

# Package ‘OmicCircos’

December 2, 2025

**Version** 1.48.0

**Date** 2015-02-23

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

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

**Maintainer** Ying Hu <yhu@mail.nih.gov>

**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

**git\_url** <https://git.bioconductor.org/packages/OmicCircos>

**git\_branch** RELEASE\_3\_22

**git\_last\_commit** de926fd

**git\_last\_commit\_date** 2025-10-29

**Repository** Bioconductor 3.22

**Date/Publication** 2025-12-01

## Contents

|                        |    |
|------------------------|----|
| OmicCircos-package     | 2  |
| circos                 | 2  |
| segAnglePo             | 5  |
| segAnglePo-methods     | 7  |
| sim.circos             | 7  |
| TCGA.BC.cnv.2k.60      | 9  |
| TCGA.BC.fus            | 9  |
| TCGA.BC.gene.exp.2k.60 | 9  |
| TCGA.BC.sample60       | 10 |
| TCGA.BC_Her2_cnv_exp   | 10 |
| TCGA.PAM50_genefu_hg18 | 10 |
| UCSC.chr.colors        | 10 |
| UCSC.hg18              | 11 |
| UCSC.hg18.chr          | 11 |
| UCSC.hg19              | 11 |
| UCSC.hg19.chr          | 11 |

|                         |           |
|-------------------------|-----------|
| UCSC.mm10 . . . . .     | 12        |
| UCSC.mm10.chr . . . . . | 12        |
| UCSC.mm9 . . . . .      | 12        |
| UCSC.mm9.chr . . . . .  | 12        |
| <b>Index</b>            | <b>13</b> |

---

|                    |                           |
|--------------------|---------------------------|
| OmicCircos-package | <i>OmicCircos package</i> |
|--------------------|---------------------------|

---

**Description**

OmicCircos is for generating high-quality circular plots for omics 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

---

|        |                      |
|--------|----------------------|
| circos | <i>draw circular</i> |
|--------|----------------------|

---

**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                                                                                                                                                                                                                                                                                            |

|                            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
|----------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>cir</code>           | genome reference name (hg19, mm10 ...) or data frame from <code>segAnglePo</code> function or data frame from user's mapping data                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| <code>.</code>             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| <code>type</code>          | <p>the type is one of</p> <ul style="list-style-type: none"> <li>• "arc": arcs with variable radii</li> <li>• "arc2": arcs with the fixed radius</li> <li>• "b": bar charts</li> <li>• "b2": bar charts (opposite side of cutoff value)</li> <li>• "b3": bar charts with the same height</li> <li>• "box": box plots</li> <li>• "chr": plots of chromosomes or segments</li> <li>• "chr2": plots of chromosomes or segments of partial genome</li> <li>• "ci95": 95% confidence interval lines</li> <li>• "h": histograms</li> <li>• "heatmap": heatmaps</li> <li>• "heatmap2": heatmaps with genomic coordinates</li> <li>• "highlight.link": link lines for zoom</li> <li>• "hist": polygons for multiple samples</li> <li>• "hl": highlight</li> <li>• "l": lines</li> <li>• "label": gene labels or text annotations</li> <li>• "label2": gene labels or text annotations with the same circumference coordinate</li> <li>• "lh": horizontal lines</li> <li>• "link.pg": link polygons based on Bezier curve</li> <li>• "link": link lines based on Bezier curve</li> <li>• "link2": link lines with smaller intra-chromosome arcs</li> <li>• "ls": lines in stair steps</li> <li>• "ml": multiple lines (for more than 1 samples)</li> <li>• "ml2": multiple horizontal lines</li> <li>• "ml3": multiple lines in stair steps</li> <li>• "ms": multiple points</li> <li>• "quant75": 75% quantile lines</li> <li>• "quant90": 90% quantile lines</li> <li>• "s": dots</li> <li>• "s2": dots with the fixed radius</li> <li>• "s.sd": dots proportional to standard deviation</li> <li>• "ss": dot sizes proportional to the values</li> <li>• "sv": dot sizes proportional to the variances</li> </ul> |
| <code>col.v</code>         | column number. The column value will be displayed. If <code>type=heatmap</code> , the number is as the first column.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| <code>B</code>             | logical: draw background?                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| <code>print.chr.lab</code> | logical: draw chromosomes or segment labels?                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| <code>col.bar</code>       | logical: draw col.bar? It is for <code>type=heatmap</code> .                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| <code>col.bar.po</code>    | 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: fond 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] 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    <- "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()
```

---

```
segAnglePo-methods      ~~ Methods for Function segAnglePo ~~
```

---

**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] PMCID: 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 | <i>copy number data of TCGA Breast Cancer</i> |
|-------------------|-----------------------------------------------|

---

**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 | <i>TCGA Breast Cancer gene fusion data.</i> |
|-------------|---------------------------------------------|

---

**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 | <i>TCGA BRCA expression data</i> |
|------------------------|----------------------------------|

---

**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 | <i>TCGA BRCA Sample names and subtypes</i> |
|------------------|--------------------------------------------|

---

**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 | <i>TCGA BRCA expression and cnv association</i> |
|----------------------|-------------------------------------------------|

---

**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 | <i>BRCA PAM50 gene list (hg18)</i> |
|------------------------|------------------------------------|

---

**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 | <i>chromosome banding colors</i> |
|-----------------|----------------------------------|

---

**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 circumference coordinates</i> |
|-----------|---------------------------------------------|

---

**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 | <i>human hg18 segment data.</i> |
|---------------|---------------------------------|

---

**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 | <i>human hg19 circumference coordinates</i> |
|-----------|---------------------------------------------|

---

**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 | <i>human hg19 segment data</i> |
|---------------|--------------------------------|

---

**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>

# Index

## \* **methods**

segAnglePo-methods, [7](#)

circos, [2](#)

OmicCircos (OmicCircos-package), [2](#)

OmicCircos-package, [2](#)

segAnglePo, [5](#)

segAnglePo, data.frame-method  
(segAnglePo-methods), [7](#)

segAnglePo, GRanges-method  
(segAnglePo-methods), [7](#)

segAnglePo-methods, [7](#)

sim.circos, [7](#)

TCGA.BC.cnv.2k.60, [9](#)

TCGA.BC.fus, [9](#)

TCGA.BC.gene.exp.2k.60, [9](#)

TCGA.BC.sample60, [10](#)

TCGA.BC\_Her2\_cnv\_exp, [10](#)

TCGA.PAM50\_genefu\_hg18, [10](#)

UCSC.chr.colors, [10](#)

UCSC.hg18, [11](#)

UCSC.hg18.chr, [11](#)

UCSC.hg19, [11](#)

UCSC.hg19.chr, [11](#)

UCSC.mm10, [12](#)

UCSC.mm10.chr, [12](#)

UCSC.mm9, [12](#)

UCSC.mm9.chr, [12](#)