

Package ‘OmicCircos’

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Title High-quality circular visualization of omics data

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biocViews Visualization,Statistics,Annotation

Depends R (>= 2.14.0), methods,GenomicRanges

Description OmicCircos is an R application and package for generating high-quality circular plots for omics data.

License GPL-2

NeedsCompilation no

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OmicCircos-package *OmicCircos package*

Description

OmicCircos is for generating high-quality circular plots for omics data.

Author(s)

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References

OmicCircos: an R package for simple and circular visualization of omics data. *Cancer Inform.* 2014 Jan 16;13:13-20. doi: 10.4137/CIN.S13495. eCollection 2014. PMID: 24526832 [PubMed] PMCID: PMC3921174

circos *draw circular*

Description

This is the main function of OmicCircos to draw circular plots.

Usage

```
circos(mapping=mapping, xc=400, yc=400, R=400, W=W, cir="", type="n",
        col.v=3, B=FALSE, print.chr.lab=TRUE, col.bar=FALSE, col.bar.po = "topleft",
        cluster=FALSE, order=NULL, scale=FALSE, cutoff = "n", zoom="", cex=1, lwd=1,
        col=rainbow(10, alpha=0.8)[7], side="")
```

Arguments

| | |
|---------|--|
| mapping | data frame or matrix containing mapping information and values. Column 1: the segment or chromosome ID; column 2: the position; column 3: the position label (optional) or the value and additional columns are the values. such as gene expression and copy number. Missing values are allowed and will be ignored. |
| xc | integer, the circle center x coordinate |
| yc | integer, the circle center y coordinate |
| R | integer, the circle radius |
| W | integer, the circle width |
| cir | genome reference name (hg19, mm10 ...) or data frame from segAnglePo function or data frame from user's mapping data. |
| type | the type is one of <ul style="list-style-type: none"> • "arc": arcs with variable radii • "arc2": arcs with the fixed radius • "b": bar charts |

- "b2": bar charts (opposite side of cutoff value)
- "b3": bar charts with the same height
- "box": box plots
- "chr": plots of chromosomes or segments
- "chr2": plots of chromosomes or segments of partial genome
- "ci95": 95% confidence interval lines
- "h": histograms
- "heatmap": heatmaps
- "heatmap2": heatmaps with genomic coordinates
- "highlight.link": link lines for zoom
- "hist": polygons for multiple samples
- "hl": highlight
- "l": lines
- "label": gene labels or text annotations
- "label2": gene labels or text annotations with the same circumference coordinate
- "lh": horizontal lines
- "link.pg": link polygons based on Bezier curve
- "link": link lines based on Bezier curve
- "link2": link lines with smaller intra-chromosome arcs
- "ls": lines in stair steps
- "ml": multiple lines (for more than 1 samples)
- "ml2": multiple horizontal lines
- "ml3": multiple lines in stair steps
- "ms": multiple points
- "quant75": 75% quantile lines
- "quant90": 90% quantile lines
- "s": dots
- "s2": dots with the fixed radius
- "s.sd": dots proportional to standard deviation
- "ss": dot sizes proportional to the values
- "sv": dot sizes proportional to the variances

| | |
|---------------|---|
| col.v | column number. The column value will be displayed. If type=heatmap, the number is as the first column. |
| B | logical: draw background? |
| print.chr.lab | logical: draw chromosomes or segment labels? |
| col.bar | logical: draw col.bar? It is for type=heatmap. |
| col.bar.po | draw col.bar position, e.g. topleft, bottomright. |
| cluster | logical: cluster and draw Dendrogram at left coner? It is for type=heatmap only. |
| order | vector: chromosome or segment order |
| scale | logical: draw scale? |
| cutoff | numeric: for multiple samples |
| zoom | vector containing six values: start chromosome, end chromosome, start position, end position, start angle and end angle |

| | |
|------|---|
| lwd | numeric: line width |
| cex | numeric: font or point sizes |
| col | character or vector: color names |
| side | character (in or out): for type=label(2) only |
| ... | ... |

Author(s)

Ying Hu <yhu@mail.nih.gov> Chunhua Yan <yanch@mail.nih.gov>

References

OmicCircos: an R package for simple and circular visualization of omics data. *Cancer Inform.* 2014 Jan 16;13:13-20. doi: 10.4137/CIN.S13495. eCollection 2014. PMID: 24526832 [PubMed] PMID: PMC3921174

Examples

```
library(OmicCircos);
options(stringsAsFactors = FALSE);

set.seed(1234);

## initial values for simulation data
seg.num    <- 10;
ind.num    <- 20;
seg.po     <- c(20:50);
link.num   <- 10;
link.pg.num <- 4;
## output simulation data
sim.out <- sim.circos(seg=seg.num, po=seg.po, ind=ind.num, link=link.num,
  link.pg=link.pg.num);

seg.f     <- sim.out$seg.frame;
seg.v     <- sim.out$seg.mapping;
link.v    <- sim.out$seg.link
link.pg.v <- sim.out$seg.link.pg
seg.num   <- length(unique(seg.f[,1]));

## select segments
seg.name <- paste("chr", 1:seg.num, sep="");
db       <- segAnglePo(seg.f, seg=seg.name);

colors   <- rainbow(seg.num, alpha=0.5);

pdffile  <- "OmicCircos4vignette1.pdf";
pdf(pdffile, 8, 8);
par(mar=c(2, 2, 2, 2));
plot(c(1,800), c(1,800), type="n", axes=FALSE, xlab="", ylab="", main="");

circos(R=400, cir=db, type="chr", col=colors, print.chr.lab=TRUE, W=4, scale=TRUE);
circos(R=360, cir=db, W=40, mapping=seg.v, col.v=3, type="l", B=TRUE, col=colors[1], lwd=2, scale=TRUE);
circos(R=320, cir=db, W=40, mapping=seg.v, col.v=3, type="ls", B=FALSE, col=colors[9], lwd=2, scale=TRUE);
circos(R=280, cir=db, W=40, mapping=seg.v, col.v=3, type="lh", B=TRUE, col=colors[7], lwd=2, scale=TRUE);
```

```

circos(R=240, cir=db, W=40, mapping=seg.v, col.v=19, type="ml", B=FALSE, col=colors, lwd=2, scale=TRUE);
circos(R=200, cir=db, W=40, mapping=seg.v, col.v=19, type="ml2", B=TRUE, col=colors, lwd=2);
circos(R=160, cir=db, W=40, mapping=seg.v, col.v=19, type="ml3", B=FALSE, cutoff=5, lwd=2);
circos(R=150, cir=db, W=40, mapping=link.v, type="link", lwd=2, col=colors[c(1,7)]);
circos(R=150, cir=db, W=40, mapping=link.pg.v, type="link.pg", lwd=2, col=sample(colors,link.pg.num));

dev.off()

## Not run:
demo(OmicCircos4vignette1)
demo(OmicCircos4vignette2)
demo(OmicCircos4vignette3)
demo(OmicCircos4vignette4)
demo(OmicCircos4vignette5)
demo(OmicCircos4vignette6)
demo(OmicCircos4vignette7)
demo(OmicCircos4vignette8)
demo(OmicCircos4vignette9)
demo(OmicCircos4vignette10)

## End(Not run)

```

segAnglePo

generate circular skeleton data from user's mapping data

Description

This function creates a data frame and converts the segment pointer positions (linear coordinates) into angle values (the angle based coordinates along circumference). In the data frame, column 1 is unique segment or chromosome names; column 2 is the start angle; column 3 is the end angle; column 4 is the accumulative start position; column 5 is the accumulative end position; column 6 is the start position and column 7 is the end position for each segment or chromosome.

Usage

```
segAnglePo(seg.dat=seg.dat, seg=seg, angle.start=angle.start, angle.end=angle.end);
```

Arguments

| | |
|-------------|---|
| seg.dat | the segment data should be a matrix or a data frame: column 1 is the segment name or chromosome name; column 2 is the segment start; column 3 is the segment end; column 4 is segment name2 (optional); and column 5 is segment description (optional). |
| seg | vector: segment names (optional) |
| angle.start | numeric: plot start angle, angle.start=0 by default (optional) |
| angle.end | numeric: plot end angle, angle.end=360 by default (optional) |

Author(s)

Ying Hu <yhu@mail.nih.gov> Chunhua Yan <yanch@mail.nih.gov>

References

OmicCircos: an R package for simple and circular visualization of omics data. *Cancer Inform.* 2014 Jan 16;13:13-20. doi: 10.4137/CIN.S13495. eCollection 2014. PMID: 24526832 [PubMed] PMCID: PMC3921174

Examples

```
library(OmicCircos);
options(stringsAsFactors = FALSE);
set.seed(1234);

## initial values for simulation data
seg.num    <- 10;
ind.num    <- 20;
seg.po     <- c(20:50);
link.num   <- 10;
link.pg.num <- 4;
## output simulation data
sim.out <- sim.circos(seg=seg.num, po=seg.po, ind=ind.num, link=link.num,
  link.pg=link.pg.num);

seg.f      <- sim.out$seg.frame;
seg.v      <- sim.out$seg.mapping;
link.v     <- sim.out$seg.link
link.pg.v  <- sim.out$seg.link.pg
seg.num    <- length(unique(seg.f[,1]));

## select segments
seg.name   <- paste("chr", 1:seg.num, sep="");
db         <- segAnglePo(seg.f, seg=seg.name);

colors    <- rainbow(seg.num, alpha=0.5);
pdffile   <- "OmicCircos4vignette2.pdf";
pdf(pdffile, 8, 8);
par(mar=c(2, 2, 2, 2));
plot(c(1,800), c(1,800), type="n", axes=FALSE, xlab="", ylab="", main="");

circos(R=400, type="chr", cir=db, col=colors, print.chr.lab=TRUE, W=4, scale=TRUE);
circos(R=360, cir=db, W=40, mapping=seg.v, col.v=8, type="box", B=TRUE, col=colors[1], lwd=0.1, scale=TRUE);
circos(R=320, cir=db, W=40, mapping=seg.v, col.v=8, type="hist", B=TRUE, col=colors[3], lwd=0.1, scale=TRUE);
circos(R=280, cir=db, W=40, mapping=seg.v, col.v=8, type="ms", B=TRUE, col=colors[7], lwd=0.1, scale=TRUE);
circos(R=240, cir=db, W=40, mapping=seg.v, col.v=3, type="h", B=FALSE, col=colors[2], lwd=0.1);
circos(R=200, cir=db, W=40, mapping=seg.v, col.v=3, type="s", B=TRUE, col=colors, lwd=0.1);
circos(R=160, cir=db, W=40, mapping=seg.v, col.v=3, type="b", B=FALSE, col=colors, lwd=0.1);
circos(R=150, cir=db, W=40, mapping=link.v, type="link", lwd=2, col=colors[c(1,7)]);
circos(R=150, cir=db, W=40, mapping=link.pg.v, type="link.pg", lwd=2, col=sample(colors,link.pg.num));

dev.off()
```

Description

~~ Methods for function segAnglePo ~~

Methods

```
signature(seg.dat = "data.frame")
signature(seg.dat = "GRanges")
```

Author(s)

Ying Hu <yhu@mail.nih.gov> Chunhua Yan <yanch@mail.nih.gov>

References

OmicCircos: an R package for simple and circular visualization of omics data. *Cancer Inform.* 2014 Jan 16;13:13-20. doi: 10.4137/CIN.S13495. eCollection 2014. PMID: 24526832 [PubMed] PMID: PMC3921174

sim.circos

circular data simulation

Description

This function generates data for user to test the circos functions

Usage

```
sim.circos(seg=10, po=c(20,50), ind=10, link=10, link.pg=10);
```

Arguments

| | |
|---------|--|
| seg | integer, the segment number. The default is 10. |
| po | vector, the segment positions. The default is c(20:50) |
| ind | integer, the number of samples. The default is 10. |
| link | integer, the number of links. The default is 10. |
| link.pg | integer, the number of link ploygons. The default is 10. |

Value

sim.circos returns a list containing at least the following components:

| | |
|-------------|-------------------------------|
| seg.frame | data.frame, segment data |
| seg.mapping | data.frame, mapping data |
| seg.link | data.fame, link data |
| seg.link.pg | data.frame, link polygon data |

Author(s)

Ying Hu <yhu@mail.nih.gov> Chunhua Yan <yanch@mail.nih.gov>

References

OmicCircos: an R package for simple and circular visualization of omics data. *Cancer Inform.* 2014 Jan 16;13:13-20. doi: 10.4137/CIN.S13495. eCollection 2014. PMID: 24526832 [PubMed] PMCID: PMC3921174

Examples

```

library(OmicCircos);
options(stringsAsFactors = FALSE);
set.seed(1234);

## initial values for simulation data
seg.num <- 10;
ind.num <- 20;
seg.po <- c(20:50);
link.num <- 10;
link.pg.num <- 4;
## output simulation data
sim.out <- sim.circos(seg=seg.num, po=seg.po, ind=ind.num, link=link.num,
  link.pg=link.pg.num);

seg.f <- sim.out$seg.frame;
seg.v <- sim.out$seg.mapping;
link.v <- sim.out$seg.link
link.pg.v <- sim.out$seg.link.pg
seg.num <- length(unique(seg.f[,1]));

## select segments
seg.name <- paste("chr", 1:seg.num, sep="");
db <- segAnglePo(seg.f, seg=seg.name);

colors <- rainbow(seg.num, alpha=0.5);
pdffile <- "OmicCircos4vignette3.pdf";
pdf(pdffile, 8, 8);
par(mar=c(2, 2, 2, 2));
plot(c(1,800), c(1,800), type="n", axes=FALSE, xlab="", ylab="", main="");

circos(R=400, type="chr", cir=db, col=colors, print.chr.lab=TRUE, W=4, scale=TRUE);
circos(R=360, cir=db, W=40, mapping=seg.v, col.v=8, type="quant90", B=FALSE, col=colors, lwd=2, scale=TRUE);
circos(R=320, cir=db, W=40, mapping=seg.v, col.v=3, type="sv", B=TRUE, col=colors[7], scale=TRUE);
circos(R=280, cir=db, W=40, mapping=seg.v, col.v=3, type="ss", B=FALSE, col=colors[3], scale=TRUE);
circos(R=240, cir=db, W=40, mapping=seg.v, col.v=8, type="heatmap", lwd=3);
circos(R=200, cir=db, W=40, mapping=seg.v, col.v=3, type="s.sd", B=FALSE, col=colors[4]);
circos(R=160, cir=db, W=40, mapping=seg.v, col.v=3, type="ci95", B=TRUE, col=colors[4], lwd=2);
circos(R=150, cir=db, W=40, mapping=link.v, type="link", lwd=2, col=colors[c(1,7)]);
circos(R=150, cir=db, W=40, mapping=link.pg.v, type="link.pg", lwd=2, col=sample(colors,link.pg.num));

the.col1=rainbow(10, alpha=0.5)[3];
highlight <- c(160, 410, 6, 2, 6, 10, the.col1, the.col1);
circos(R=110, cir=db, W=40, mapping=highlight, type="hl", lwd=1);

the.col1=rainbow(10, alpha=0.1)[3];
the.col2=rainbow(10, alpha=0.5)[1];
highlight <- c(160, 410, 3, 12, 3, 20, the.col1, the.col2);
circos(R=110, cir=db, W=40, mapping=highlight, type="hl", lwd=2);

```


dev.off()

TCGA.BC.cnv.2k.60 *copy number data of TCGA Breast Cancer*

Description

Examples of TCGA Breast Cancer DNA copy number data from 500 genes and 60 samples.

Author(s)

Ying Hu <yhu@mail.nih.gov> Chunhua Yan <yanch@mail.nih.gov>

TCGA.BC.fus *TCGA Breast Cancer gene fusion data.*

Description

Examples of TCGA Breast Cancer gene fusion data from 18 fusion proteins

Author(s)

Ying Hu <yhu@mail.nih.gov> Chunhua Yan <yanch@mail.nih.gov>

TCGA.BC.gene.exp.2k.60
TCGA BRCA expression data

Description

Examples of TCGA Breast Cancer expression data from 500 genes and 60 samples

Author(s)

Ying Hu <yhu@mail.nih.gov> Chunhua Yan <yanch@mail.nih.gov>

TCGA.BC.sample60 *TCGA BRCA Sample names and subtypes*

Description

Names and subtypes of 60 samples for TCGA Breast Cancer expression and copy number data

Author(s)

Ying Hu <yhu@mail.nih.gov> Chunhua Yan <yanch@mail.nih.gov>

TCGA.BC_Her2_cnv_exp *TCGA BRCA expression and cnv association*

Description

The p-values of associations between the TCGA Breast Cancer copy number and gene expression data.

Author(s)

Ying Hu <yhu@mail.nih.gov> Chunhua Yan <yanch@mail.nih.gov>

TCGA.PAM50_geneFu_hg18
BRCA PAM50 gene list (hg18)

Description

Breast cancer PAM 50 gene list (hg18).

Author(s)

Ying Hu <yhu@mail.nih.gov> Chunhua Yan <yanch@mail.nih.gov>

UCSC.chr.colors *chromosome banding colors*

Description

Chromosome banding colors from UCSC Genome Browser

Author(s)

Ying Hu <yhu@mail.nih.gov> Chunhua Yan <yanch@mail.nih.gov>

UCSC.hg18 *human hg18 circumference coordinates*

Description

Human hg18 circumference coordinates (angles) are calculated from hg18 chromosome size data using the seqAnglPo function. The chromosome size data stored in UCSC.hg18.chr.

Author(s)

Ying Hu <yhu@mail.nih.gov> Chunhua Yan <yanch@mail.nih.gov>

UCSC.hg18.chr *human hg18 segment data.*

Description

Human hg18 chromome size and binding data obtained from UCSC Genome Browser cytogenetics table.

Author(s)

Ying Hu <yhu@mail.nih.gov> Chunhua Yan <yanch@mail.nih.gov>

UCSC.hg19 *human hg19 circumference coordinates*

Description

Human hg19 circumference coordinates (angles) are calculated from hg19 chromosome size data using the seqAnglPo function. The chromosome size data stored in UCSC.hg19.chr.

Author(s)

Ying Hu <yhu@mail.nih.gov> Chunhua Yan <yanch@mail.nih.gov>

UCSC.hg19.chr *human hg19 segment data*

Description

Human hg19 chromome size and binding data obtained from UCSC Genome Browser cytogenetics table.

Author(s)

Ying Hu <yhu@mail.nih.gov> Chunhua Yan <yanch@mail.nih.gov>

UCSC.mm10 *mouse mm10 circumference coordinates*

Description

Mouse mm10 circumference coordinates (angles) are calculated from mm10 chromosome size data using the seqAnglPo function. The mouse chromosome size data stored in UCSC.mm10.chr.

Author(s)

Ying Hu <yhu@mail.nih.gov> Chunhua Yan <yanch@mail.nih.gov>

UCSC.mm10.chr *mouse mm10 segment data.*

Description

Mouse mm10 chromosome size and binding data obtained from UCSC Genome Browser cytogenetics table.

Author(s)

Ying Hu <yhu@mail.nih.gov> Chunhua Yan <yanch@mail.nih.gov>

UCSC.mm9 *mouse mm9 circumference coordinates*

Description

Mouse mm9 circumference coordinates (angles) are calculated from mm9 chromosome size data using the seqAnglPo function. The mouse chromosome size data stored in UCSC.mm9.chr.

Author(s)

Ying Hu <yhu@mail.nih.gov> Chunhua Yan <yanch@mail.nih.gov>

UCSC.mm9.chr *mouse mm9 segment data.*

Description

Mouse mm9 chromosome size and binding data obtained from UCSC Genome Browser cytogenetics table.

Author(s)

Ying Hu <yhu@mail.nih.gov> Chunhua Yan <yanch@mail.nih.gov>

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