the X circle (default is "blue")
bg_c	(Optional) The background colour (default is "white")
width	(Optional) The width of the output file (in pixels for BMP/JPEG/PNG/TIF or in centiinch for PDF/SVG; default is 1000)
height	(Optional) The height of the output file (in pixels for BMP/JPEG/PNG/TIF or in centiinch for PDF/SVG; default is 1000)
output	(Optional) Output format: "bmp","jpg","pdf","png","svg" or "tif" (anything else writes to the screen; default is "screen")
filename	(Optional) The name of the output file (default is "biovenn" + extension of the selected output format)
map2ens	(Optional) Map from Entrez or Affymetrix IDs to Ensembl IDs (default is FALSE)

Details

When using a BioVenn diagram for a publication, please cite: BioVenn - an R and Python package for the comparison and visualization of biological lists using area-proportional Venn diagrams T. Hulsen, Data Science 2021, 4 (1): 51-61 https://dx.doi.org/10.3233/DS-210032

Value

An image of the Venn diagram is generated in the desired output format.

Also returns an object with thirteen lists: X, Y, Z, X only, Y only, Z only, XY, XZ, YZ, XY only, XZ only, YZ only, XYZ.

Examples

```
list_x <- c("1007_s_at","1053_at","117_at","121_at","1255_g_at","1294_at")
list_y <- c("1255_g_at","1294_at","1316_at","1320_at","1405_i_at")
list_z <- c("1007_s_at","1405_i_at","1255_g_at","1431_at","1438_at","1487_at","1494_f_at")
biovenn <- draw.venn(list_x, list_y, list_z, subtitle="Example diagram", nrtype="abs")
```

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