Package 'chromPlot'

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Type Package

Title Global visualization tool of genomic data

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Description Package designed to visualize genomic data along the chromosomes, where the vertical chromosomes are sorted by number, with sex chromosomes at the end.

License GPL (>= 2)

LazyLoad yes

LazyData yes

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Contents

`chromPlot-package` *Global visualization tool of genomic data*

Description

Package designed to visualize genomic data along the chromosomes, where the vertical chromosomes are sorted by number, with sex chromosomes at the end.

Details

Package:	chromPlot
Type:	Package
Version:	0.0.1
Date:	2016-01-05
License:	GPL (>= 2)
LazyLoad:	yes

Author(s)

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`chromPlot` *Global visualization tool of genomic data*

Description

Package designed to visualize genomic data along the chromosomes, where the vertical chromosomes are sorted by number, with sex chromosomes at the end.

Usage

```
chromPlot(annot1, annot2, annot3, annot4, stat, stat2,
scale.title="Counts", statTyp="p", scex=1, spty=20, statCol, statCol2,
statName="Statistic", statName2="Statistic2", bands, bandsDesc, gaps,
gapsDesc, segment, segmentDesc, segment2=NULL, segment2Desc=NULL, chr,
bin=1e6, yAxis=TRUE, figCols=NULL, colBand="lightgray", colAnnot1="brown",
colAnnot2="gold", colAnnot3="darkgreen", colAnnot4="blue", colSegments=c("darkgreen",
"orange", "blue", "darkslategray2", "cyan", "blueviolet", "goldenrod3", "darkseagreen4",
"red", "green", "salmon", "darkolivegreen", "maroon", "purple"),
colSegments2=colSegments[-1L], colStat="blue", colStat2="orange", title=NULL,
plotRndchr=FALSE, maxSegs=200, noHist=FALSE, segLwd=3, sortSegs=TRUE,
chrSide=c(-1, -1, -1, -1, 1, -1, -1, 1), cex=0.75, legChrom, org=NULL, strand=NULL,
stack=TRUE, statThreshold=NULL, statThreshold2=NULL, statSumm="none")
```

Arguments

annot1	Genome annotations
annot2	Genome annotations, subset of annot1
annot3	Genome annotations, subset of annot2
annot4	Genome annotations, subset of annot3
stat	Genome annotations associated to quantitative values
stat2	Second track of genome annotations associated to quantitative values
statCol	Name column in stat with the values to plot
statCol2	Name column in stat2 with the values to plot
statTyp	Type of plot for stat ("l", "p", NULL)
statName	Description for stat (default="Statistic")
statName2	Description for stat2 (default="Statistic")
bands	Genome annotations to be plotted on chromosomal body (e.g G bands)
bandsDesc	Description for bands
gaps	Chromosome alignment gaps (only centromers and telomers used)
gapsDesc	Description for gaps
segment	Genomic segments. Can contain a 'Group' column with categories
segmentDesc	Description for segment
segment2	second track of genomic segments. Can contain a 'Group' column with categories
segment2Desc	Description for segment2
chr	Vector of chromosome names to plotted (optional)
bin	Bin size for histograms in base pairs
yAxis	Should I draw the y-axis (logical)
figCols	Maximum number of chromosomes in a row
colBand	Color for chromosome bands
colAnnot1	Color for histograms for annot1
colAnnot2	Color for histograms for annot2
colAnnot3	Color for histograms for annot3
colAnnot4	Color for histograms for annot4
colSegments	Color for chromosome segment (ignored if segment are grouped (see details)
colSegments2	Color for chromosome segment2 (ignored if segment2 are grouped (See details)
colStat	Color for stat
colStat2	Color for stat2
title	Plot title
plotRndchr	Include random scaffolds
maxSegs	Maximum number of segments. If the segment or segment2 tracks contain more segments than this value, a histogram of segments is drawn instead
noHist	If TRUE, segments are never drawn as histograms, even they are more than maxSegs or if the largest segment is smaller than the bin size.
segLwd	Line width for segments

sortSegs	Sort overlapping segments by size
chrSide	Chromosome side where to draw annot1, annot2, annot3, annot4, segments, segments2, stat and stat2, respectively. 1=right, -1=left
cex	Cex for plot (see ?par for details)
legChrom	Legend chromosome (character string). Place legend after this chromosome
scale.title	Title for histograms scales
scex	Cex for stat track
spty	A character specifying the type of plot region to be used in stat
org	Organism name, e.g. mmusculus, hsapiens
strand	Strand "+" or "-" for local view using GenomeGraphs
stack	Stack overlapping segments in segment and segment2 in clusters
statThreshold	Only plot segments in stat with values above this threshold
statThreshold2	Only plot segments in stat2 with values above this threshold
statSumm	Type of statistical function for apply to the data ("mean", "median","sum", "none"), if the value is 'none', chromPlot will not apply some statistical function.

Details

chromPlot package creates an idiogram with all chromosomes including the sex chromosomes. The package is able to plot genomic data on both sides of chromosome as histograms or vertical segments. Histograms represent the number of genomic elements in each bin of size bin. The parameters annot1, annot2, annot3, annot4, segment, segment2, stat, stat2, band, gaps should be data.frames with at leas these columns: 'Chrom', 'Start', 'End'. The gaps and bands arguments are used to plot the chromosomal ideogram.The argument band should also have a 'Group' column with categories for classifying each annotation element. Arguments stat and stat2 should have a statCol and stat2Col column respectively with continuoos values.

If plotted on the same chromosomal side, tracks will be plotted on top of each other, in the order they are in the function's syntax. This can be used for plotting stacked barplots if, for instance, annot1, annot2, annot3, and annot4 are supersets of ecah other. This, however, is not enforced nor checked. An alternative way to create a stacked histogram is providing a single track with Group category. The user can modify the side tracks are plotted on by modifying chrSide.

The segment and segment2 tracks are plotted as vertical bars by default. However, the their elements exceed in number given to maxSegs or if the maximum segment size is smaller than bin, they are plotted as histograms. This behaviour can be modified by setting noHist = TRUE.

For more details and usage examples see the vignette.

Value

Karyotype diagram in device.

Author(s)

Ricardo Verdugo and Karen Orostica

Examples

```
data(hg_cytoBandIdeo)
data(hg_gap)
chromPlot(bands=hg_cytoBandIdeo, gaps=hg_gap)
```

hg_cytoBandIdeo *cytoBandIdeo human*

Description

Describes the positions of cytogenetic bands with a chromosome of human.

Usage

```
data(hg_cytoBandIdeo)
```

Format

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

`Chrom` a character vector

`Start` a numeric vector

`End` a numeric vector

`Name` a character vector

`gieStain` a character vector

Details

This file describes the cytogenetics positions on chromosomes of human. specifically it has 5 columns Chrom, Start, End, Name y Group. Chrom referenced to the chromosomes, the Start and End columns indicated the start and end positions, while that Name indicated the name of cytogenetics Bands, finally, Group column contains informations associated to the Giemsa stain results.

Value

data.frame that contain the positions of cytogenetic bands with a chromosome of human.

Examples

```
data(hg_cytoBandIdeo)
## maybe str(hg_cytoBandIdeo) ; plot(hg_cytoBandIdeo) ...
```

hg_gap *Human Gap*

Description

This track depicts gaps in the assembly of the human genome.

Usage

```
data(hg_gap)
```

Format

A data frame with 457 observations on the following 4 variables.

`Chrom` a character vector

`Start` a numeric vector

`End` a numeric vector

`Name` a character vector

Details

This track depicts gaps in the assembly of human genome. Gaps are represented as black boxes in this track. This assembly contains the following principal types of gaps: (In this context, a contig is a set of overlapping sequence reads.) Clone - gaps between clones (114 gaps). Contig - gaps between map contigs, various sizes (104 gaps). Telomere - 42 gaps for telomeres (100,000 Ns) Centromere - 20 gaps for centromeres (size: 2,890,000 Ns) Short_arm - 21 gaps for the short arm (10,000 Ns) at base positions 100, 001-110,000 of each chromosome. other - sequence of Ns in the assembly that were not marked as gaps in the AGP assembly definition file, various sizes (384 gaps). Fragment - a single gap of 31 bases in chrX_GL456233_random.

Value

data.frame that contain the gaps in the assembly of the human genome.

Examples

```
data(hg_gap)
## maybe str(hg_gap) ; plot(hg_gap) ...
```

`mm10_cytoBandIdeo` *cytoBandIdeo*

Description

Describes the positions of cytogenetic bands with a chromosome of mouse.

Usage

```
data(mm10_cytoBandIdeo)
```

Format

A data frame with 448 observations on the following 5 variables.

`Chrom` a character vector

`Start` a numeric vector

`End` a numeric vector

`Name` a character vector

`gieStain` a character vector

Details

This file describes the cytogenetics positions on chromosomes of mouse. specifically it has 5 columns Chrom, Start, End, Name y Group. Chrom referenced to the chromosomes, the Start and End columns indicated the start and end positions, while that Name indicated the name of cytogenetics Bands, finally, Group column contains informations associated to the Giemsa stain results.

Value

data.frame that contain the positions of cytogenetic bands with a chromosome of mouse.

Examples

```
data(mm10_cytoBandIdeo)
## maybe str(mm10_cytoBandIdeo) ; plot(mm10_cytoBandIdeo) ...
```

---

mm10_gap *Gaps*

Description

This track depicts gaps in the assembly of the mouse genome.

Usage

```
data(mm10_gap)
```

Format

A data frame with 686 observations on the following 4 variables.

`Chrom` a character vector

`Start` a numeric vector

`End` a numeric vector

`Name` a character vector

Details

This track depicts gaps in the assembly (Dec. 2011, Genome Reference Consortium Mouse Build 38 (GCA_000001635.2)) of the mouse genome. Gaps are represented as black boxes in this track. This assembly contains the following principal types of gaps: (In this context, a contig is a set of overlapping sequence reads.) Clone - gaps between clones (114 gaps). Contig - gaps between map contigs, various sizes (104 gaps). Telomere - 42 gaps for telomeres (100,000 Ns) Centromere - 20 gaps for centromeres (size: 2,890,000 Ns) Short_arm - 21 gaps for the short arm (10,000 Ns) at base positions 100,001-110,000 of each chromosome. other - sequence of Ns in the assembly that were not marked as gaps in the AGP assembly definition file, various sizes (384 gaps). Fragment - a single gap of 31 bases in chrX_GL456233_random.

Value

data.frame that contain the gaps in the assembly of the mouse genome.

Examples

```
data(mm10_gap)
## maybe str(mm10_gap) ; plot(mm10_gap) ...
```

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