Package 'RCircos'

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Type Package

Title Circos 2D Track Plot

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Description RCircos package provides a simple and flexible way to
generate Circos 2D track plot images for genomic data visualization. The types of plots include: connector, text,heatmap, histogram, line, scatter, link, and tiles. All
functions require only R graphics package that comes with R base installation.

License GPL (>= 2)

Depends R (>= 2.10)

URL <http://bitbucket.org/henryhzhang/rcircos>

R topics documented:

RCircos-package   *Circos-like Plot of Genomic Data*

Description

This is the R implement of basic Circos plots of genimic data for: chromosome ideogram, connectors, gene labels, heatmap, histogram, line, links, scatter, and tiles.

Details

Package:	RCircos
Type:	Package
Version:	1.0
Date:	2013-02-11
License:	GPL (>=2)

Author(s)

Hongen Zhang

Maintainer: Hongen Zhang <hzhang@mail.nih.gov>

References

Hongen Zhang, Paul Meltzer, and Sean Davis. RCircos: an R package for Circos 2D track plots. To be published soon.

Examples

```
library(RCircos)
```

```
RCircos.Base.Plot.Positions
```
Base Positions of Points for Circos Plot

Description

Calculate x- and y-coordinates of points for a circular line which serves as the basis of plot locations for all Crircos tracks and data points.

Usage

```
RCircos.Base.Plot.Positions(cyto.band, RCircos.Par)
```

Arguments

cyto.band   A data frame returned from RCircos.Cytoband.Data(cyto.info, chr.exclude, RCircos.Par) and containing plot data for chromosome ideogram .

RCircos.Par   A list returned from RCircos.Initialize.Parameters() and containing graphicarameters specific for Circos plots.

Details

This function calculates x- and y-coordinates of a set of points that forms a circular line with radius of 1. The coordinates start from (0,1) and move on clockwise. Plot positions for chromosome ideogram, data tracks, data points, and text labels are all derived from these coordinates.

Value

A data frame that contains the x- and y-coordinates of each point on a circular line as well as degrees of text rotation at each point.

Author(s)

Hongen Zhang

```
RCircos.Chromosome.Ideogram
```
Draw Chromosome Ideogram

Description

Draw a circular chromosome ideogram with all or subset of chromosomes, chromosome names, and chromosome highlights. Graphic device must be initialized before drawing.

Usage

```
RCircos.Chromosome.Ideogram(cyto.band, base.positions, RCircos.Par)
```

Arguments

`cyto.band`	A data frame returned from RCircos.Cytoband.Data(cyto.info, chr.exclude, RCircos.Par) and containing plot data for chromosome ideogram .
`base.positions`	
	A data frame returned from RCircos.Base.Plot.Positions(cyto.band, RCircos.Par) and containing x- and y-coordinates of a circlular line as well as degrees of text rotation at each point.
`RCircos.Par`	A list returned from RCircos.Initialize.Parameters() containing graphics parameters specific for Circos plot.

Author(s)

Hongen Zhang

`RCircos.Connector`   *Circos-like Connector Plot*

Description

Draw a set of connectors between two tracks (three lines for each connector). Graphics device must be initialized before drawing.

Usage

```
RCircos.Connector(cyto.band, base.positions, connect.data, track.num, side, RCir
```

Arguments

`cyto.band`	A data frame returned from RCircos.Cytoband.Data(cyto.info, chr.exclude, RCircos.Par) and containing plot data for chromosome ideogram .
`base.positions`	
	A data frame returned from RCircos.Base.Plot.Positions(cyto.band, RCircos.Par) and containing x- an dy-coordinates of a circular lines as well as degrees of text rotation at each point.
`connect.data`	A data frame containing index of plot points for outer (e.g., chromosome ideogram) and inner track (e.g., gene names).
`track.num`	Integer, the number of the plot track inside or outside of chromosome ideogram.
`side`	Character vector, either "in" or "out" representing the position related to chromosome ideogram.
`RCircos.Par`	A list returned from RCircos.Initialize.Parameters() containing graphics paramters specific for Circos plot.

Author(s)

Hongen Zhang

```
RCircos.Cytoband.Data
```
Chromosome Ideogram Data

Description

This function sorts chromosome ideogram data by chromosome and cytoband, calculate band length (number of base pairs), number of points needed to cover the band, relavent locations of each band on the circular layout, and assign colors to chromosome highlights and each band.

Usage

```
RCircos.Cytoband.Data(cytoband, chr.exclude = NULL, RCircos.Par)
```

Arguments

cytoband   A data frame returned from RCircos.Cytoband.Data(cyto.info, chr.exclude, RCircos.Par) and containing plot data for chromosome ideogram .

chr.exclude   Character vector containing of chromosome name(s) that should be excluded from data frame to be returned, or NULL if all chromosomes are included.

RCircos.Par   A list returned from RCircos.Initialize.Parameters() and containing graphic parameters specific for Circos plot.

Value

Chromosome   chromosome name with prefix of "chr"

ChromStar   start position of the band

ChromEnd   end position of the band

Band   band name

Stain   intensity of Giemsa staining

Length   band length in base pairs

Unit   total number of points (chromosome units) to draw for the band

Location   index of last points of the band on the circular line

BandColor   RGB color of the band shown on the Circos image

ChrColor   highlight color of the chromosome

Author(s)

Hongen Zhang

RCircos.Data.Point *Convert Genomic Position to Index of Circos Plot Position*

Description

Calculate the index of Circos plot positions (a set of x- and y-coordinates for a circular line) for a genomic position (chromosome and start position).

Usage

```
RCircos.Data.Point(cyto.band, chromosome, start)
```

Arguments

cyto.band	A data frame returned from RCircos.Cytoband.Data(cyto.info, chr.exclude, RCircos.Par) and containing plot data for chromosome ideogram.
chromosome	Character vector, a chromosome name with or without prefix of "chr".
start	Integer, start position of a genomic interval (e.g, a gene or a band) on the chromosome.

Value

An integer representing the index of Circos plot positions.

Author(s)

Hongen Zhang

RCircos.Gene.Label *Circos-like Gene Label Plot*

Description

Label gene names along chromosome ideogram or a data track.

Usage

```
RCircos.Gene.Label(base.positions, gene.data, name.col, track.num, side, RCircos
```

Arguments

base.positions	A data frame returned from RCircos.Base.Plot.Positions(cyto.band, RCircos.Par) containing x- and y-coordinates for a circular line as well as degrees of text rotation at each position.
gene.data	A data frame containing gene annotation data. The first three columns should be chromosome name, start position, and end position. One column is for gene names and the last column is for Circos plot location of each gene.
name.col	Integer, the number of column for gene name in the gene.data object.

track.num   Integer, the number of plot track inside or outside of chromosome ideogram.

side   Character vector, either "in" or "out", representing the position related to chromosome ideogram.

RCircos.Par   A list returned from RCircos.Initialize.Parameters() containing graphics parameters specific for Circos plot.

Author(s)

Hongen Zhang

RCircos.Gene.Label.Data

Sample Data for Gene Labels

Description

RCircos.Gene.Label.Data contains genomic position information for 192 genes. Each row of the data contains genomic position and gene name for one gene in the order of chromosome name, start position, end position, and gene name.

Usage

    data(RCircos.Gene.Label.Data)

Format

A data frame with 192 observations on the following 4 variables.

Chromosome a factor with levels chr1 chr10 chr11 chr12 chr13 chr14 chr15 chr16 chr17 chr18 chr19 chr2 chr20 chr21 chr22 chr3 chr4 chr5 chr6 chr7 chr8 chr9 chrX

chromStart a numeric vector

chromEnd a numeric vector

Gene a factor with levels ABL1 ACN9 ACVR1B AKT1 ALK APC ARHGEF2 ARID1A ASXL1 ATM ATRX BAG3 BAI3 BAP1 BCAN BCL2 BRAF BRCA1 BRCA2 CA12 CA9 CALU CARD11 CBL CCND1 CD34 CDC73 CDH1 CDK4 CDKN2A CDX2 CEACAM7 CEBPA CES3 CRLF2 CSF1R CSF3 CTNNA1 CTNNB1 CUL2 CYLD CYP1A1 DAXX DCC DES DIRAS1 DIRC2 DKK3 DLD DMBT1 DNMT3A DPYD EGF EGFR EGR3 EIF4G2 EML4 ENO1 ENO2 ERBB2 ERBB3 ERBB4 ERG EZH2 F10 FAM123B FBXW7 FGFR1 FGFR2 FGFR3 FH FHIT FLCN FLT3 FOXL2 FZR1 GATA1 GATA2 GATA3 GFAP GNA11 GNAQ GNAS GRP GSTM1 HIVEP3 HNF1A HRAS IDH1 IDH2 IFNA1 IL2 ITGB5 JAK1 JAK2 JAK3 KDR KIT KRAS KRT20 MAGI1 MAP2K4 MEN1 MET MGMT MIB1 MKI67 MLH1 MPL MSH2 MSH6 MUC1 MUC17 MUC2 MUTYH MVP MYC MYD88 NAT1 NAT2 NES NF1 NF2 NOTCH1 NOTCH2 NPM1 NRAS PBRM1 PCNA PDGFRA PDZD4 PGR PHOX2B PIK3CA PMS2 PPP2R1A PRCC PRKAR1A PTCH1 PTEN PTGS2 PTPN11 RB1 REEP5 RET RNF139 RNF2 RPS15 RUNX1 SDHA SDHAF1 SDHAF2 SDHB SDHC SDHD SELT SETD2 SLC38A1 SLC6A2 SLTM SMAD4 SMARCA4 SMARCB1 SMO SMOX SMUG1 SOCS1 SRC SST STC1 STK11 SUFU SYP TCF7L2 TET2 TFE3 TFEB TMEM97 TNFAIP3 TNFSF13 TP53 TPD52L2 TPM4 TSC1 TSC2 TSHR TYK2 VHL VIM WT1 XRCC1 ZNF135

Source

Unpublished data.

```
RCircos.Get.Label.Locations
```
                 Calculate New Position for Gene or Data Point Labels

---

Description

This function is used to derive a new plot position from genomic position for gene or data point labeling. In case there are too many data points in a genomic interval, text and lines for the lables may become overlapped so that correct numbers and new plot positions are often needed to make the labels readable. This function will remove extra label data points if they cannot fit in the given genomic interval.

Usage

```
RCircos.Get.Label.Locations(cyto.band, genomic.data, label.type = c("text", "lin
```

Arguments

`cyto.band`	A data frame containing plot data for chromosome ideogram returned from RCircos.Cytoband.Data(cyto.info, chr.exclude, RCircos.Par).
`genomic.data`	A data frame containing genomic and Circos plot position data returned from RCircos.Get.Plot.Data(genomic.data, cyto.band).
`label.type`	Character vector, either "text", "line", or "point".
`RCircos.Par`	A list returned from RCircos.Initialize.Parameters() and containing graphics parameters specific for Circos plot.

Value

A data frame containing same contents as the genomic.data plus one column with new Circos plot positions.

Author(s)

Hongen Zhang

```
RCircos.Get.Plot.Data
```
Convert Genomic Data to Circos Plot Data

Description

This function calculates the Circos plot position from genomic position for a dataset. The Circos plot position is the row index of matrix that contains x- and y-coordinates of a circular line. A new column for Circos plot positions is appended to the input genomic.data and returned.

Usage

```
RCircos.Get.Plot.Data(genomic.data, cyto.band)
```

Arguments

`genomic.data`	A data frame with the first three columns as chromosome name, start and end position followed by data values for one or more samples.
`cyto.band`	A data frame containing Circos plot data for chromosome ideogram returned from RCircos.Cytoband.Data(cyto.info, chr.exclude, RCircos.Par).

Value

A data frame with same contents as the genomic.data plus a new column with Circos plot position.

Author(s)

Hongen Zhang

```
RCircos.Heatmap          Circos-like Heamap Plot
```

Description

Draw one track of heatmap. Graphic device must be initialized before drawing and the first four columns of input heatmap.data must be chromosome name, start position, end position, and gene names.

Usage

```
RCircos.Heatmap(cyto.band, base.positions, heatmap.data, data.col, track.num, si
```

Arguments

`cyto.band`	A data frame containing plot data for chromosoem ideogram returned from RCircos.Cytoband.Data(cyto.info, chr.exclude, RCircos.Par).
`base.positions`	
	A data frame returned from RCircos.Base.Plot.Positions(cyto.band, RCircos.Par) containing x- and y-coordinates for a circular line as well as degrees of text rotation at each position.
`heatmap.data`	A data frame, converted from genomic data by RCircos.Get.Plot.Data(genomic.data, cyto.band), containing genomic positions, genomic data values, and Circos plot positions.
`data.col`	Integer, the number of column for the data to be plotted.
`track.num`	Integer, the number of the plot track inside or outside of chromosome ideogram.
`side`	Character vector, either "in" or "out" representing the position related to chromosome ideogram.
`RCircos.Par`	A list returned from RCircos.Initialize.Parameters() containing graphics paramters specific for Circos plot.

Author(s)

Hongen Zhang

`RCircos.Heatmap.Data`
                              Sample Data for RCircos Heatmap Plot

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Description

A dataset with the first three columns as chromosome names, start position, and end position followed by a column of gene names then columns of gene expression values.

Usage

```
data(RCircos.Heatmap.Data)
```

Format

A data frame with 6660 observations on the following 10 variables.

Chromosome a factor with levels `chr1 chr10 chr11 chr12 chr13 chr14 chr15 chr16`
    `chr17 chr18 chr19 chr2 chr20 chr21 chr22 chr3 chr4 chr5 chr6 chr7 chr8`
    `chr9 chrX chrY`

`chromStart` a numeric vector

`chromEnd` a numeric vector

`GeneName` a character vector

`X786.O` a numeric vector

`A498` a numeric vector

`A549.ATCC` a numeric vector

`ACHN` a numeric vector

`BT.549` a numeric vector

`CAKI.1` a numeric vector

Source

Modified from NCBI GEO dataset: GSE32474.

RCircos.Histogram   *Circos-like Histogram Plot*

Description

Draw one track of histogram. Graphic device must be initialized before drawing and the first three columns of input hist.data must be chromosome name, start position, end position.

Usage

```
RCircos.Histogram(cyto.band, base.positions, hist.data, data.col, track.num, sid
```

Arguments

cyto.band	A data frame containing plot data for chromosoem ideogram returned from RCircos.Cytoband.Data(cyto.info, chr.exclude, RCircos.Par).
base.positions	
	A data frame returned from RCircos.Base.Plot.Positions(cyto.band, RCircos.Par) containing x- and y-coordinates for a circular line as well as degrees of text rotation at each position.
hist.data	A data frame, converted from genomic data by RCircos.Get.Plot.Data(genomic.data, cyto.band), containing genomic positions, genomic data values, and Circos plot positions.
data.col	Integer, the number of column for the data to be plotted.
track.num	Integer, the number of the plot track inside or outside of chromosome ideogram.
side	Character vector, either "in" or "out" representing the position related to chromosome ideogram.
RCircos.Par	A list returned from RCircos.Initialize.Parameters() containing graphics parameters specific for Circos plot.

Author(s)

Hongen Zhang

`RCircos.Histogram.Data`

Sample Data for Circos Histogram Plot

Description

A dataset with the first three columns as chromosome names, start position, and end position followed by a column of histogram data.

Usage

```
data(RCircos.Histogram.Data)
```

Format

A data frame with 324 observations on the following 4 variables.

Chromosome a factor with levels `chr1 chr10 chr11 chr12 chr13 chr14 chr15 chr16`
`chr17 chr18 chr19 chr2 chr20 chr21 chr22 chr3 chr4 chr5 chr6 chr7 chr8`
`chr9 chrX chrY`

chromStart a numeric vector

chromEnd a numeric vector

Data a numeric vector

Source

Unpulished data.

`RCircos.Initialize.Parameters`

Initialize Graphics Parameters for Circos Plot

Description

Set up default values for parameters of chromosome ideogram and data plots. All parameters are held in a list and returned for outside use.

Usage

```
RCircos.Initialize.Parameters()
```

Value

base.per.unit

Integer, number of base pairs covered by one plot point, default: 3000.

chrom.paddings

Integer, padding length between two chromosomes in chromosome units, default: 3000.

radius.len   Float number, radius of circular line to calculate all plot positions, default: 1.0.

chr.ideog.pos

Float number, location of chromosome ideogram, default: radius.len + 0.1.

highlight.pos

Float number, location of chromosome highlight, default: radius.len + 0.2 .

chr.name.pos

Float number, location of chromosome name labels, default: radius.len + 0.3.

plot.radius   Float, the radius of maximum plot area, default: radius.len + 0.5.

track.in.start

Float number, location of first track inside of chromosome ideogram, default: chr.ideog.pos - 0.05.

track.out.start

Float number, location of first track outside of chromosome ideigram, default: radius.len + 0.4.

chrom.width   Float number, width of chromosomes on ideogram, default: 0.08.

track.padding

Float number, padding width beteen two plot tracks, default: 0.02.

track.height

Float number, height of data plot track, default: 0.1.

highlight.width

Integer, line type of chromosome highlight, default: 1.

hist.width   Integer, width of histogram columns, in chromosome units, default: 1000.

text.size   Float number, cex value of gene names for circular label, default: 0.4.

heatmap.width

Integer, heatmap cell width, in chromosome units, default: 100.

point.type   Character type for point plot, default: ".".

point.size   Integer, character size for point plot, default: 1.

max.layers   Integer, maximum number of layers for tile plot, default: 5.

Author(s)

Hongen Zhang

RCircos.Line.Data   *Sample Data for Circos Line Plot*

Description

A data frame with the first three columns as chromosome name, start and end position followed by columns of DNA copy number variant data (num.mark and seg.mean).

Usage

```
data(RCircos.Line.Data)
```

Format

A data frame with 2037 observations on the following 5 variables.

chromosome a factor with levels 1 10 11 12 13 14 15 16 17 18 19 2 20 21 22 3 4 5 6 7 8
    9 X Y

start a numeric vector

stop a numeric vector

num.mark a numeric vector

seg.mean a numeric vector

Source

Unpublished data.

RCircos.Line.Plot   *Circos-like Line Plot*

Description

Draw one track of line plot. Graphics device must bae initialized before drawing.

Usage

```
RCircos.Line.Plot(cyto.band, base.positions, line.data, data.col, track.num, sid
```

Arguments

cyto.band   A data frame containing plot data for chromosoem ideogram returned from
                RCircos.Cytoband.Data(cyto.info, chr.exclude, RCircos.Par).

base.positions
                A data frame returned from RCircos.Base.Plot.Positions(cyto.band, RCircos.Par)
                containing x- and y-coordinates for a circular line as well as degrees of text rotation at each position.

line.data   A data frame, converted from genomic data by RCircos.Get.Plot.Data(genomic.data,
                cyto.band), containing genomic positions, genomic data values, and Circos plot positions.

`data.col`	Integer, the number of column for the data to be plotted.
`track.num`	Integer, the number of the plot track inside or outside of chromosome ideogram.
`side`	Character vector, either "in" or "out" representing the position related to chromosome ideogram.
`RCircos.Par`	A list returned from RCircos.Initialize.Parameters() containing graphics paramters specific for Circos plot.

Author(s)

Hongen Zhang

`RCircos.Link.Data`   *Sample Data for Circos Link Plot*

Description

A data frame containing paired genomic position data for each row. The content of each row must be in the order of name, start and end position of chromosome A then name, start and end position of chromosome B. This data frame is directly used to draw link lines without extra processing.

Usage

```
data(RCircos.Link.Data)
```

Format

A data frame with 71 observations on the following 6 variables.

Chromosome a factor with levels `chr1 chr10 chr11 chr12 chr14 chr15 chr17 chr19 chr2 chr21 chr22 chr3 chr4 chr5 chr6 chr7 chr8 chr9 chrX`

chromStart a numeric vector

chromEnd a numeric vector

Chromosome.1 a factor with levels `chr1 chr10 chr11 chr12 chr14 chr15 chr16 chr17 chr18 chr19 chr2 chr20 chr21 chr22 chr3 chr4 chr5 chr6 chr7 chr8 chr9 chrX`

chromStart.1 a numeric vector

chromEnd.1 a numeric vector

Source

Unpublished data.

RCircos.Link.Line   *Draw A Circos Link Line*

Description

Calculate and draw a quandratic Bezire curve between two points with (0,0) as control points. Graphic device must be initialized before drawing.

Usage

```
RCircos.Link.Line(point.locations, point.one, point.two, color)
```

Arguments

`point.locations`

> A data frame returned from RCircos.Base.Plot.Positions(cyto.band, RCircos.Par) containing x- and y-coordinates for a circular line as well as degrees of text rotation at each position.

`point.one`   The first point (start point) of the Bezier curve.

`point.two`   The last point (end point) of the Bezier curve.

`color`   Color for the Bezier curve.

Author(s)

Hongen Zhang

RCircos.Link.Plot   *ircos-like Link Line Plot*

Description

Draw lines(quandratic Bezier curves) between paired genomic positions. Graphic device must be initialize before drawing. Link lines are always in the most inner of data plot area.

Usage

```
RCircos.Link.Plot(cyto.band, base.positions, link.data, track.num, by.chromosome
```

Arguments

`cyto.band`   A data frame containing plot data for chromosome ideogram returned from RCircos.Cytoband.Data(cyto.info, chr.exclude, RCircos.Par).

`base.positions`

> A data frame returned from RCircos.Base.Plot.Positions(cyto.band, RCircos.Par) containing x- and y-coordinates for a circular line as well as degrees of text rotation at each position.

`link.data`   A data frame that contains data for links between genomic positions. The first three columns of the data frame are chromosome name, start position, and end position for first genomic position followed by the chromosome name, start, and end position for second genomic position.

`track.num`   Integer, the number of the plot track inside or outside of chromosome ideogram.

`by.chromosome`

Boolean, If true, red color will be used for links between positions of same chromosomes and blue color for links between different chromosomes. Otherwise, different colors will be automatically assigned for each line.

`RCircos.Par` A list returned from RCircos.Initialize.Parameters() containing graphics paramters specific for Circos plot.

Author(s)

Hongen Zhang

`RCircos.List.Parameters`
Print out Graphic Parameters to Standard Output

Description

Display all graphic parameters specific for Circos plot on standard output.

Usage

```
RCircos.List.Parameters(RCircos.Par)
```

Arguments

`RCircos.Par` A list returned from RCircos.Initialize.Parameters() that contains graphics parameters specific for Circos plot.

Author(s)

Hongen Zhang

`RCircos.Mouse.Expr.Data`
Sample Data of Mouse Gene Expression

Description

A data frame containing mouse genomic position information and gene expresio n values.

Usage

```
data(RCircos.Mouse.Expr.Data)
```

Format

A data frame with 16499 observations on the following 5 variables.

Chromosome a factor with levels `chr1 chr10 chr11 chr12 chr13 chr14 chr15 chr16 chr17 chr18 chr19 chr2 chr3 chr4 chr5 chr6 chr7 chr8 chr9 chrX chrY`

txStart a numeric vector

txEnd a numeric vector

Gene a character vector

Expr.Mean a numeric vector

Source

Modified from GEO dataset: GSE42081.

`RCircos.Rat.Expr.Data`

Sample Data of Rat Gene Expression

Description

A data frame containing rat genes, genomic position and expression values of these genes.

Usage

```
data(RCircos.Rat.Expr.Data)
```

Format

A data frame with 11426 observations on the following 5 variables.

Chromosome a factor with levels `chr1 chr10 chr11 chr12 chr13 chr14 chr15 chr16 chr17 chr18 chr19 chr2 chr20 chr3 chr4 chr5 chr6 chr7 chr8 chr9 chrX`

txStart a numeric vector

txEnd a numeric vector

Gene a character vector

Expr.Mean a numeric vector

Source

Modified from GEO dataset: GSE42081.

```
RCircos.Reset.Ideogram.Position
```
Reset Graphics Parameters Derived from Radius

Description

Reset parameters derived from radius length such as plot positions for chromosome ideogram, chromosome highlight, chromosome names, inside and outside tracks, and radius of plot area.

Usage

```
RCircos.Reset.Ideogram.Position(RCircos.Par, radius.len)
```

Arguments

RCircos.Par   A list returned from RCircos.Initialize.Parameters() containing graphics paramters specific for Circos plot.

radius.len   Float number, radius length of the circular line which served as the basis for calculation of Circos plot position.

Details

Parameters to be changed and their values: chr.ideog.pos(radius.len + 0.1), highlight.pos(radius.len + 0.2), chr.name.pos(radius.len + 0.3), track.in.start(chr.ideog.pos - 0.05), track.out.start(chr.name.pos + 0.1), and plot.radius (radius.len + 0.5).

Value

A list with updataed values of contents same as the input argument.

Author(s)

Hongen Zhang

```
RCircos.Scatter.Data
```
Sample Data for Circos Scatter Plot

Description

A data frame with the first three columns as chromosome name, start and end position followed by columns of DNA copy number variant data (num.mark and seg.mean).

Usage

```
data(RCircos.Scatter.Data)
```

Format

A data frame with 1757 observations on the following 5 variables.

chromosome a factor with levels 1 10 11 12 13 14 15 16 17 18 19 2 20 21 22 3 4 5 6 7 8 9 X Y

start a numeric vector

stop a numeric vector

num.mark a numeric vector

seg.mean a numeric vector

RCircos.ScatterPlot

Circos-like Scatter Plot

Description

Draw one track of scatter plot. Graphics device must be initialized before drawing.

Usage

```
RCircos.ScatterPlot(cyto.band, base.positions, scatter.data, data.col, track.num
```

Arguments

cyto.band	A data frame containing plot data for chromosoem ideogram returned from RCircos.Cytoband.Data(cyto.info, chr.exclude, RCircos.Par).
base.positions	A data frame returned from RCircos.Base.Plot.Positions(cyto.band, RCircos.Par) containing x- and y-coordinates for a circular line as well as degrees of text rotation at each position.
scatter.data	A data frame, converted from genomic data by RCircos.Get.Plot.Data(genomic.data, cyto.band), containing genomic positions, scatterplot data values, and Circos plot positions.
data.col	Integer, the number of column for the data to be plotted.
track.num	Integer, the number of the plot track inside or outside of chromosome ideogram.
side	Character vector, either "in" or "out" representing the position related to chromosome ideogram.
by.fold	Zero or a positive float number, if it is greater than zero, any data point with a value greater or equal to the by.fold will be plot as red color and data points with values less or equal to negative by.fold will be plot as blue colr. Otherwise, black color is used.
RCircos.Par	A list returned from RCircos.Initialize.Parameters() containing graphics paramters specific for Circos plot.

Author(s)

Hongen Zhang

RCircos.Tile.Data   *Sample Data for Circos Tile Plot*

Description

A data frame contining genomic position data only (chromosome, start and end positions).

Usage

```
data(RCircos.Tile.Data)
```

Format

A data frame with 152 observations on the following 3 variables.

Chromosome a factor with levels `chr1 chr10 chr11 chr12 chr13 chr14 chr15 chr16`
    `chr17 chr18 chr19 chr2 chr20 chr21 chr22 chr3 chr4 chr5 chr6 chr7 chr8`
    `chr9 chrX chrY`

chromStart a numeric vector

chromEnd a numeric vector

Source

Unpublished Data.

RCircos.Tile.Plot   *Circos-like Tile Plot*

Description

Draw one track of Tiles. Graphics device must be initialized before drawing.

Usage

```
RCircos.Tile.Plot(cyto.band, base.positions, tile.data, track.num, side, RCircos
```

Arguments

cyto.band
: A data frame containing plot data for chromosoem ideogram returned from RCircos.Cytoband.Data(cyto.info, chr.exclude, RCircos.Par).

base.positions
: A data frame returned from RCircos.Base.Plot.Positions(cyto.band, RCircos.Par) containing x- and y-coordinates for a circular line as well as degrees of text rotation at each position.

tile.data
: A data frame, converted from genomic data by RCircos.Get.Plot.Data(genomic.data, cyto.band), containing genomic positions (chromose name, start and end positions) and Circos plot positions.

track.num
: Integer, the number of the plot track inside or outside of chromosome ideogram.

side   Character vector, either "in" or "out" representing the position related to chro-
              mosome ideogram.

RCircos.Par   A list returned from RCircos.Initialize.Parameters() containing graphics paramters
              specific for Circos plot.

Author(s)

Hongen Zhang

RCircos.Track.Outline
Draw Outline of Data Plot Track

Description

Draw outline with subtracks for one data plot track.

Usage

```
RCircos.Track.Outline(cyto.band, base.positions, out.pos, in.pos, num.subtrack,
```

Arguments

cyto.band   A data frame containing plot data for chromosome ideogram returned from
               RCircos.Cytoband.Data(cyto.info, chr.exclude, RCircos.Par).

base.positions
               A data frame returned from RCircos.Base.Plot.Positions(cyto.band, RCircos.Par)
               containing x- and y-coordinates for a circular line as well as degrees of text ro-
               tation at each position.

out.pos   Float number, the outside position of a data track.

in.pos   Float number, the inside position of a data track.

num.subtrack   Integer, total number of subtrack in a data plot track.

RCircos.Par   A list returned from RCircos.Initialize.Parameters() containing graphics paramter
               specific for Circos plot.

Author(s)

Hongen Zhang

```
RCircos.Track.Positions
```
Calculate Track Position For A Data Plot Track

Description

Calculate inner and outer plot positions for a data track.

Usage

```
RCircos.Track.Positions(side = "in", track.num, RCircos.Par)
```

Arguments

`side`	Character vector either "in" or "out" representing the position related to chromosome ideogram.
`track.num`	Integer, number of data track to be plotted.
`RCircos.Par`	A list returned from RCircos.Initialize.Parameters() that contains graphics parameters specific for Circos plot.

Value

Vector of two float numbers for outer and inner positions of a data track.

Author(s)

Hongen Zhang

```
RCircos.Validate.Genomic.Data
```
Validate Input Genomic Data

Description

Validate Input Genomic Data. Column(s) for chromosome names will be converted to character vectors. Start and end positions will be checked for correct ranges.

Usage

```
RCircos.Validate.Genomic.Data(genomic.data, cyto.band, plot.type = c("plot", "li
```

Arguments

`genomic.data`	A data frame with the first three columns as chromosome name, start and end position followed by data values for one or more samples.
`cyto.band`	A data frame containing Circos plot data for chromosome ideogram returned from RCircos.Cytoband.Data(cyto.info, chr.exclude, RCircos.Par).
`plot.type`	Character vector either "plot" for dataset with one set of genomic position data or "link" for dataset with paired genomic position data .

Value

A data frame with same dimmensions of input data.

Author(s)

Hongen Zhang

`UCSC.Baylor.3.4.Rat.cytoBandIdeogram`
Cytoband Information for Rat Chromosome Ideogram

Description

A data frame containing chromosome name, start and end position, band name, and intensity of Giemsa stains for each cytoband.

Usage

```
data(UCSC.Baylor.3.4.Rat.cytoBandIdeogram)
```

Format

A data frame with 246 observations on the following 5 variables.

Chromosome a factor with levels `chr1 chr10 chr11 chr12 chr13 chr14 chr15 chr16 chr17 chr18 chr19 chr2 chr20 chr3 chr4 chr5 chr6 chr7 chr8 chr9 chrX`

ChromStart a numeric vector

ChromEnd a numeric vector

Band a factor with levels `p11 p12 p13 p14 p15 p16 p21 p22 q11 q12 q12.1 q12.2 q12.3 q12.4 q12.5 q13 q14 q15 q16 q21 q22 q23 q24 q25 q26 q27 q31 q32 q32.1 q32.2 q32.3 q33 q34 q35 q36 q37 q38 q41 q42 q43 q44 q45 q51 q52 q53 q54 q55`

Stain a factor with levels `gneg gpos gvar`

Source

http://genome.ucsc.edu

```
UCSC.HG19.Human.CytoBandIdeogram
```
Cytoband Information for Human Chromosome Ideogram

Description

A data frame containing chromosome name, start and end position, band name, and intensity of Giemsa stains for each cytoband.

Usage

```
data(UCSC.HG19.Human.CytoBandIdeogram)
```

Format

A data frame with 862 observations on the following 5 variables.

`Chromosome` a factor with levels `chr1 chr10 chr11 chr12 chr13 chr14 chr15 chr16 chr17 chr18 chr19 chr2 chr20 chr21 chr22 chr3 chr4 chr5 chr6 chr7 chr8 chr9 chrX chrY`

`ChromStart` a numeric vector

`ChromEnd` a numeric vector

`Band` a factor with levels `p11 p11.1 p11.11 p11.12 p11.2 p11.21 p11.22 p11.23 p11.3 p11.31 p11.32 p11.4 p12 p12.1 p12.2 p12.3 p12.31 p12.32 p12.33 p13 p13.1 p13.11 p13.12 p13.13 p13.2 p13.3 p13.31 p13.32 p13.33 p14 p14.1 p14.2 p14.3 p15 p15.1 p15.2 p15.3 p15.31 p15.32 p15.33 p15.4 p15.5 p16.1 p16.2 p16.3 p21 p21.1 p21.2 p21.3 p21.31 p21.32 p21.33 p22 p22.1 p22.11 p22.12 p22.13 p22.2 p22.3 p22.31 p22.32 p22.33 p23 p23.1 p23.2 p23.3 p24.1 p24.2 p24.3 p25.1 p25.2 p25.3 p26.1 p26.2 p26.3 p31.1 p31.2 p31.3 p32.1 p32.2 p32.3 p33 p34.1 p34.2 p34.3 p35.1 p35.2 p35.3 p36.11 p36.12 p36.13 p36.21 p36.22 p36.23 p36.31 p36.32 p36.33 q11 q11.1 q11.2 q11.21 q11.22 q11.221 q11.222 q11.223 q11.23 q12 q12.1 q12.11 q12.12 q12.13 q12.2 q12.3 q13 q13.1 q13.11 q13.12 q13.13 q13.2 q13.3 q13.31 q13.32 q13.33 q13.4 q13.41 q13.42 q13.43 q13.5 q14 q14.1 q14.11 q14.12 q14.13 q14.2 q14.3 q15 q15.1 q15.2 q15.3 q16.1 q16.2 q16.3 q21 q21.1 q21.11 q21.12 q21.13 q21.2 q21.21 q21.22 q21.23 q21.3 q21.31 q21.32 q21.33 q22 q22.1 q22.11 q22.12 q22.13 q22.2 q22.3 q22.31 q22.32 q22.33 q23 q23.1 q23.2 q23.3 q23.31 q23.32 q23.33 q24 q24.1 q24.11 q24.12 q24.13 q24.2 q24.21 q24.22 q24.23 q24.3 q24.31 q24.32 q24.33 q25 q25.1 q25.2 q25.3 q25.31 q25.32 q25.33 q26 q26.1 q26.11 q26.12 q26.13 q26.2 q26.3 q26.31 q26.32 q26.33 q27 q27.1 q27.2 q27.3 q28 q28.1 q28.2 q28.3 q29 q31.1 q31.2 q31.21 q31.22 q31.23 q31.3 q31.31 q31.32 q31.33 q32 q32.1 q32.11 q32.12 q32.13 q32.2 q32.3 q32.31 q32.32 q32.33 q33 q33.1 q33.2 q33.3 q34 q34.1 q34.11 q34.12 q34.13 q34.2 q34.3 q35 q35.1 q35.2 q35.3 q36.1 q36.2 q36.3 q37.1 q37.2 q37.3 q41 q42.11 q42.12 q42.13 q42.2 q42.3 q43 q44`

`Stain` a factor with levels `acen gneg gpos100 gpos25 gpos50 gpos75 gvar stalk`

Source

http://genome.ucsc.edu

```
UCSC.Mouse.GRCm38.CytoBandIdeogram
```
Cytoband Inforamtion for Mouse Chromosome Ideogram

Description

A data frame containing chromosome name, start and end position, band name, and intensity of Giemsa stains for each cytoband.

Usage

```
data(UCSC.Mouse.GRCm38.CytoBandIdeogram)
```

Format

A data frame with 403 observations on the following 5 variables.

Chromosome a factor with levels chr1 chr10 chr11 chr12 chr13 chr14 chr15 chr16
    chr17 chr18 chr19 chr2 chr3 chr4 chr5 chr6 chr7 chr8 chr9 chrX chrY

ChromStart a numeric vector

ChromEnd a numeric vector

Band a factor with levels qA qA1 qA1.1 qA1.2 qA1.3 qA2 qA3 qA3.1 qA3.2 qA3.3 qA4
    qA5 qA5.1 qA5.2 qA5.3 qA6 qA7.1 qA7.2 qA7.3 qB qB1 qB1.1 qB1.2 qB1.3
    qB2 qB2.1 qB2.2 qB2.3 qB3 qB3.1 qB3.2 qB3.3 qB4 qB5 qB5.1 qB5.2 qB5.3
    qC qC1 qC1.1 qC1.2 qC1.3 qC2 qC3 qC3.1 qC3.2 qC3.3 qC4 qC5 qC6 qC7 qD
    qD1 qD2 qD2.1 qD2.2 qD2.3 qD3 qE qE1 qE1.1 qE1.2 qE1.3 qE2 qE2.1 qE2.2
    qE2.3 qE3 qE3.1 qE3.2 qE3.3 qE4 qE5 qF qF1 qF2 qF2.1 qF2.2 qF2.3 qF3
    qF4 qF5 qG1 qG1.1 qG1.2 qG1.3 qG2 qG3 qH1 qH2 qH2.1 qH2.2 qH2.3 qH3 qH4
    qH5 qH6

Stain a factor with levels gneg gpos100 gpos33 gpos66 gpos75

Source

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Index