Package ‘chromPlot’

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**Type** Package

**Title** Global visualization tool of genomic data

**Version** 1.30.0

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**Author** Ricardo A. Verdugo and Karen Y. Orostica

**Maintainer** Karen Y. Orostica <korostica09@gmail.com>

**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

**Depends** stats, utils, graphics, grDevices, datasets, base, biomaRt,
GenomicRanges, R (>= 3.1.0)

**Suggests** qtl, GenomicFeatures, TxDb.Hsapiens.UCSC.hg19.knownGene

**biocViews** DataRepresentation, FunctionalGenomics, Genetics,
Sequencing, Annotation, Visualization

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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.

Details

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

Author(s)

Author: Ricardo Verdugo and Karen Orostica
Maintainer: Karen Orostica <korostica09@alumnos.utalca.cl>

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", statType="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"),
```
arguments = c(annot1, annot2, annot3, annot4, stat, stat2, statCol, statCol2, statTyp, statName, statName2, bands, bandsDesc, gaps, gapsDesc, segment, segmentDesc, segment2, segment2Desc, chr, bin, yAxis, figCols, colBand, colAnnot1, colAnnot2, colAnnot3, colAnnot4, colSegments, colSegments2, colStat, colStat2)

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 least 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 continuous 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 each 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, their elements
exceed in number given to maxSegs or if the maximum segment size is smaller than bin, they are
plotted as histograms. This behavior 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)

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**

```r
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**

```r
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**

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