Package 'RCircos'

October 30, 2013

Type Package

Title Circos 2D Track Plot

Version 1.1.2

Date 2013-10-28

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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: heatmap, histogram, lines, scatterplot, tiles and plot items for further decorations include connector, link (lines and ribbons), and text (gene) label. 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

NeedsCompilation no

Repository CRAN

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R topics documented:

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

Description

This is the R implement of basic Circos plots of genimic data.

Details

Package:	RCircos
Type:	Package
Version:	1.1.2
Date:	2013-10-22
License:	GPL (>=2)

RCircos package provides a simple and flexible way to make Circos 2D track plots with R and could be easily integrated into other R data processing and graphic manipulation pipelines for presenting large-scale multi-sample genomic research data. It can also serve as a base tool to generate complex Circos images. Currently, RCircos supports genomic data plot for three species: human, mouse, and rat. Data plots include chromosome ideogram with cytoband, heatmap, histogram, lines, scatterplot, and tiles. Plot items for further decorations have connectors, links (lines and ribbons), and text (gene) labels. Each plot is implemented with a specific function and input data for all functions are data frames which can be objects read from text files or generated with other R pipelines.

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. BMC Bioinformatics, 2013, 14:244.

RCircos.Chromosome.Ideogram.Plot
Draw Chromosome Ideogram

Description

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

Usage

```
RCircos.Chromosome.Ideogram.Plot()
```

Author(s)

Hongen Zhang

Examples

```
# Load RCircos libaray
# ---------------------------------------------------
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

library(RCircos);


# Load human chromosome ideogram
# ---------------------------------------------------
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(UCSC.HG19.Human.CytoBandIdeogram);


# Set RCircso core components
# ---------------------------------------------------
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
cyto.info <- UCSC.HG19.Human.CytoBandIdeogram;
chr.exclude <- NULL;
num.inside <- 5;
num.outside <- 0;
## Not run: RCircos.Set.Core.Components(cyto.info,
chr.exclude, num.inside, num.outside);
## End(Not run)


# Initialize graphic device and plot chromosome
# ideogram
# ---------------------------------------------------
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

## Not run: RCircos.Set.Plot.Area();
## Not run: RCircos.Chromosome.Ideogram.Plot();
```

RCircos.Clear.Track   *Erase One or More Data Tracks*

Description

Erase one data track or all tracks from current track to the center of plot plot area.

Usage

```
RCircos.Clear.Track(track.num, side, to.center = FALSE)
```

Arguments

track.num	Integer, representing the ordinal number of the plot track to be erased.
side	Character vector, either "in" or "out", representing the position related to chromosome ideogram.
to.center	Logic, FALSE for erasing current track only and TRUE for erasing all tracks from current track to the center of plot plot area.

Author(s)

Hongen Zhang

Examples

```
# Load RCircos libaray
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

library(RCircos);


# Load human chromosome ideogram
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(UCSC.HG19.Human.CytoBandIdeogram);
data(RCircos.Link.Data);


# Set RCircso core components
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

cyto.info <- UCSC.HG19.Human.CytoBandIdeogram;
chr.exclude <- c("chrX", "chrY");
tracks.inside <- 5;
tracks.outside <- 0;
## Not run: RCircos.Set.Core.Components(cyto.info,
            chr.exclude, num.inside, num.outside);
## End(Not run)


# Initialize graphic device, plot chromosome ideogram
# and scatters
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

## Not run: RCircos.Set.Plot.Area();
```

```
## Not run: RCircos.Chromosome.Ideogram.Plot();

data(RCircos.Scatter.Data);
data.col <- 5;
track.num <- 1;
side <- "in";
by.fold <- 1;
## Not run: RCircos.Scatter.Plot(RCircos.Scatter.Data,
                data.col, track.num, side, by.fold);
## End(Not run)

track.num <- 3;
## Not run: RCircos.Link.Plot(RCircos.Link.Data,
                        track.num, TRUE);
## End(Not run)

track.num <- 1;
side <- "in";
to.center <- FALSE;
## Not run: RCircos.Clear.Track(track.num, side, to.center);
to.center <- TRUE;
## Not run: RCircos.Clear.Track(track.num, side, to.center);
```

RCircos.Data.Point   *Convert a Genomic Position to an 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 name and start position). This function is for internal use only.

Usage

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

Arguments

chromosome	Character vector, a chromosome name with prefix of "chr", e.g., "chr1".
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 RCircos plot positions.

Author(s)

Hongen Zhang

RCircos.Env   *RCircos Environment*

Description

RCircos.Env is the user environment to hold RCircos core components and each component in the environment can be viewed with get mothod.

Format

The format is: <environment: 0x14f6c10>

RCircos.Gene.Connector.Plot

         Draw Connectors between Chromosome Ideogram and Gene Names

Description

Draw a set of connectors (three lines for each connector) between chromosome ideogram or a data track and gene names. RCircos core components and graphics device must be initialized before drawing.

Usage

```
RCircos.Gene.Connector.Plot(genomic.data, track.num, side)
```

Arguments

genomic.data   A data frame with the first four columns for chromosome names, start positions, end positions, and gene names.

track.num   Integer, representing the ordinal number of the plot track where the connectors are plotted.

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

Author(s)

Hongen Zhang

Examples

```
# Load RCircos libaray
# ------------------------------------------------
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

library(RCircos);


# Load human chromosome ideogram and sample data
# ------------------------------------------------
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(RCircos.Gene.Label.Data);
data(UCSC.HG19.Human.CytoBandIdeogram);


# Set RCircso core components
# ------------------------------------------------
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

cyto.info <- UCSC.HG19.Human.CytoBandIdeogram;
chr.exclude <- NULL;
tracks.inside <- 5;
tracks.outside <- 0;
## Not run: RCircos.Set.Core.Components(cyto.info,
        chr.exclude, tracks.inside, tracks.outside);
## End(Not run)


# Initialize graphic device, plot chromosome ideogram
# and connectors
# ------------------------------------------------
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

gene.data <- RCircos.Gene.Label.Data;
## Not run: RCircos.Set.Plot.Area();
## Not run: RCircos.Chromosome.Ideogram.Plot();
## Not run: RCircos.Gene.Connector.Plot(gene.data,
                                1, "in");
## End(Not run)
```

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.Gene.Name.Plot

Draw Gene Names on a Data Track

Description

Label gene names along chromosome ideogram or a data track. RCircos core components and graphic device must be initialized before drawing.

Usage

```
RCircos.Gene.Name.Plot(gene.data, name.col, track.num, side)
```

Arguments

gene.data   A data frame. The first three columns should be chromosome name, start posi-
              tion, end position.

name.col   Integer, representing the ordinal number of the column in input data that contains
              gene names.

track.num   Integer, representing the ordinal number of the plot track where the gene names
              are plotted.

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

Author(s)

Hongen Zhang

Examples

```
# Load RCircos libaray
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

library(RCircos);


# Load human chromosome ideogram and sample data
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(UCSC.HG19.Human.CytoBandIdeogram);
data(RCircos.Gene.Label.Data);


# Set RCircso core components
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

cyto.info <- UCSC.HG19.Human.CytoBandIdeogram;
chr.exclude <- c("chrX", "chrY");
num.inside <- 5;
num.outside <- 0;
## Not run: RCircos.Set.Core.Components(cyto.info,
        chr.exclude, num.inside, num.outside);
## End(Not run)

# Initialize graphic device, plot chromosome ideogram
# and gene names
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

## Not run: RCircos.Set.Plot.Area();
## Not run: RCircos.Chromosome.Ideogram.Plot();
```

```
name.col <- 4;
track.num <- 2;
side <- "in";
gene.data <- RCircos.Gene.Label.Data;
## Not run: RCircos.Gene.Name.Plot(gene.data, name.col,
                                   track.num, side);
## End(Not run)
```

RCircos.Get.Gene.Label.Locations
Calculate New Position for Gene Labels

Description

This function calculates new plot position from genomic positions for gene labeling. In case there are too many genes in a genomic interval, 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.

This function is for internal use only.

Usage

```
RCircos.Get.Gene.Label.Locations(genomic.data)
```

Arguments

genomic.data   A data frame. The first three columns should be chromosome name, start position, end position.

Value

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

Author(s)

Hongen Zhang

RCircos.Get.Heatmap.ColorScales

Generate Color Scales for Heatmap Plot

Description

Create color scales for heatmap plot. Currently there are six color scales could be generated:

BlueWhiteRed: colors from blue (lowest) to white then red (highest)
GreenWhiteRed: colors from green (lowest) to white then red (highest)
GreenYellowRed: colors from green (lowest) to yellow then red (highest)
GreenBlackRed: colors from green (lowest) to black then red (highest)
YellowToRed: colors from yellow (lowest) to red (highest)
BlackOnly: black only

This function is mainly for internal use only.

Usage

```
RCircos.Get.Heatmap.ColorScales(heatmap.color)
```

Arguments

heatmap.color   Character vector, one of "BlueWhiteRed", "GreenWhiteRed", "GreenYellowRed",
                 "GreenBlackRed", "YellowToRed", and "BlackOnly".

Value

A vector or two column matrix of rgb colors.

Author(s)

Hongen Zhang

Examples

```
## Not run: colorScales <- RCircos.Get.Heatmap.ColorScales(heatmap.color);
```

```
RCircos.Get.Link.Colors
```
Set up Colors for Link Lines or Ribbons

Description

Assign colors for link lines or Ribbons. The defult colors are rainbow with lenght of total link lines or ribbons. If by.chromosome is set to TRUE, red color will be used for links between positions of same chromosomes and blue color for links between different chromosomes. Users can also define their own colors by appending a column with color names to link data and give the column name as "PlotColor".

This function is for internal use only.

Usage

```
RCircos.Get.Link.Colors(link.data, by.chromosome)
```

Arguments

link.data	A data frame with paired genomic positions in each row. The first three columns are for chromosome names, start and end position of one genomic position followed by three columns for chromosome names, start and end position of the second genomic position.
by.chromosome	Logic. If true, red color will be used for links between positions of same chromosomes and blue color for links between different chromosomes. Otherwise, user defined or random colors (rainbow) will be automatically assigned for each line.

Value

A vector of color names with length same as the rows of input data.

Author(s)

Hongen Zhang

```
RCircos.Get.Plot.Colors
```
Assign Plot Colors for Non-Link Data Plot

Description

Assign plot colors for each data point of genomic data except of link plot (link lines or ribbons). Users can define their own colors by appending a column with color names to plot data and give the column name as "PlotColor". Otherwise, default colors will be used.

This function is for internal use only.

Usage

```
RCircos.Get.Plot.Colors(plot.data, color)
```

Arguments

plot.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.

color   Character vector of color names.

Value

A vector of color names with length same as the rows of input data.

Author(s)

Hongen Zhang

RCircos.Get.Plot.Data   *Convert Genomic Data to RCircos Plot Data*

Description

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

This function is mainly for internal use.

Usage

```
RCircos.Get.Plot.Data(genomic.data, plot.type)
```

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.

plot.type   Character vector, either "plot" or "link".

Value

Updated genomic data (with a new column for RCircos plot positions)

Author(s)

Hongen Zhang

```
RCircos.Get.Plot.Ideogram
```
Get Chromosome Ideogram Object

Description

Get the chromosome ideogram object used during current RCircos session. RCircos core components must be initialized first. This function is mainly for internal use.

Usage

```
RCircos.Get.Plot.Ideogram()
```

Value

A data frame containing all information for chromosome ideogram plot. The first five column are orginal cytoband data and following are chromosome highlight colors, and plot colors, length, number of chromosome unit, and relative location on the circular layout of each band.

Author(s)

Hongen Zhang

```
RCircos.Get.Plot.Parameters
```
Get All RCircos Plot Parameters

Description

Get all parameters used in current RCircos session in order to check and reset plot parameters. RCircos core components must be initialized first.

Usage

```
RCircos.Get.Plot.Parameters()
```

Value

A list of all parameters used for RCircos plot.

Author(s)

Hongen Zhang

Examples

```
# Load RCircos libaray
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

library(RCircos);


# Load human chromosome ideogram
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(UCSC.HG19.Human.CytoBandIdeogram);


# Set RCircso core components
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

cyto.info <- UCSC.HG19.Human.CytoBandIdeogram;
chr.exclude <- c("chrX", "chrY");
num.inside <- 5;
num.outside <- 0;
## Not run: RCircos.Set.Core.Components(cyto.info,
        chr.exclude, tracks.inside, tracks.outside);
## End(Not run)


# Get RCircos plot parameters
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

## Not run: params <- RCircos.Get.Plot.Parameters();
## Not run: params
```

RCircos.Get.Plot.Positions

Get RCircos Plot Position Object

Description

Get the data frame of base plot positions which are used to derive all other positions of RCircos plot. RCircos core components must be initialized first. This function is mainly for internal use.

Usage

```
RCircos.Get.Plot.Positions()
```

Value

A data frame with three columns for x, and y coordinates of a circular line with radius of 1 as well as the degrees used for text rotation at each point of the positions.

Author(s)

Hongen Zhang

Examples

```
# Load RCircos libaray
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

library(RCircos);


# Load human chromosome ideogram
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(UCSC.HG19.Human.CytoBandIdeogram);


# Set RCircso core components
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

cyto.info <- UCSC.HG19.Human.CytoBandIdeogram;
chr.exclude <- c("chrX", "chrY");
num.inside <- 5;
num.outside <- 0;
## Not run: RCircos.Set.Core.Components(cyto.info,
        chr.exclude, tracks.inside, tracks.outside);
## End(Not run)


# Get RCircos base plot positions
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

## Not run: positions <- RCircos.Get.Plot.Positions();
## Not run: head(positions);
```

RCircos.Heatmap.Data   *Sample Data for RCircos Heatmap Plot*

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.Heatmap.Plot   *Circos-like Heamap Plot*

Description

Draw one track of heatmap. RCircos core components and graphic device must be initialized before drawing.

Usage

```
RCircos.Heatmap.Plot(heatmap.data, data.col, track.num, side)
```

Arguments

`heatmap.data`	A data frame with the first three columns as chromosome names, start position and end position of each data point followed by data values for one or more samples.
`data.col`	Integer, representing the ordinal number of the column in input data set that contains the data to be plotted.
`track.num`	Integer, representing the ordinal number of the plot track where the heatmap will be plotted.
`side`	Character vector, either "in" or "out", representing the position related to chromosome ideogram.

Author(s)

Hongen Zhang

Examples

```
# Load RCircos libaray
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

library(RCircos);


# Load human chromosome ideogram and sample data
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(UCSC.HG19.Human.CytoBandIdeogram);
data(RCircos.Heatmap.Data);


# Set RCircso core components
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

cyto.info <- UCSC.HG19.Human.CytoBandIdeogram;
chr.exclude <- c("chrX", "chrY");
num.inside <- 5;
num.outside <- 0;
## Not run: RCircos.Set.Core.Components(cyto.info,
             chr.exclude, num.inside, num.outside);
## End(Not run)


# Initialize graphic device, plot chromosome ideogram
# and one heatmap track
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
```

```
## Not run: RCircos.Set.Plot.Area();
## Not run: RCircos.Chromosome.Ideogram.Plot();

data.col <- 5
track.num <- 4;
side <- "in";
## Not run: RCircos.Heatmap.Plot(RCircos.Heatmap.Data,
                   data.col, track.num, side);
## End(Not run)
```

RCircos.Histogram.Data

Sample Data for RCircos 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.Histogram.Plot
```
Circos-like Histogram Plot

Description

Draw one track of histogram. RCircos core components and graphic device must be initialized before drawing.

Usage

```
RCircos.Histogram.Plot(hist.data, data.col, track.num, side)
```

Arguments

hist.data	A data frame with the first three columns as chromosome names, start position and end position of each data point followed by data values for one or more samples.
data.col	Integer, representing the ordinal number of the column in input data that contains the data to be plotted.
track.num	Integer, representing the ordinal number of the plot track where the histogram will be plotted.
side	Character vector, either "in" or "out", representing the position related to chromosome ideogram.

Author(s)

Hongen Zhang

Examples

```
# Load RCircos libaray
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

library(RCircos);


# Load human chromosome ideogram and sample data
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(UCSC.HG19.Human.CytoBandIdeogram);
data(RCircos.Histogram.Data);


# Set RCircso core components
# _____
```

```
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

cyto.info <- UCSC.HG19.Human.CytoBandIdeogram;
chr.exclude <- c("chrX", "chrY");
num.inside <- 5;
num.outside <- 0;
## Not run: RCircos.Set.Core.Components(cyto.info,
           chr.exclude, num.inside, num.outside);
## End(Not run)


# Initialize graphic device, plot chromosome ideogram
# and histogram track
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

## Not run: RCircos.Set.Plot.Area();
## Not run: RCircos.Chromosome.Ideogram.Plot();

data.col <- 4;
track.num <- 4;
side <- "in";
## Not run: RCircos.Histogram.Plot(RCircos.Histogram.Data,
                      data.col, track.num, side);
## End(Not run)
```

RCircos.Initialize.Parameters

Initialize RCircos Plot Parameters

Description

Setup default values for RCircos plot. All parameters are held in one list. This function is for internal use.

Usage

```
RCircos.Initialize.Parameters(tracks.inside, tracks.outside)
```

Arguments

tracks.inside   Integer, how many tracks will be put inside of chromosome ideogram.

tracks.outside   Integer, how many tracks will be put outside of chromosome ideogram.

Author(s)

Hongen Zhang

RCircos.Line.Data   *Sample Data for RCircos 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. RCircos core components and graphics device must bae initialized before drawing.

Usage

```
RCircos.Line.Plot(line.data, data.col, track.num, side)
```

Arguments

line.data	A data frame with the first three columns as chromosome names, start position and end position of each data point followed by data values for one or more samples.
data.col	Integer, representing the ordinal number of the column in input dataset that contains the data to be plotted.
track.num	Integer, representing the ordinal number of the plot track where the lines will be plotted.
side	Character vector, either "in" or "out", representing the position related to chromosome ideogram.

Author(s)

Hongen Zhang

Examples

```
# Load RCircos libaray
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

library(RCircos);


# Load human chromosome ideogram and sample data
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(UCSC.HG19.Human.CytoBandIdeogram);
data(RCircos.Line.Data);


# Set RCircso core components
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

cyto.info <- UCSC.HG19.Human.CytoBandIdeogram;
chr.exclude <- c("chrX", "chrY");
num.inside <- 5;
num.outside <- 0;
## Not run: RCircos.Set.Core.Components(cyto.info,
            chr.exclude, num.inside, num.outside);
## End(Not run)


# Initialize graphic device, plot chromosome ideogram
# and one track of lines
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
```

```
## Not run: RCircos.Set.Plot.Area();
## Not run: RCircos.Chromosome.Ideogram.Plot();

data.col <- 5;
track.num <- 4;
side <- "in";
## Not run: RCircos.Line.Plot(RCircos.Line.Data, data.col,
                            track.num, side);
## End(Not run)
```

RCircos.Link.Data   *Sample Data for RCircos 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 *Calculate x and y Coordinates for a Bezire Curve*

Description

Calculate a quandratic Bezire curve between two points with (0,0) as control points. This function is for internal use.

Usage

```
RCircos.Link.Line(line.start, line.end)
```

Arguments

line.start   The position (a point) where the Bezier curve starts.

line.end   The position (a point) where the Bezier curve ends.

Author(s)

Hongen Zhang

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

Description

Draw lines (quandratic Bezier curves) between paired genomic positions. RCircos core components and graphic device must be initialize before drawing. Link lines are always in the center of plot area.

Usage

```
RCircos.Link.Plot(link.data, track.num, by.chromosome = FALSE)
```

Arguments

link.data   A data frame with paired genomic positions in each row. The first three columns are for chromosome names, start and end position of one genomic position followed by three columns for chromosome names, start and end position of the second genomic position.

track.num   Integer, representing the ordinal number of the plot track where the link lines will start.

by.chromosome   Logic. If true, red color will be used for links between positions of same chromosomes and blue color for links between different chromosomes. Otherwise, user defined or random colors (rainbow) will be automatically assigned for each line.

Author(s)

Hongen Zhang

Examples

```
# Load RCircos libaray
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

library(RCircos);


# Load human chromosome ideogram and sample data
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(UCSC.HG19.Human.CytoBandIdeogram);
data(RCircos.Link.Data);


# Set RCircso core components
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

cyto.info <- UCSC.HG19.Human.CytoBandIdeogram;
chr.exclude <- c("chrX", "chrY");
num.inside <- 5;
num.outside <- 0;
## Not run: RCircos.Set.Core.Components(cyto.info,
            chr.exclude, num.inside, num.outside);
## End(Not run)


# Initialize graphic device, plot chromosome ideogram
# and link lines
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

## Not run: RCircos.Set.Plot.Area();
## Not run: RCircos.Chromosome.Ideogram.Plot();

track.num <- 4;
## Not run: RCircos.Link.Plot(RCircos.Link.Data,
                    track.num, TRUE);
## End(Not run)
```

RCircos.List.Parameters

Print RCircos Parameters to Standard Output

Description

Display all graphic parameters used by current RCircos session on standard output. RCircos core components must be initialized first.

Usage

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

Author(s)

Hongen Zhang

Examples

```
# Load RCircos libaray
# ---------------------------------------------------
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

library(RCircos);


# Load human chromosome ideogram
# ---------------------------------------------------
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(UCSC.HG19.Human.CytoBandIdeogram);


# Set RCircso core components
# ---------------------------------------------------
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

cyto.info <- UCSC.HG19.Human.CytoBandIdeogram;
chr.exclude <- c("chrX", "chrY");
num.inside <- 5;
num.outside <- 0;
## Not run: RCircos.Set.Core.Components(cyto.info,
        chr.exclude, tracks.inside, tracks.outside);
## End(Not run)


# List RCircos plot parameters
# ---------------------------------------------------
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

## Not run: RCircos.List.Parameters();
```

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.Multiple.Species.Core.Components

Setup RCircos Core Components with Multiple Species

Description

Setup RCircos core components with chromosome ideograms of multiple species for visulization
of similarity and difference of genomic data between different species.

Usage

```
RCircos.Multiple.Species.Core.Components(cyto.info.list,
                        species.list, chr.exclude = NULL,
                        tracks.inside, tracks.outside)
```

Arguments

cyto.info.list	A List contains data frames for chromosome ideogram data of different species. All data frames in the list must have same columns.
species.list	Character vector represent multiple species. Each one will be used as prefix of chromosome names for relavant species. The order of species must match the order of the species in cyto.info.list.
chr.exclude	Character vector of chromosome names to be excluded from plot, e.g., chr.exclude <- c("chrX", "chrY");
tracks.inside	Integer, total number of data tracks inside of chromosome ideogram.
tracks.outside	Integer, total number of data tracks outside of chromosome ideogram.

Author(s)

Hongen Zhang

Examples

```
# Load RCircos libaray
# ---------------------------------------------------
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

library(RCircos);


# Load mouse and rat chromosome ideograms and make
# a multiple species cytoband data
# ---------------------------------------------------
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(UCSC.Mouse.GRCm38.CytoBandIdeogram);
data(UCSC.Baylor.3.4.Rat.cytoBandIdeogram);
cyto.list <- list(UCSC.Mouse.GRCm38.CytoBandIdeogram,
            UCSC.Baylor.3.4.Rat.cytoBandIdeogram);
species <- c("M", "R");


# Set RCircso core components with multiple species
# cytoband data
# ---------------------------------------------------
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

chr.exclude <- c("chrX", "chrY");
tracks.inside <- 5;
tracks.outside <- 0;
## Not run: RCircos.Multiple.Species.Core.Components(
      cyto.list, species, chr.exclude,
      tracks.inside, tracks.outside);
## End(Not run)
```

RCircos.Multiple.Species.Dataset

Construct A Dataset from Multiple Genomic Data of Different Species

Description

Combine plot datasets from different species as one data frame for RCircos plot with multiple sets of chromosome ideogram.

Usage

```
RCircos.Multiple.Species.Dataset(data.list, species)
```

Arguments

data.list   A List contains data frames for genomic data of different species. All data frames in the list must have same columns.

species   Character vector represent multiple species. Each one will be used as prefix of chromosome names for relavant species. The order of species must match the order of the species in data.list.

Value

A data frame contains all input plot data.

Author(s)

Hongen Zhang

Examples

```
# Load RCircos libaray
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

library(RCircos);


# Load mouse and rat gene expression datasets
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(RCircos.Mouse.Expr.Data);
data(RCircos.Rat.Expr.Data);
data.list <- list(RCircos.Mouse.Expr.Data,
                  RCircos.Rat.Expr.Data);
species <- c("M", "R");
```

```
# Generate data frome that contains both mouse and
# rat gene expression data
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

## Not run: new.data <- RCircos.Multiple.Species.Dataset(
                            data.list, species);
## End(Not run)
```

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.Plot.Ideogram

Reset RCircos Ideogram Plot Data

Description

Reset chromosome ideogram plot data. Reserved for advanced usage.

Usage

```
RCircos.Reset.Plot.Ideogram(chromIdeo)
```

Arguments

chromIdeo   An object obtained from RCircos.Get.Plot.Ideogram() with/without modifications.

Author(s)

Hongen Zhang

RCircos.Reset.Plot.Parameters

Reset RCircos Plot Parameters

Description

Reset RCircos plot parameters after they were initialized. Also update chromosome ideogram and base positions when necessary. Among the parameters, chromosome padding is automatically calculated with base.per.unit unless the padding is set to zero. Parameters related to radius are automatically adjusted based on radius.

Usage

```
RCircos.Reset.Plot.Parameters(new.params)
```

Arguments

new.params   An list contains all plot parameters with updated values.

Author(s)

Hongen Zhang

Examples

```
# Load RCircos libaray
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

library(RCircos);


# Load human chromosome ideogram
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(UCSC.HG19.Human.CytoBandIdeogram);
cyto.info <- UCSC.HG19.Human.CytoBandIdeogram;


# Set RCircso core components
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

chr.exclude <- c("chrX", "chrY");
tracks.inside <- 5;
tracks.outside <- 0;
## Not run: RCircos.Set.Core.Components(cyto.info,
      chr.exclude, tracks.inside, tracks.outside);
## End(Not run)


# List RCircos plot parameters then get RCircos plot
# parameters, reset base.per.unit to 30000 and then
# reset RCircos plot parameters. List RCircos plot
# parameters again to see the change
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

## Not run: RCircos.List.Parameters();
## Not run: params <- RCircos.Get.Plot.Parameters();
## Not run: params$base.per.unit <- 30000;
## Not run: RCircos.Reset.Plot.Parameters(params);
## Not run: RCircos.List.Parameters();
```

RCircos.Ribbon.Data   *Sample Data for RCircos Ribbon Plot*

Description

A data frame containing paired genomic position data for each row. The contents of each row are
in the order of name, start and end positions of chromosome A then name, start and end positions
of chromosome B. This data frame is directly used to draw ribbons without extra processing.

Usage

```
data(RCircos.Ribbon.Data)
```

Format

A data frame with 4 observations on the following 6 variables.

chromA a factor with levels `chr1 chr5 chr8`

chromStartA a numeric vector

chromEndA a numeric vector

chromB a factor with levels `chr10 chr13 chr17 chr18`

chromStartB a numeric vector

chromEndB a numeric vector

Source

Unpublished data.

RCircos.Ribbon.Plot *Draw Ribbon between Two Genomic Regions*

Description

Draw various ribbons instead of lines with uniform thickness. The thickness of ribbons are relative to the size of the genomic regions to be linked.

Usage

```
RCircos.Ribbon.Plot(ribbon.data, track.num, by.chromosome = FALSE, twist = FALSE)
```

Arguments

ribbon.data	A data frame with paired genomic positions in each row. The first three columns of each row are for chromosome name, start and end positions of one genomic position followed by three columns for chromosome name, start and end positions of the second genomic position.
track.num	Integer, representing the ordinal number of the plot track where the ribbons will start.
by.chromosome	Logic, If true, red color will be used for ribbons between positions of same chromosomes and blue color for ribbons between different chromosomes. Otherwise, different colors will be automatically assigned for each ribbon.
twist	Logic, TRUE for the ribbons with twisted shape and FALSE for no twist.

Author(s)

Hongen Zhang

Examples

```
# Load RCircos libaray
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

library(RCircos);


# Load human chromosome ideogram and sample data
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(UCSC.HG19.Human.CytoBandIdeogram);
data(RCircos.Link.Data);
data(RCircos.Ribbon.Data);


# Set RCircso core components
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

cyto.info <- UCSC.HG19.Human.CytoBandIdeogram;
chr.exclude <- c("chrX", "chrY");
num.inside <- 5;
num.outside <- 0;
## Not run: RCircos.Set.Core.Components(cyto.info,
            chr.exclude, num.inside, num.outside);
## End(Not run)


# Initialize graphic device, plot chromosome ideogram
# and link lines
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

## Not run: RCircos.Set.Plot.Area();
## Not run: RCircos.Chromosome.Ideogram.Plot();

track.num <- 4;
## Not run: RCircos.Link.Plot(RCircos.Link.Data,
                    track.num, TRUE);
## End(Not run)
## Not run: RCircos.Ribbon.Plot(RCircos.Ribbon.Data,
                    track.num, FALSE, FALSE);
## End(Not run)
```

RCircos.Scatter.Data   *Sample Data for RCircos 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.Scatter.Plot   *Circos-like Scatter Plot*

Description

Draw one track of scatter plot. RCircos core components and graphics device must be initialized before drawing.

Usage

```
RCircos.Scatter.Plot(scatter.data, data.col, track.num, side, by.fold = 0)
```

Arguments

scatter.data	A data frame with the first three columns as chromosome name, start position and end position of each data point followed by data values for one or more samples.
data.col	Integer, representing the ordinal number of the column in input dataset that contains the data to be plotted.
track.num	Integer, representing the ordinal number of the plot track where the data will be plotted.
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.

Author(s)

Hongen Zhang

Examples

```
# Load RCircos libaray
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

library(RCircos);


# Load human chromosome ideogram
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(UCSC.HG19.Human.CytoBandIdeogram);
cyto.info <- UCSC.HG19.Human.CytoBandIdeogram;


# Set RCircso core components
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

chr.exclude <- c("chrX", "chrY");
tracks.inside <- 5;
tracks.outside <- 0;
## Not run: RCircos.Set.Core.Components(cyto.info,
          chr.exclude, num.inside, num.outside);
## End(Not run)


# Initialize graphic device, plot chromosome ideogram
# and scatters
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

## Not run: RCircos.Set.Plot.Area();
## Not run: RCircos.Chromosome.Ideogram.Plot();

data(RCircos.Scatter.Data);
data.col <- 5;
track.num <- 4;
side <- "in";
by.fold <- 1;
## Not run: RCircos.Scatter.Plot(RCircos.Scatter.Data,
            data.col, track.num, side, by.fold);
## End(Not run)
```

```
RCircos.Set.Base.Plot.Positions
```
Setup Base Plot Positions

Description

Calculate x and y coordinates for a circular line that served as base plot positions to derive positions for all other plot items. Total number of coordinates are based on total chromosome units and padding. Degrees that text should be rotated at each point are also calculated. This function is for internal use.

Usage

```
RCircos.Set.Base.Plot.Positions()
```

Author(s)

Hongen Zhang

```
RCircos.Set.Core.Components
```
Initialize Core Components for RCircos Plot

Description

Setup core components for RCircos Plot including plot parameters, cytoband data, and base plot positions. This function must be called before chromosome ideogram and any other data plot.

Usage

```
RCircos.Set.Core.Components(cyto.info, chr.exclude = NULL,
                           tracks.inside, tracks.outside)
```

Arguments

cyto.info   A data frame with chromosome ideogram data and columns are ordered by chromosome names, start position, end position, band names, and stain intensity for each chromosome band.

chr.exclude   Character vector of chromosome names to be excluded from plot, e.g., chr.exclude <- c("chrX", "chrY");

tracks.inside   Integer, total number of data tracks inside of chromosome ideogram.

tracks.outside   Integer, total number of data tracks outside of chromosome ideogram.

Author(s)

Hongen Zhang

Examples

```
# Load RCircos libaray
# ------------------------------------------------
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

library(RCircos);


# Load human chromosome ideogram
# ------------------------------------------------
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(UCSC.HG19.Human.CytoBandIdeogram);
cyto.info <- UCSC.HG19.Human.CytoBandIdeogram;


# Set RCircso core components
# ------------------------------------------------
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

chr.exclude <- c("chrX", "chrY");
tracks.inside <- 5;
tracks.outside <- 0;
## Not run: RCircos.Set.Core.Components(cyto.info,
       chr.exclude, tracks.inside, tracks.outside);
## End(Not run)
```

RCircos.Set.Cytoband.data

Setup Chromosome Cytoband Data for RCircos Plot

Description

Calculate band length (number of base pairs), number of chromosome units (plot points needed to cover the band), relavent locations of each band on the circular layout, and assign colors to chromosome highlights and each band. This function is for internal use.

Usage

```
RCircos.Set.Cytoband.data(cyto.band.info)
```

Arguments

cyto.band.info   A data frame with chromosome ideogram data and columns are ordered by chromosome names, start position, end position, band names, and stain intensity for each chromosome band.

Author(s)

Hongen Zhang

RCircos.Set.Plot.Area   *Setup Plot Area for RCircos Plot*

Description

Open an new window for plotting. RCircos core components must be initialized before call this function. All four margins are set to 0.25 and window size are set to plot.radius in RCircos parameters. This function is optional and could be replaced by call par(), plot.new(), and plot.window() if users want control the plot window by themselves.

Usage

```
RCircos.Set.Plot.Area()
```

Author(s)

Hongen Zhang

Examples

```
# Load RCircos libaray
# ------------------------------------------------
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

library(RCircos);


# Load human chromosome ideogram
# ------------------------------------------------
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(UCSC.HG19.Human.CytoBandIdeogram);
cyto.info <- UCSC.HG19.Human.CytoBandIdeogram;


# Set RCircso core components
# ------------------------------------------------
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

chr.exclude <- c("chrX", "chrY");
```

```
tracks.inside <- 5;
tracks.outside <- 0;
## Not run: RCircos.Set.Core.Components(cyto.info,
        chr.exclude, tracks.inside, tracks.outside);
## End(Not run)


# Set plot area, i.e., initialize graphic device
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

## Not run: RCircos.Set.Plot.Area();
```

RCircos.Tile.Data   *Sample Data for RCircos 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. RCircos core components and graphics device must be initialized before drawing.

Usage

```
RCircos.Tile.Plot(tile.data, track.num, side)
```

Arguments

tile.data   A data frame with three columns for chromosome name, start and end positions of each data point. Columns for data values are optional.

track.num   Integer, representing the ordinal number of the plot track where the data will be plotted.

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

Author(s)

Hongen Zhang

Examples

```
# Load RCircos libaray
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

library(RCircos);


# Load human chromosome ideogram
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(UCSC.HG19.Human.CytoBandIdeogram);
cyto.info <- UCSC.HG19.Human.CytoBandIdeogram;


# Set RCircso core components
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

cyto.info <- UCSC.HG19.Human.CytoBandIdeogram;
chr.exclude <- c("chrX", "chrY");
tracks.inside <- 5;
```

```
tracks.outside <- 0;
## Not run: RCircos.Set.Core.Components(cyto.info,
            chr.exclude, num.inside, num.outside);
## End(Not run)



# Initialize graphic device and plot chromosome
# ideogram
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

## Not run: RCircos.Set.Plot.Area();
## Not run: RCircos.Chromosome.Ideogram.Plot();



# Load tile data and plot one track of tiles
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(RCircos.Tile.Data);
track.num <- 4;
side <- "in";
## Not run: RCircos.Tile.Plot(RCircos.Tile.Data,
                          track.num, side);
## End(Not run)
```

RCircos.Track.Outline   *Draw Outline for A Data Plot Track*

Description

Draw outline with subtracks for one data plot track. RCircos core components and graphic device must be initialized first. This function is mainly for internal use.

Usage

```
RCircos.Track.Outline(out.pos, in.pos, num.layers)
```

Arguments

out.pos	Float number, the outside position of a data track.
in.pos	Float number, the inside position of a data track.
num.layers	Integer, total number of subtrack in a data plot track.

Author(s)

Hongen Zhang

Examples

```
# Load RCircos libaray
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

library(RCircos);


# Load human chromosome ideogram
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(UCSC.HG19.Human.CytoBandIdeogram);
cyto.info <- UCSC.HG19.Human.CytoBandIdeogram;


# Set RCircso core components
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

cyto.info <- UCSC.HG19.Human.CytoBandIdeogram;
chr.exclude <- c("chrX", "chrY");
tracks.inside <- 5;
tracks.outside <- 0;
## Not run: RCircos.Set.Core.Components(cyto.info,
            chr.exclude, num.inside, num.outside);
## End(Not run)


# Initialize graphic device and plot chromosome
# ideogram
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

## Not run: RCircos.Set.Plot.Area();
## Not run: RCircos.Chromosome.Ideogram.Plot();


# Plot one track outline
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

side <- "in";
track.num <- 1;
locations <- RCircos.Track.Positions(side, track.num);
out.pos <- locations[1];
in.pos <- locations[2];
subtracks <- 5;
## Not run: RCircos.Track.Outline(out.pos, in.pos,
                      subtracks);
## End(Not run)
```

RCircos.Track.Positions
Calculate Data Plot Track Positions

Description

Calculate inner and outer plot positions for a data track. RCircos core components must be initialized first. This function is for internal use only.

Usage

```
RCircos.Track.Positions(side, track.num)
```

Arguments

side	Character vector, either "in" or "out", representing the position related to chromosome ideogram.
track.num	Integer, representing the ordinal number of the plot track

Author(s)

Hongen Zhang

RCircos.Validate.Cyto.Info
Validate Chromosome Ideogram Data

Description

Validate chromosome ideogram information including of chromosome names, order of chromosomes, chromosome start and chromosome end positions for each chromosome band. This function is mainly for internal use.

Usage

```
RCircos.Validate.Cyto.Info(cyto.info, chr.exclude)
```

Arguments

cyto.info	A data frame with chromosome ideogram data includes chromosome names, start position, end position, band names, and stain intensity for each chromosome band.
chr.exclude	Character vector of chromosome names to be excluded from plot, e.g., chr.exclude <- c("chrX", "chrY");

Value

Data frame with validated chromosome ideogram information.

Author(s)

Hongen Zhang

RCircos.Validate.Genomic.Data

Validate Genomic Data for RCircos Plot

Description

Validate input dataset for correct chromosome names, chromosome start, and chromosome end positions. Chromosome names will be converted to character vectors if they are factor variables. This function is for internal use.

Usage

```
RCircos.Validate.Genomic.Data(genomic.data, plot.type = c("plot", "link"))
```

Arguments

genomic.data   A data frame with the first three columns as chromosome names, start and end positions. Following columns may be another set of chromosome names, start and end positions then zero or more data columns.

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

The validated data frame.

Author(s)

Hongen Zhang

RCircos.Workflow   *Print Out RCircos Workflow*

Description

Display RCircos plot workflow on stardard output device for a quick quide.

Usage

```
RCircos.Workflow()
```

Author(s)

Hongen Zhang

Examples

```
library(RCircos);
RCircos.Workflow();
```

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

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

http://genome.ucsc.edu

Index