

# Package ‘circularDNACircos’

August 12, 2025

**Type** Package

**Title** Circos Plotting Tools

**Version** 0.99.0

**Description** Imports the circular pairs information from the csv or text files and creates circular visualizations using the R circlize library of these circular pairs.

**Depends** R (>= 4.4)

**License** MIT + file LICENSE

**Encoding** UTF-8

**Imports** circlize, readr, grDevices

**Suggests** knitr, rmarkdown, testthat (>= 3.0.0), BiocStyle

**biocViews** Software, Visualization, DataImport, StructuralVariants, Genome

**RoxygenNote** 7.3.2

**URL** <https://github.com/hjp7ht/circularDNACircos>

**BugReports** <https://github.com/hjp7ht/circularDNACircos/issues>

**Config/testthat/edition** 3

**VignetteBuilder** knitr

**NeedsCompilation** no

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dual_circos_plot	<i>dual_circos_plot</i>
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## Description

Generates two circos plots from two files and saves as images in the same directory.

## Usage

```
dual_circos_plot(
    file1,
    file2,
    outer_track_height = 0.3,
    inner_track_height = 0.13,
    max_pairs_per_outer_bin = 20,
    max_pairs_per_inner_bin = 15,
    outer_track_arrow_head_width = 0.08,
    outer_track_arrow_head_length = 0.07,
    inner_track_arrow_head_width = 0.1,
    inner_track_arrow_head_length = 0.07,
    png1 = "circos_plot1.png",
    png2 = "circos_plot2.png"
)
```

## Arguments

file1	First CSV or TXT file.
file2	Second CSV or TXT file.
outer_track_height	can be in between(0 to 1 ideally 0.25)
inner_track_height	can be in between( 0 to 1 ideally < 0.2)
max_pairs_per_outer_bin	number of pairs you want to show in the bin ( ideally 20 for track height of 0.25)
max_pairs_per_inner_bin	number of pairs you want to show in the bin ( ideally 20 for track height of 0.25)
outer_track_arrow_head_width	arrow head width (ideally in between 0.05-0.2)
outer_track_arrow_head_length	arrow head length( ideally in between 0.05-0.4)
inner_track_arrow_head_width	arrow head width (ideally in between 0.05-0.2)
inner_track_arrow_head_length	arrow head length( ideally in between 0.05-0.4)
png1	name of the first circos plot
png2	name of the second circos plot

## Value

Invisibly returns the widget object.

**Examples**

```
# Minimal runnable example: create two tiny datasets and plot to temp files
df1 <- data.frame(
  chromosome = c("chr1", "chr1", "chr1", "chr1"),
  start1     = c(1000, 1300, 1050, 1020),
  end1       = c(1150, 1450, 1100, 1070),
  start2     = c(1350, 1650, 1900, 1930),
  end2       = c(1500, 1800, 1950, 1980),
  orientation = c("FR", "RF", "FF", "RR"),
  stringsAsFactors = FALSE
)
df2 <- data.frame(
  chromosome = c("chr1", "chr1"),
  start1     = c(1050, 1020),
  end1       = c(1100, 1070),
  start2     = c(1900, 1930),
  end2       = c(1950, 1980),
  start3     = c(1300, 1700),
  end3       = c(1450, 1850),
  orientation = c("FFR", "RRF"),
  stringsAsFactors = FALSE
)

f1 <- tempfile(fileext = ".csv")
f2 <- tempfile(fileext = ".csv")
utils::write.csv(df1, f1, row.names = FALSE)
utils::write.csv(df2, f2, row.names = FALSE)

out1 <- file.path(tempdir(), "circos1.png")
out2 <- file.path(tempdir(), "circos2.png")

dual_circos_plot(
  file1 = f1, file2 = f2,
  outer_track_height = 0.25, inner_track_height = 0.13,
  max_pairs_per_outer_bin = 20, max_pairs_per_inner_bin = 15,
  outer_track_arrow_head_width = 0.08, outer_track_arrow_head_length = 0.07,
  inner_track_arrow_head_width = 0.10, inner_track_arrow_head_length = 0.07,
  png1 = out1, png2 = out2
)
file.exists(out1) && file.exists(out2)
```