

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

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

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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 ideogram 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, if 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 | <i>cytoBandIdeo human</i> |
|-----------------|---------------------------|

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 | <i>cytoBandIdeo</i> |
|-------------------|---------------------|

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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