

# Package: circplot (via r-universe)

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**Title** Circular Plots

**Description** Tools to make circular plots.

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**Depends** R (>= 3.1.0)

**Imports** graphics, qtl2

**Suggests** devtools, roxygen2

**License** GPL-3

**URL** <https://github.com/kbroman/circplot>

**BugReports** <https://github.com/kbroman/circplot/issues>

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plot\_scan1\_circ      *plot a genome scan as a circle*

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### Description

Plot LOD curves for a genome scan as a circle

### Usage

```
plot_scan1_circ(
  x,
  map,
  lodcolumn = 1,
  chr = NULL,
  gap = NULL,
  rlim = c(5, 6),
  start_angle = pi,
  clockwise = TRUE,
  xlim = NULL,
  ylim = NULL,
  chr_labels = TRUE,
  lwd = 2,
  col = "slateblue",
  lty = 1,
  add = FALSE,
  ...
)
```

### Arguments

x	Output of <code>qt12::scan1()</code>
map	A list of vectors of marker positions, as produced by <code>qt12::insert_pseudomarkers()</code> .
lodcolumn	LOD score column to plot (a numeric index, or a character string for a column name). Only one value allowed.
chr	Selected chromosomes to plot; a vector of character strings.
gap	Gap between chromosomes. The default is 1% of the total genome length.
rlim	radius limits
start_angle	angle to start
clockwise	If true, go clockwise
xlim	x-axis limits
ylim	y-axis limits
chr_labels	Whether to add chromosome labels
lwd	line width for LOD curves

col	color for LOD curves
lty	line type for LOD curves
add	Add curves to previous plot (need care about matching rlim and ylim)
...	Additional graphics parameters

**Value**

No return value

**Examples**

```
library(qtl2)
iron <- read_cross2(system.file("extdata", "iron.zip", package="qtl2"))
map <- insert_pseudomarkers(iron$gmap, step=1)
probs <- calc_genoprob(iron, map, error_prob=0.002)
pheno <- iron$pheno
covar <- match(iron$covar$sex, c("f", "m")) # make numeric
names(covar) <- rownames(iron$covar)
Xcovar <- get_x_covar(iron)

out <- scan1(probs, pheno, addcovar=covar, Xcovar=Xcovar)
kinship <- calc_kinship(probs, "loco")
out_lmm <- scan1(probs, pheno, kinship, covar, Xcovar)

max_lod <- max(c(maxlod(out), maxlod(out_lmm)))
plot_scan1_circ(out, map, ylim=c(0, max_lod), rlim=c(5, 7))
plot_scan1_circ(out_lmm, map, col="violetred", lty=2, add=TRUE,
               ylim=c(0, max_lod), rlim=c(5, 7))
```

xy2circ

*convert cartesian coordinates to circular coordinates***Description**

convert standard cartesian coordinates to coordinates in a circular plot

**Usage**

```
xy2circ(
  x,
  y = NULL,
  xlim = NULL,
  ylim = NULL,
  rlim = c(1, 2),
  start_angle = pi,
  clockwise = TRUE
)
```

**Arguments**

x	vector of x coordinates, or a 2-column matrix with columns x and y
y	vector of y coordinates (ignored if x is a 2-column matrix)
xlim	x-axis limits
ylim	y-axis limits
rlim	radius limits for plot
start_angle	angle to start
clockwise	If true, go clockwise

**Value**

2-column data frame of (x,y) locations in circle plot

**Examples**

```
x <- seq(0, 18*pi, len=251)
y <- sin(x)
rlim <- c(4, 7)
xl <- c(-rlim[2], rlim[2])*1.1
yl <- range(y)
par(bty="n", pty="s")
plot(0, 0, type="n", xaxs="i", yaxs="i", xlim=xl, ylim=yl,
     xaxt="n", yaxt="n", xlab="", ylab="")
pos <- xy2circ(x, y, rlim=rlim)
lines(pos, lwd=2, col="slateblue")
circ <- xy2circ(x, rep(0, length(x)), rlim=rlim, ylim=yl)
lines(circ, lwd=2)
```

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