Package ‘SNPchip’

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arrangeFigs

Arranging two trellis objects on a grid.

Description
Helper function for arranging multipanel displays of log R ratios and B allele frequencing in a single figure.

Usage
arrangeFigs(lattice.figs, ...)

Arguments
lattice.figs A named list ('lrr' and 'baf') of two trellis object.
...

Value
nothing

Author(s)
R. Scharpf

See Also
latticeFigs, arrangeSideBySide

arrangeSideBySide

Helper function to arrange two trellis objects side by side on a grid.

Description
For visualizing copy number alterations, it is often helpful to plot estimates of copy number along with the corresponding estimate of the B allele frequencies. Creating a trellis object for the copy number estimates and a separate trellis object for the B allele frequencies, this function can be used to arrange the two trellis objects side by side on a grid.

Usage
arrangeSideBySide(object1, object2)

Arguments
object1 A trellis object (e.g., a trellis object of the copy number estimates).
object2 A trellis object (e.g., a trellis object of the B allele frequencies).
centromere

Author(s)
Rob Scharpf

See Also
xypanel, xyplot

centromere       Coordinates of centromere

Description
Extracts coordinates of centromere for a particular chromosome

Usage
centromere(chromosome, build, verbose=FALSE)

Arguments

  chromosome       Chromosome name. Several formats for specifying chromosome are allowed (see examples).
  build            character string. Supported UCSC builds are ‘hg18’ and ‘hg19’.
  verbose          Logical. Displays build used to annotate the centromere coordinates when TRUE

Value
integer: start and stop coordinates of centromere in basepairs

Author(s)
R. Scharpf

Examples

  centromere(1, "hg18")
  centromere("1", "hg18")
  centromere("chr1", "hg18")
  centromere(1, "hg19")
  centromere("X", "hg18")
dataFrame-methods

Generic function for coercing gSet objects to data.frame

Description

Generic function for coercing gSet objects to data.frame as a precursor to plotting with lattice

Usage

dataFrame(range, data, ...)

Arguments

range  A GenomicRanges object containing interval(s) for which low-level data should be plotted
data   A container for the low-level data (e.g., BafLrrSet) or a RangedSummarizedExperiment...

Value

A data.frame with column labels that depend on the class of data.

Author(s)

R. Scharpf

dataFrame-methods

Construct a data.frame from genomic data for plotting

Description

Construct a data.frame of genomic data (log R ratios and BAFs) from a RangedSummarizedExperiment with markers in the interval given by the GRanges object.

Methods

signature(range = "GRanges", data = "gSet")  The argument range is often intervals from a hidden Markov model fit to the genomic data in the data object. gSet-derived classes contain assay data on copy number and allele frequencies.
signature(range = "GRanges", data = "RangedSummarizedExperiment")  The argument range is often intervals from a hidden Markov model fit to the genomic data in the data object. The RangedSummarizedExperiment is assumed to contain log R ratio (lrr) and B allele frequency (baf) assays.
getCytoband

Description
This function generates a data.frame with the respective cytoband names, chromosomes, Giemsa stain, and the start and end positions. These tables can then be used to plot chromosome idiograms. Currently, cytoband annotation for UCSC genome builds hg18 and hg19 are supported.

Usage
getCytoband(build)

Arguments
build A character string indicating UCSC build ("hg18" or "hg19").

Value
data.frame

Author(s)
Michael Considine

See Also
plotIdiogram

Examples
cytoband <- getCytoband("hg19")
cytoband <- cytoband[cytoband$chr == "chr1",]
plotIdiogram(1, "hg18", cytoband=cytoband, cex.axis=0.6)

latticeFigs

Generate trellis objects of log R ratios and B allele frequencies

Description
Generate trellis objects of log R ratios and B allele frequencies

Usage
latticeFigs(gr, data, colors, ...)

Arguments
gr A GRanges object
data A RangedSummarizedExperiment with assays "lrr" and "baf"
colors Colors for copy number states
... Additional arguments to panel.xyplot
A list (length 2) of trellis objects with names 'lrr' and 'baf'.

R. Scharpf

**Description**

Draw an idiogram for the specified chromosome.

**Usage**

```r
plotIdiogram(chromosome, build, cytoband, cytoband.ycoords, xlim, ylim=c(0, 2),
new=TRUE, label.cytoband=TRUE, label.y=NULL, srt, cex.axis=1,
outer=FALSE, taper=0.15, verbose=FALSE, unit=c("bp", "Mb"),
is.lattice=FALSE,...)
plotCytoband2(chromosome, build, cytoband, xlim, xaxs="r", new=TRUE,
label.cytoband=TRUE, cex.axis=1, outer=FALSE, verbose=TRUE, ...)
```

**Arguments**

- `chromosome`: character string or integer: which chromosome to draw the cytoband
- `build`: UCSC genome build. Supported builds are "hg18" and "hg19".
- `cytoband`: data.frame containing cytoband information
- `cytoband.ycoords`: numeric: y coordinates
- `xlim`: x-axis limits
- `xaxs`: numeric. See `par`
- `ylim`: y-axis limits
- `new`: logical: new plotting device
- `label.cytoband`: logical: if TRUE, labels the cytobands
- `label.y`: numeric: height (y-coordinate) for cytoband label
- `srt`: string rotation for cytoband labels. See `par`
- `cex.axis`: size of cytoband labels. See `par`
- `outer`: logical: whether to draw the labels in the outer margins. See `par`
- `taper`: tapering for the ends of the cytoband
- `verbose`: Logical. If TRUE, displays human genome build used to annotated the cytoband coordinates.
- `unit`: Character string indicating the unit for physical position on the x-axis. Available options are basepairs (bp) or Mb.
- `is.lattice`: logical indicating whether your drawing the cytoband on a lattice graphic.
- `...`: additional arguments to plot
Author(s)

Robert Scharpf and Jason Ting

Examples

```r
plotIdiogram("1", "hg18")
plotIdiogram("1", "hg19")
plotIdiogram("1", build="hg19", cex=0.8, label.cytoband=FALSE)
## user-defined coordinates
plotIdiogram("1", build="hg19", cex=0.8, label.cytoband=FALSE,
ylim=c(0,1), cytoband.ycoords=c(0.1, 0.3))
```

```r
library(oligoClasses)
sl <- getSequenceLengths("hg19")[c(paste("chr", 1:22, sep=""), "chrX", "chrY")]
ybottom <- seq(0, 1, length.out=length(sl)) - 0.01
ytop <- seq(0, 1, length.out=length(sl)) + 0.01
for(i in seq_along(sl)){
  chr <- names(sl)[i]
  if(i == 1){
    plotIdiogram("1", build="hg19", cex=0.8, label.cytoband=FALSE, ylim=c(-0.05,1.05), cytoband.ycoords=c(ybottom[1], ytop[1]),
xlim=c(0, max(sl)))
  }
  if(i > 1){
    plotIdiogram(names(sl)[i], build="hg19", cex=0.8, label.cytoband=FALSE, cytoband.ycoords=c(ybottom[i], ytop[i]),
    new=FALSE)
  }
}
axis(1, at=pretty(c(0, max(sl)), n=10), labels=pretty(c(0, max(sl)), n=10)/1e6, cex.axis=0.8)
mtext("position (Mb)", 1, line=2)
par(las=1)
axis(2, at=ybottom+0.01, names(sl), cex.axis=0.6)
```

---

xypanel

A panel function for plotting copy number versus physical position

Description

A panel function for `xyplot` for plotting copy number versus physical position.

Usage

```r
xypanel(x, y, gt, is.snp, range, col.hom = "grey20", fill.hom = 
"lightblue", col.het = "grey20", fill.het = "salmon", col.np = "grey20",
fill.np = "grey60", show.state=TRUE, state.cex=1, col.state="blue", ..., subscripts)
```

Arguments

- `x` Physical position in megabases.
- `y` Copy number estimates.
- `gt` Genotype calls.
- `is.snp` Logical. Whether the marker is polymorphic.
- `range` A RangedData or IRanges object. Note that we expect the units returned by start and end to be basepairs.
col.hom  A specification for the color of plotting symbols for homozygous genotypes.
fill.hom  A specification for the fill color of plotting symbols for homozygous genotypes.
col.het  A specification for the color of plotting symbols for heterozygous genotypes.
fill.het  A specification for the fill color of plotting symbols for heterozygous genotypes.
col.np   A specification for the color of plotting symbols for nonpolymorphic markers.
fill.np   A specification for the fill color of plotting symbols for nonpolymorphic genotypes.
show.state Logical. Whether to display the predicted state in each panel.
state.cex Numeric. cex for state label. Ignored if show.state is FALSE.
col.state Character. color for state label. Ignored if show.state is FALSE.
... Additional arguments passed to lattice functions xyplot, lpoints, and lrect.
subscripts See the panel functions in lattice for more information.

Details
The order of plotting is (1) nonpolymorphic markers, (2) homozygous SNPs, and (3) heterozygous SNPs. Stretches of homozygosity should appear as blue using the default color scheme.

Note
To make the drawing of the range object border invisible, one can use border="white".

Author(s)
R. Scharpf

See Also
xyplot

Examples
## Not run:
if(require("crlmm") & require("VanillaICE") & require("IRanges")){
  library(lattice)
  library(oligoClasses)
data(oligoSetExample, package="oligoClasses")
  oligoSet <- oligoSet[chromosome(oligoSet) == 1, ]
cn <- copyNumber(oligoSet)/100
cn <- log2((2^cn)/2)
  gt <- calls(oligoSet)[,]
  ## simulate BAFs
  bf <- rep(NA, length(gt))
  u <- runif(length(gt))
  bf[gt==1 & u > 0.5] <- runif(sum(gt==1 & u > 0.5), 0, 0.05)
  bf[gt==1 & u <= 0.5] <- runif(sum(gt==1 & u <= 0.5), 0.95, 1)
  bf[gt==2] <- runif(sum(gt==2), 0.45, 0.55)
  bf[900:1200] <- runif(length(900:1200), 0, 0.03)
  gr <- GRanges(paste0("chr", chromosome(featureData(oligoSet))),
                IRanges(position(oligoSet), width=1))
  cn <- as.matrix(cn)
  bf <- as.matrix(bf)
xypanelBaf <- Panel function for plotting copy number and B allele frequencies for a genomic interval.

Description

Panel function for plotting copy number and B allele frequencies for a genomic interval.

Usage

xypanelBaf(x, y, gt, baf, is.snp, range, col.hom = "grey20", fill.hom = "lightblue", col.het = "grey20", fill.het = "salmon", col.np = "grey20", fill.np = "grey60", show.state = TRUE, state.cex = 1, col.state = "blue", ...)

Arguments

x
physical position in basepairs

y
total copy number (relative or absolute)

gt
Genotypes coded as integers (1=AA, 2=AB, 3=BB). This is optional. If provided one can color code the plotting symbols by the genotype.

baf
B allele frequencies.

is.snp
Logical. Indicator of whether the marker hybridized to a known SNP or a non-polymorphic region of the genome.

range
A RangedDataCNV-derived object indicating the genomic interval to plot.

col.hom
Color to use for homozygous genotypes.

fill.hom
Fill color to use for homozygous genotypes.

col.het
Color to use for heterozygous genotypes.

fill.het
Fill color to use for heterozygous genotypes.

col.np
Color to use for nonpolymorphic markers

fill.np
Fill color for nonpolymorphic markers.
show.state Logical indicating whether to display the copy number state for a RangedDataHMM object.
state.cex Size of the font for displaying the HMM state. Ignored if show.state is FALSE.
col.state Color for displaying the state.
... Additional arguments passed to panel.xyplot.
subscripts See panel.xyplot

Details
Function for plotting B allele frequencing and copy number on a trellis display. Intended to be passed to the panel argument of the function xyplotLrrBaf and should not be called directly by the user.

Author(s)
R.Scharpf

See Also
xyplotLrrBaf

xyplot
Plot copy number and physical position for a set of genomic intervals.

Description
Plot copy number and physical position given by a CNSet object for a set of genomic intervals stored in a RangedDataCVN object.

Usage
xyplot2(x, data, range, frame=50e3L, ...)

Arguments
x A formula. Currently, the formula must be one of cn~x, cn ~ x | id or cn ~ x | range when data is a CNSet. If data is a BeadStudioSet, the formula has the form lrr ~ x| range or baf ~ x | range.
data A CNSet, BeadStudioSet, or SnpSet object.
... A RangedDataCNV object must be passed by the name 'range'. Arguments for xyplot are passed to xyplot2. Additional arguments are passed to xypanel and panel.xyplot.
range A RangedDataCNV object.
frame The genomic distance (basepairs) to the left and right of the start and stop coordinates in the range object.
Details

These functions plot copy number estimates versus physical position. The function is particularly useful for multi-panel displays in which the copy number estimates for a single range of a GRanges object appears in one panel. The size of the multi-panel display depends on the number of ranges (rows) in the GRanges object.

Value

An object of class trellis.

Author(s)

R. Scharpf

See Also

xyplot, xypanel

To modify the plot appearance from the default, additional arguments can be passed to panel.xyplot, lpoints, and lrect.

Examples

## simulated data
library(oligoClasses)
library(IRanges)
library(VanillaICE)
data(oligoSetExample, package="oligoClasses")
## The oligoSnpSet class will likely be deprecated and made defunct
## in a future release. Instead, we favor
## RangedSummarizedExperiment-derived classes defined in VanillaICE
oligoSet <- oligoSet[chromosome(oligoSet) == 1, ]
cn <- copyNumber(oligoSet)/100
cn <- log2((2^cn)/2)
gt <- calls(oligoSet)[,]
## simulate BAFs
bf <- rep(NA, length(gt))
ู <- runif(length(gt))
bf[gt==1 & ู > 0.5] <- runif(sum(gt==1 & ู > 0.5), 0, 0.05)
bf[gt==1 & ู <= 0.5] <- runif(sum(gt==1 & ู <= 0.5), 0.95, 1)
bf[gt==2] <- runif(sum(gt==2), 0.45, 0.55)
bf[900:1200] <- runif(length(900:1200), 0, 0.03)
gr <- GRanges(paste0("chr", chromosome(featureData(oligoSet))),
IRanges(position(oligoSet), width=1))
cn <- as.matrix(cn)
bf <- as.matrix(bf)
dimnames(cn) <- dimnames(bf) <- list(featureNames(oligoSet), sampleNames(oligoSet))
se <- SnpArrayExperiment(cn=cn,
    baf=bf,
    rowRanges=gr,
    isSnp=rep(TRUE, length(gr)))
fit <- hmm2(se)
g <- as(segs(fit), "GRanges")
## To visualize each range in it’s own panel surrounded by a
## frame of 2,000,000 bases:
## (here the frames are overlapping, but the method could be
xyplotLrrBaf

xyplot lattice function for RangedData and oligoSnpSet objects

Description

For each genomic interval in the ranged data, a plot of the log R ratios and B allele frequencies stored in the oligoSnpSet are plotted.

Usage

xyplotLrrBaf(rd, object, frame, ...) 

Arguments

rd An instance of RangedDataCNV or GRanges.
object A oligoSnpSet or BeadStudioSet object with assayData elements for log R ratios and B allele frequencies.
frame The genomic distance in basepairs to plot on either side of the genomic interval in the rd object.

Details

The xypanelBaf function is a panel function that does the actual plotting of the genomic data.

Value

A trellis object.

Author(s)

R. Scharpf

See Also

xypanelBaf
Examples

```r
## Not run:
library(crlmm)
library(SummarizedExperiment)
library(VanillaICE)
data(cnSetExample, package="crlmm")
oligoSetList <- BafLrrSetList(cnSetExample[, 1])
oligoSet <- oligoSetList[[1]]
cn <- copyNumber(oligoSet)/100
cn <- log2((2^cn)/2)
gt <- calls(oligoSet)[,]
## simulate BAFs
bf <- baf(oligoSet)[, ]/1000
gr <- GRanges(paste0("chr", chromosome(featureData(oligoSet))),
IRanges(position(oligoSet), width=1))
cn <- as.matrix(cn)
bf <- as.matrix(bf)
dimnames(cn) <- dimnames(bf) <- list(featureNames(oligoSet), sampleNames(oligoSet))
se <- SnpArrayExperiment(cn=cn,
  baf=bf,
  rowRanges=gr,
  isSnp=rep(TRUE, length(gr)))
fit <- hmm2(se)
##rd <- fit[sampleNames(fit)="NA19007", ]
rd <- as(segs(fit), "GRanges")
## We're interested in this range
range <- GRanges("chr8", IRanges(3.7e6, 5.9e6), sample="NA19007")
index <- subjectHits(findOverlaps(range, rd))
xyplotLrrBaf(rd[index, ], oligoSetList[[1]], frame=1e6,
  panel=xpanelBaf, cex=0.2,
scales=list(x=list(relation="free"),
y=list(alternating=1,
at=c(-1, 0, log2(3/2), log2(4/2)),
lables=expression(-1, 0, log[2](3/2), log[2](4/2))),
par.strip.text=list(cex=0.7),
ylim=c(-3,1),
col.hom="grey50",
col.het="grey50",
col.np="grey20",
xlab="physical position (Mb)",
ylab=expression(log[2]("R ratios")),
key=list(text=list(c(expression(log[2]("R ratios")), expression("B allele frequencies")),
col=c("grey", "blue")), columns=2))
## Or, plot each range of the GRanges instance in a separate panel
xyplotLrrBaf(rd, oligoSetList[[1]], frame=1e6,
  panel=xpanelBaf, cex=0.2,
scales=list(x=list(relation="free"),
y=list(alternating=1,
at=c(-1, 0, log2(3/2), log2(4/2)),
lables=expression(-1, 0, log[2](3/2), log[2](4/2))),
par.strip.text=list(cex=0.7),
ylim=c(-3,1),
col.hom="grey50",
col.het="grey50",
```
col=np="grey20",
xlab="physical position (Mb)",
ylab=expression(log[2]("R ratios")),
key=list(text=list(c(expression(log[2]("R ratios")), expression("B allele frequencies")),
col=c("grey", "blue"), columns=2))

## End(Not run)
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