

# Package ‘OmicCircos’

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**Title** High-quality circular visualization of omic data

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**Depends** R (>= 2.14.0),methods,GenomicRanges

**Description** OmicCircos is an R application and package for generating high-quality circular maps for omic data

**License** GPL-2

**VignetteBuilder** knitr

**Suggests** knitr

**biocViews** Visualization, StatisticalMethod, Annotation

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OmicCircos-package	<i>OmicCircos package</i>
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## Description

OmicCircos is for generating high-quality circular maps for omic data.

## Author(s)

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

## References

OmicCircus: an R package for simple and circular visualization of omic data (in press)

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circos	<i>draw circular</i>
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## Description

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

## Usage

```
circos(mapping=mapping, xc=400, yc=400, R=400, W=W, cir="", type="n", col.v=3, B=F,
print.chr.lab=T, col.bar=F, col.bar.po = "topleft", cluster=F, order=NULL, scale=F,
cutoff = "n", zoom="", lwd=1, col=rainbow(10, alpha=0.5)[7], side="")
```

**Arguments**

mapping	matrix or data frame or character containing draw values with mapping information (please have a look at the format of example data sets) In general, the first column is the segment or chromosome ID, the second column is the positions, the third column is the position label (option) and next column(s) is(are) the values. 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 wide
cir	given genome reference name (hg19, mm10 ...) or data frame (user's mapping data)
type	the type is one of "b": bar chart, "box": boxplot, "h": histogram, "hist": polygon for multiple samples, "hl": highlight, "l": line graph, "link": linked line based on Bezier curve, "link.pg": linked polygon based on Bezier curve, "heatmap": heatmap, "label": gene label or text annotation.
col.v	number of column. The column value will be drawn. If type=heatmap, the number is as the first column.
B	logical: draw background?
print.chr.lab	logical: draw chromosome or segment labels?
col.bar	logical: draw col.bar? It is for type=heatmap only by the version.
col.bar.po	draw col.bar position (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
col	character or vector: color name(s).
side	character (in or out): for type=label only.
...	...

**Author(s)**

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

**References**

OmicCircus: an R package for simple and circular visualization of omic data

## Examples

```

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

set.seed(1234);

## initial
seg.num    <- 10;
ind.num    <- 20;
seg.po     <- c(20:50);
link.num   <- 10;
link.pg.num <- 10;

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]));

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=0.1, scale=TRUE);
circos(R=320, cir=db, W=40, mapping=seg.v, col.v=3, type="ls", B=FALSE, col=colors[3], lwd=0.1, scale=TRUE);
circos(R=280, cir=db, W=40, mapping=seg.v, col.v=3, type="lh", B=TRUE, col=colors[7], lwd=0.1, scale=TRUE);
circos(R=240, cir=db, W=40, mapping=seg.v, col.v=19, type="ml", B=FALSE, col=colors, lwd=0.1, scale=TRUE);
circos(R=200, cir=db, W=40, mapping=seg.v, col.v=19, type="ml2", B=TRUE, col=colors, lwd=0.1);
circos(R=160, cir=db, W=40, mapping=seg.v, col.v=19, type="ml3", B=FALSE, cutoff=5, lwd=0.1);
circos(R=150, cir=db, W=40, mapping=link.v, type="link", lwd=2, col=colors);
circos(R=150, cir=db, W=40, mapping=link.pg.v, type="link.pg", lwd=2, col=colors);

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 by user's mapping data*

---

## Description

This function creates a matrix for the draw circular. In the matrix, column 1 is unique segment or chromosome names; column 2 is for the angle start, column 3 the angle end, column 4 is for the accumulative start point number, column 5 is for the accumulative end point number, column 6 is for the start point number, column 6 is for the end point number.

## Usage

```
segAnglePo(seg.dat=seg.dat, seg=seg);
```

## Arguments

seg.dat	the data should be matrix or data frame. column 1 is segment name or chromosome name, column 2 is segment start, column 3 is segment end, column 4 is segment name2 (option) and column 5 is segment discription (option).
seg	vector: segment names (option)

## Author(s)

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

## References

OmicCircus: an R package for simple and circular visualization of omic data

## Examples

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

## initial
seg.num <- 10;
ind.num <- 20;
seg.po <- c(20:50);
link.num <- 10;
```

```

link.pg.num <- 10;

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]));

##
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, mapping=seg.v, 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);
circos(R=150, cir=db, W=40, mapping=link.pg.v, type="link.pg", lwd=2, col=colors);

dev.off()

```

---

segAnglePo-methods      *~~ Methods for Function segAnglePo ~~*

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## 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

OmicCircus: an R package for simple and circular visualization of omic data

---

sim.circos	<i>circular data simulation</i>
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---

## 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	the segment nubers, integer. The default is 10.
po	the position number at one segment, vector. The default is c(20:50)
ind	the individual number, iteger. The default is 10.
link	the link number, integer. The default is 10.
link.pg	the link ploygon number, integer. The default is 10.

## Value

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

seg.s	data.frame, db information
seg.v	data.frame, mapping data
link.v	data.fame, mapping data for link
seg.v	data.frame, mapping data for link polygon

## Author(s)

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

## References

OmicCircus: an R package for simple and circular visualization of omic data

## Examples

```

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

## initial
seg.num    <- 10;
ind.num    <- 20;
seg.po     <- c(20:50);
link.num   <- 10;
link.pg.num <- 10;

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(mapping=seg.v, 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=0.1, scale=TRUE);
circos(R=320, cir=db, W=40, mapping=seg.v, col.v=3, type="sv", B=TRUE, col=colors[7], lwd=0.1, scale=TRUE);
circos(R=280, cir=db, W=40, mapping=seg.v, col.v=3, type="ss", B=FALSE, col=colors[3], lwd=0.1, 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], lwd=0.1);
circos(R=160, cir=db, W=40, mapping=seg.v, col.v=3, type="ci95", B=TRUE, col=colors[4], lwd=0.1);
circos(R=150, cir=db, W=40, mapping=link.v, type="link", lwd=2, col=colors);
circos(R=150, cir=db, W=40, mapping=link.pg.v, type="link.pg", lwd=2, col=colors);

the.col1=rainbow(10, alpha=0.3)[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=2);

the.col1=rainbow(10, alpha=0.01)[3];
the.col2=rainbow(10, alpha=0.8)[1];
highlight <- c(160, 410, 6, 12, 7, 10, the.col1, the.col2);
circos(R=110, cir=db, W=40, mapping=highlight, type="hl", lwd=2);

dev.off()

```



---

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

---

**Description**

This data set is the sub DNA copy number data of TCGA Breast Cancer.

**Author(s)**

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

---

TCGA.BC.fus      *gene fusion (partly) of TCGA Breast Cancer*

---

**Description**

This data set is the gene fusion data of TCGA Breast Cancer.

**Author(s)**

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

---

TCGA.BC.fus.lab      *gene fusion (partly) of TCGA Breast Cancer*

---

**Description**

This data set is the fusion gene symbols of TCGA Breast Cancer.

**Author(s)**

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

---

TCGA.BC.gene.exp.2k.60      *sub gene expression data of TCGA Breast Cancer*

---

**Description**

This data set is the sub gene expression data of TCGA Breast Cancer.

**Author(s)**

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

---

TCGA.BC.sample60      *sub types of TCGA Breast Cancer sub data set*

---

**Description**

This data set is the sub types of TCGA Breast Cancer sub data set

**Author(s)**

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

---

TCGA.BC\_Her2\_cnv\_exp      *the pvalues of the association between the copy number and gene expression of sub TCGA Breast Cancer data set*

---

**Description**

This data set is the pvalues of the association between the copy number and gene expression of sub TCGA Breast Cancer data set.

**Author(s)**

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

---

TCGA.PAM50\_genefu\_hg18  
*PAM50 gene list (hg18)*

---

**Description**

This data set is the PAM 50 gene list (hg18).

**Author(s)**

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

---

UCSC.chr.colors	<i>chromosome banding colors from UCSC Genome Browser</i>
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**Description**

chromosome banding colors from UCSC Genome Browser

**Author(s)**

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

---

UCSC.hg18	<i>human hg18 mapping reference by UCSC cytogenetics table</i>
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---

**Description**

This data set is the human hg18 mapping reference by UCSC cytogenetics table. It was generated by hg18.chr data set using seg.angle.po function.

**Author(s)**

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

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UCSC.hg18.chr	<i>human hg18 cytogenetics table from UCSC Genome Browser</i>
---------------	---

---

**Description**

This data set is the human hg18 cytogenetics data by UCSC.

**Author(s)**

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

---

UCSC.hg19	<i>human hg19 mapping reference by UCSC cytogenetics table</i>
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---

**Description**

This data set is the human hg19 mapping reference by UCSC cytogenetics table. It was generated by hg19.chr data set using seg.angle.po function.

**Author(s)**

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

---

UCSC.hg19.chr

*human hg19 cytogenetics table from UCSC Genome Browser*

---

**Description**

This data set is the human hg19 cytogenetics data by UCSC.

**Author(s)**

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

---

UCSC.hg19.mac3

*seg.angle.po output of human hg19 and monkey rhemac3 by UCSC Genome Browser*

---

**Description**

This data set is the seg.angle.po output of human hg19 and monkey rhemac3 by UCSC Genome Browser.

**Author(s)**

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

---

UCSC.hg19.mac3.chr

*human hg19 and monkey rhemac3 cytogenetics tables from UCSC Genome Browser*

---

**Description**

This data set is human hg19 and monkey rhemac3 cytogenetics tables from UCSC Genome Browser.

**Author(s)**

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

---

UCSC.hg19.mm10	<i>seg.angle.po output of human hg19 and mouse mm10 by UCSC Genome Browser</i>
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---

**Description**

This data set is the seg.angle.po output of the human hg19 and mouse mm10 by UCSC Genome Browser.

**Author(s)**

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

---

UCSC.hg19.mm10.chr	<i>human hg19 and mouse mm10 cytogenetics tables from UCSC Genome Browser</i>
--------------------	---

---

**Description**

This data set is human hg19 and mouse mm10 cytogenetics tables from UCSC Genome Browser.

**Author(s)**

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

---

UCSC.hs_cyto_mac	<i>genome comparison of human hg19 and Macaca mulatta Mac3 by UCSC Genome Browser</i>
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**Description**

This data set is the genome comparison of the human hg19 and Macaca mulatta Mac3 by UCSC Genome Browser.

**Author(s)**

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

---

UCSC.hs_cyto_mm	<i>genome comparison of human hg19 and mouse mm10 by UCSC Genome Browser</i>
-----------------	--

---

**Description**

This data set is the genome comparison of the human hg19 and mouse mm10 by UCSC Genome Browser.

**Author(s)**

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

---

UCSC.mm10	<i>mouse mm10 mapping reference by UCSC cytogenetics table</i>
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---

**Description**

This data set is the mouse mm10 mapping reference by UCSC cytogenetics table. It was generated by mm10.chr data set using seg.angle.po function.

**Author(s)**

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

---

UCSC.mm10.chr	<i>mouse mm10 cytogenetics table from UCSC Genome Browser</i>
---------------	---

---

**Description**

This data set is the mouse mm10 cytogenetics data by UCSC.

**Author(s)**

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

---

UCSC.mm9

*mouse mm9 mapping reference by UCSC cytogenetics table*

---

**Description**

This data set is the mouse mm9 mapping reference by UCSC cytogenetics table. It was generated by mm9.chr data set using seg.angle.po function.

**Author(s)**

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

---

UCSC.mm9.chr

*mouse mm9 cytogenetics table from UCSC Genome Browser*

---

**Description**

This data set is the mouse mm9 cytogenetics data by UCSC.

**Author(s)**

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

---

UCSC\_cytoband\_hg19\_Mac3

*combined cytogenetics data in human hg18 and Macaca mulatta Mac3*

---

**Description**

This data set is the combined cytogenetics data in human hg18 and Macaca mulatta Mac3

**Author(s)**

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

---

UCSC\_cytoband\_hg19\_mm10

*combined cytogenetics data in human hg18 and mouse mm10*

---

**Description**

This data set is the combined cytogenetics data in human hg18 and mouse mm10

**Author(s)**

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

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