Package `ggbio`

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**Version** 1.22.3

**Title** Visualization tools for genomic data.

**Description** The ggbio package extends and specializes the grammar of graphics for biological data. The graphics are designed to answer common scientific questions, in particular those often asked of high throughput genomics data. All core Bioconductor data structures are supported, where appropriate. The package supports detailed views of particular genomic regions, as well as genome-wide overviews. Supported overviews include ideograms and grand linear views. High-level plots include sequence fragment length, edge-linked interval to data view, mismatch pileup, and several splicing summaries.

**Depends** methods, BiocGenerics, ggplot2 (>= 1.0.0)

**Imports** grid, grDevices, graphics, stats, utils, gridExtra, scales, reshape2, table, Hmisc, biovizBase (>= 1.19.1), Biobase, S4Vectors (>= 0.9.25), IRanges, GenomeInfoDb (>= 1.1.3), GenomicRanges (>= 1.21.10), SummarizedExperiment, Biostats, Rsamtools (>= 1.17.28), GenomicAlignments (>= 1.1.16), BSgenome, VariantAnnotation (>= 1.11.4), rtracklayer (>= 1.25.16), GenomicFeatures (>= 1.17.13), OrganismDbi, GGally, ensembldb (>= 1.3.8), AnnotationDbi

**VignetteBuilder** knitr


**URL** http://tengfei.github.com/ggbio/

**BugReports** https://github.com/tengfei/ggbio/issues

**License** Artistic-2.0

**LazyLoad** Yes

topics documented:

- layout_karyogram-method.R
- layout_linear-method.R
- stat_aggregate-method.R
- stat_coverage-method.R
- stat_identity-method.R
- stat_mismatch-method.R
- stat_stepping-method.R
- stat_gene-method.R
- stat_table-method.R
- stat_bin-method.R
- stat_slice-method.R
- stat_reduce-method.R
- coord Genome-method.R
- autoplot-method.R
- hack.R
- plotGrandLinear.R
- plotRangesLinkedToData.R
- plotFragLength-method.R
- plotSpliceSum-method.R
- rescale-method.R
- utils.R
- zzz.R

biovViews Infrastructure, Visualization

NeedsCompilation no

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Maintainer Michael Lawrence <lawrence.michael@gene.com>

topics documented:

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**arrangeGrobByParsingLegend**

Arrange grobs by parsing their legend.

_Usage_

`arrangeGrobByParsingLegend(..., nrow = NULL, ncol = NULL, widths = c(4, 1), legend.idx = NULL)`

_Arguments_

- `...` ggplot graphics.
- `nrow` number of row for layout.
- `ncol` number of columns for layout.
- `widths` width ratio for plot group and legend group.
- `legend.idx` legend index you want to keep.

_Value_

- `a`

_Author(s)_

Tengfei Yin

_Examples_

```r
library(ggplot2)
p1 <- qplot(x = mpg, y = cyl, data = mtcars, color = carb)
p2 <- qplot(x = mpg, y = cyl, data = mtcars, color = wt)
p3 <- qplot(x = mpg, y = cyl, data = mtcars, color = qsec)
p4 <- qplot(x = mpg, y = cyl, data = mtcars, color = gear)
arrangeGrobByParsingLegend(p1, p2, p3, p4)
arrangeGrobByParsingLegend(p1, p2, p3, p4, ncol = 1)
arrangeGrobByParsingLegend(p1, p2, p3, p4, legend.idx = 2)
```
autoplot

Generic autoplot function

Description

autoplot is a generic function to visualize various data object, it tries to give better default graphics and customized choices for each data type, quick and convenient to explore your genomic data compare to low level ggplot method, it is much simpler and easy to produce fairly complicate graphics, though you may lose some flexibility for each layer.

Usage

## S4 method for signature 'GRanges'
autoplot(object, ..., chr, xlab, ylab, main, truncate.gaps = FALSE, 
  truncate.fun = NULL, ratio = 0.0025, space.skip = 0.1, 
  legend = TRUE, geom = NULL, stat = NULL, 
  chr.weight = NULL, 
  coord = c("default", "genome", "truncate_gaps"), 
  layout = c("linear", "karyogram", "circle"))

## S4 method for signature 'GRangesList'
autoplot(object, ..., xlab, ylab, main, indName = "grl_name", 
  geom = NULL, stat = NULL, coverage.col = "gray50", 
  coverage.fill = coverage.col, group.selfish = FALSE)

## S4 method for signature 'IRanges'
autoplot(object, ..., xlab, ylab, main)

## S4 method for signature 'Seqinfo'
autoplot(object, ideogram = FALSE, ... )

## S4 method for signature 'GAlignments'
autoplot(object, ..., xlab, ylab, main, which, 
  geom = NULL, stat = NULL)

## S4 method for signature 'BamFile'
autoplot(object, ..., which, xlab, ylab, main, 
  bsgenome, geom = "line", stat = "coverage", method = c("raw", "estimate"), 
  coord = c("linear", "genome"), 
  resize.extra = 10, space.skip = 0.1, show.coverage = 
  TRUE)

## S4 method for signature 'character'
autoplot(object, ..., xlab, ylab, main, which)

## S4 method for signature 'TxDbOREnsDb'
autoplot(object, which, ..., xlab, ylab, main, truncate.gaps = 
  FALSE, truncate.fun = NULL, ratio = 0.0025,
autoplot

  mode = c("full", "reduce"), geom =
  c("alignment"), stat = c("identity", "reduce"),
  names.expr = "tx_name", label = TRUE)

## S4 method for signature 'BSgenome'
autoplot(object, which, ...,
       xlab, ylab, main, geom = NULL)

## S4 method for signature 'Rle'
autoplot(object, ..., xlab, ylab, main, binwidth, nbins = 30,
         geom = NULL, stat = c("bin", "identity", "slice"),
         type = c("viewSums", "viewMins", "viewMaxs", "viewMeans"))

## S4 method for signature 'RleList'
autoplot(object, ..., xlab, ylab, main, binwidth,
         facetByRow = TRUE, stat = c("bin", "identity", "slice"),
         geom = NULL, type = c("viewSums", "viewMins", "viewMaxs", "viewMeans"))

## S4 method for signature 'matrix'
autoplot(object, ..., xlab, ylab, main,
         geom = c("tile", "raster"), axis.text.angle = NULL,
         hjust = 0.5, na.value = NULL,
         rownames.label = TRUE, colnames.label = TRUE,
         axis.text.x = TRUE, axis.text.y = TRUE)

## S4 method for signature 'ExpressionSet'
autoplot(object, ..., type = c("heatmap", "none",
       "scatterplot.matrix", "pcp", "MA", "boxplot",
       "mean-sd"), test.method =
       "t", rotate = FALSE, pheno.plot = FALSE, main_to_pheno
       = 4.5, padding = 0.2)

## S4 method for signature 'RangedSummarizedExperiment'
autoplot(object, ..., type = c("heatmap", "link", "pcp", "boxplot", "scatterplot.matrix"),
         pheno.plot = FALSE,
         main_to_pheno = 4.5, padding = 0.2, assay.id = 1)

## S4 method for signature 'VCF'
autoplot(object, ...,
         xlab, ylab, main,
         assay.id,
         type = c("default", "geno", "info", "fixed"),
         full.string = FALSE,
         ref.show = TRUE,
         genome.axis = TRUE,
         transpose = TRUE)

## S4 method for signature 'OrganismDb'
autoplot(object, which, ..., 
  xlab, ylab, main, 
  truncate.gaps = FALSE, 
  truncate.fun = NULL, 
  ratio = 0.0025, 
  geom = c("alignment"), 
  stat = c("identity", "reduce"), 
  columns = c("TXNAME", "SYMBOL", "TXID", "GENEID"), 
  names.expr = "SYMBOL", 
  label = TRUE, 
  label.color = "gray40")

## S4 method for signature 'VRanges'
autoplot(object, ..., which = NULL, 
  arrow = TRUE, indel.col = "gray30", 
  geom = NULL, 
  xlab, ylab, main)

## S4 method for signature 'TabixFile'
autoplot(object, which, ...)

Arguments

object object to be plot.
columns columns passed to method works for TxDb, EnsDb and OrganismDb.
label.color when label turned on for gene model, this parameter controls label color.
arow arrow passed to geome_alignment function to control intron arrow attributes.
indel.col indel colors.
ideogram Weather to call plotIdeogram or not, default is FALSE, if TRUE, layout_karyogram will be called.
transpose logical value, default TRUE, always make features from VCF as x, so we can use it to map to genomic position.
axis.text.angle axis text angle.
axis.text.x logical value indicates whether to show x axis and labels or not.
axis.text.y logical value indicates whether to show y axis and labels or not.
hjust horizontal just for axis text.
rownames.label logical value indicates whether to show rownames of matrix as y label or not.
colnames.label logical value indicates whether to show colnames of matrix as y label or not.
na.value color for NA value.
rotate pheno.plot show pheno plot or not.
main_to_pheno main matrix plot width to pheno plot width ratio.
padding padding between plots.
assay.id index for assay you are going to use.
geom Geom to use (Single character for now). Please see section Geometry for details.
truncate.gaps logical value indicate to truncate gaps or not.
<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>truncate.fun</td>
<td>Shrinkage function. Please see <code>shrinkagefun</code> in package <code>biovizBase</code>.</td>
</tr>
<tr>
<td>ratio</td>
<td>Used in <code>maxGap</code>.</td>
</tr>
<tr>
<td>mode</td>
<td>Display mode for genomic features.</td>
</tr>
<tr>
<td>space.skip</td>
<td>Space ratio between chromosome spaces in coordinate genome.</td>
</tr>
<tr>
<td>coord</td>
<td>Coordinate system.</td>
</tr>
<tr>
<td>chr.weight</td>
<td>Numeric vectors which sum to &lt;1, the names of vectors has to be matched with seqnames in <code>seqinfo</code>, and you can only specify part of the seqnames, other lengths of chromosomes will be assigned proportionally to their seqlengths. For example, you could specify chr1 to be 0.5, so the chr1 will take half of the space and other chromosomes squeezed to take left of the space.</td>
</tr>
<tr>
<td>legend</td>
<td>A logical value indicates whether to show legend or not. Default is TRUE.</td>
</tr>
<tr>
<td>which</td>
<td>A <code>GRanges</code> object to subset the result, usually passed to the <code>ScanBamParam</code> function.</td>
</tr>
<tr>
<td>show.coverage</td>
<td>A logical value indicates whether to show coverage or not. This is used for geom &quot;mismatch.summary&quot;.</td>
</tr>
<tr>
<td>resize.extra</td>
<td>A numeric value used to add buffer to intervals to compute stepping levels on.</td>
</tr>
<tr>
<td>bsgenome</td>
<td>A <code>BSgenome</code> object. Only need for geom &quot;mismatch.summary&quot;.</td>
</tr>
<tr>
<td>xlab</td>
<td>X label.</td>
</tr>
<tr>
<td>ylab</td>
<td>Y label.</td>
</tr>
<tr>
<td>label</td>
<td>Logic value, default TRUE. To show label by the side of features.</td>
</tr>
<tr>
<td>facetByRow</td>
<td>A logical value, default is TRUE, facet <code>RleList</code> by row. If FALSE, facet by column.</td>
</tr>
<tr>
<td>type</td>
<td>For <code>Rle/RleList</code>, &quot;raw&quot; plot everything, so be careful, that would be pretty slow if you have too much data. For &quot;viewMins&quot;, &quot;viewMaxs&quot;, &quot;viewMeans&quot;, &quot;viewSums&quot;, require extra arguments to slice the object. So users need to at least provide lower, more details and control please refer the the manual of slice function in <code>IRanges</code>. For &quot;viewMins&quot;, &quot;viewMaxs&quot;, we use <code>viewWhichMin</code> and <code>viewWhichMax</code> to get x scale, for &quot;viewMeans&quot;, &quot;viewSums&quot;, we use window midpoint as x. For <code>ExpressionSet</code>, plotting types.</td>
</tr>
<tr>
<td>layout</td>
<td>Layout including linear, circular and karyogram. for <code>GenomicRangesList</code>, it only supports circular layout.</td>
</tr>
<tr>
<td>method</td>
<td>Method used for parsing coverage from <code>bam</code> files. <code>estimate</code> use fast estimated method and <code>raw</code> use relatively slow parsing method.</td>
</tr>
<tr>
<td>test.method</td>
<td>Test method.</td>
</tr>
<tr>
<td>...</td>
<td>Extra parameters. Usually are those parameters used in <code>autoplot</code> to control aesthetics or geometries.</td>
</tr>
<tr>
<td>main</td>
<td>Title.</td>
</tr>
<tr>
<td>stat</td>
<td>Statistical transformation.</td>
</tr>
<tr>
<td>indName</td>
<td>When coerce <code>GRangesList</code> to <code>GRanges</code>, names created for each group.</td>
</tr>
<tr>
<td>coverage.col</td>
<td>Coverage stroke color.</td>
</tr>
<tr>
<td>coverage.fill</td>
<td>Coverage fill color.</td>
</tr>
<tr>
<td>group.selfish</td>
<td>Passed to <code>addStepping</code>, control whether to show each group as unique level or not. If set to FALSE, if two groups are not overlapped with each other, they will probably be layout in the same level to save space.</td>
</tr>
</tbody>
</table>
names.expr  
names expression used for creating labels. For EnsDb objects either "tx_id", "gene_name" or "gene_id".

binwidth  
width of the bins.

nbin  
number of bins.

genome.axis  
logical value, if TRUE, whenever possible, try to parse genomic position for each column(e.g. RangedSummarizedExperiment), show column as exactly the genomic position instead of showing them side by side and indexed from 1.

full.string  
logical value. If TRUE, show full string of indels in plot for VCF.

ref.show  
logical value. If TRUE, show REF in VCF at bottom track.

chr  
characters indicates the seqnames to be subseted.

Value
A ggplot object, so you can use common features from ggplot2 package to manipulate the plot.

Introduction
autoplot is redefined as generic s4 method inside this package, user could use autoplot in the way they are familiar with, and we are also setting limitation inside this package, like

• scales X scales is always genomic coordinates in most cases, x could be specified as start/end/midpoint when it’s special geoms for interval data like point/line
• colors Try to use default color scheme defined in biovizBase package as possible as it can

Geometry
We have developed new geom for different objects, some of them may require extra parameters you need to provide. Some of the geom are more like geom + stat in ggplot2 package. e.g. "coverage.line" and "coverage.polygon". We simply combine them together, but in the future, we plan to make it more general.

This package is designed for only biological data, especially genomic data if users want to explore the data in a more flexible way, you could simply coerce the GRanges to a data.frame, then just use formal autoplot function in ggplot2, or autoplot generic for data.frame.

Some objects share the same geom so we introduce all the geom together in this section

Showing all the intervals as stepped rectangle, colored by strand automatically.
For TxDb or EnsDb objects, showing full model.

segment  
Showing all the intervals as stepped segments, colored by strand automatically.
For object BSgenome, show nucleotides as colored segment.
For Rle/RleList, show histogram-like segments.

line  
Showing interval as line, the interval data could also be just single position when start = end, x is one of start/end/midpoint, y value is unquoted name in elementMetadata column names. y value is required.

point  
Showing interval as point, the interval data could also be just single position when start = end, x is one of start/end/midpoint, y value is unquoted name in elementMetadata column names, y value is required.
For object BSgenome, show nucleotides as colored point.

coverage.line  
Coverage showing as lines for interval data.

coverage.polygon  
Coverage showing as polygon for interval data.
splice  Splicing summary. The size and width of the line and rectangle should represent the counts in each model. Need to provide model.

single  For TxDb or EnsDb objects, showing single(reduced) model only.

tx  For TxDb or EnsDb objects, showing transcripts isoforms.

mismatch.summary  Showing color coded mismatched stacked bar to indicate the proportion of mismatching at each position, the reference is set to gray.

text  For object BSgenome, show nucleotides as colored text.

rectangle  For object BSgenome, show nucleotides as colored rectangle.

Faceting

Faceting in ggbio package is a little different from ggplot2 in several ways

- The faceted column could only be seqnames or regions on the genome. So we limited the formula passing to facet argument, e.g something ~ seqnames, is accepted formula, you can change “something” to variable name in the elementMetadata. But you can not change the second part.

- Sometime, we need to view different regions, so we also have a facet_gr argument which accept a GRanges. If this is provided, it will override the default seqnames and use provided region to facet the graphics, this might be useful for different gene centric views.

Author(s)

Tengfei Yin

Examples

library(ggbio)

set.seed(1)
N <- 1000
library(GenomicRanges)
gr <- GRanges(seqnames =
sample(c("chr1", "chr2", "chr3"),
size = N, replace = TRUE),
IRanges(
    start = sample(1:300, size = N, replace = TRUE),
    width = sample(70:75, size = N,replace = TRUE)),
strand = sample(c("+", "-", "*"), size = N,
    replace = TRUE),
value = rnorm(N, 10, 3), score = rnorm(N, 100, 30),
sample = sample(c("Normal", "Tumor"),
    size = N, replace = TRUE),
pair = sample(letters, size = N,
    replace = TRUE))

idx <- sample(1:length(gr), size = 50)

# code chunk number 3: default
autoplot(gr[idx])
```r
set.seed(123)
gr.b <- GRanges(seqnames = "chr1", IRanges(start = seq(1, 100, by = 10),
    width = sample(4:9, size = 10, replace = TRUE)),
    score = rnorm(10, 10, 3), value = runif(10, 1, 100))
gr.b2 <- GRanges(seqnames = "chr2", IRanges(start = seq(1, 100, by = 10),
    width = sample(4:9, size = 10, replace = TRUE)),
    score = rnorm(10, 10, 3), value = runif(10, 1, 100))
gr.b <- c(gr.b, gr.b2)
head(gr.b)
```

```r
p1 <- autoplot(gr.b, geom = "bar")
## use value to fill the bar
p2 <- autoplot(gr.b, geom = "bar", aes(fill = value))
tracks(default = p1, fill = p2)
```
### code chunk number 10: gr-circle
seqlengths(gr) <- c(400, 500, 700)
values(gr)$to.gr <- gr[sample(1:length(gr), size = length(gr))]
idx <- sample(1:length(gr), size = 50)
gr <- gr[idx]
ggplot() + layout_circle(gr, geom = "ideo", fill = "gray70", radius = 7, trackWidth = 3) +
    layout_circle(gr, geom = "bar", radius = 10, trackWidth = 4,
        aes(fill = score, y = score)) +
    layout_circle(gr, geom = "point", color = "red", radius = 14,
        trackWidth = 3, grid = TRUE, aes(y = score)) +
    layout_circle(gr, geom = "link", linked.to = "to.gr", radius = 6, trackWidth = 1)

### code chunk number 11: seqinfo-src
data(hg19Ideogram, package = "biovizBase")
seq <- seqinfo(hg19Ideogram)
seq

### code chunk number 12: seqinfo
autoplot(seq[ paste0("chr", c(1:22, "X")) ]) 

### code chunk number 13: ir-load
set.seed(1)
N <- 100
ir <- IRanges(start = sample(1:300, size = N, replace = TRUE),
    width = sample(70:75, size = N, replace = TRUE))
# add meta data
df <- DataFrame(value = rnorm(N, 10, 3), score = rnorm(N, 100, 30),
    sample = sample(c("Normal", "Tumor"),
        size = N, replace = TRUE),
    pair = sample(letters, size = N, replace = TRUE))
values(ir) <- df
ir

### code chunk number 14: ir-exp
p1 <- autoplot(ir)
p2 <- autoplot(ir, aes(fill = pair)) + theme(legend.position = "none")
p3 <- autoplot(ir, stat = "coverage", geom = "line", facets = sample ~ .)
p4 <- autoplot(ir, stat = "reduce")
tracks(p1, p2, p3, p4)
```r
set.seed(1)
N <- 100

## simmulated GRanges
gr <- GRanges(seqnames = sample(c("chr1", "chr2", "chr3"), size = N, replace = TRUE),
              IRanges(start = sample(1:300, size = N, replace = TRUE),
                      width = sample(30:40, size = N, replace = TRUE),
                      strand = sample(c("+", "-", "*"), size = N, replace = TRUE),
                      value = rnorm(N, 10, 3), score = rnorm(N, 100, 30),
                      sample = sample(c("Normal", "Tumor"), size = N, replace = TRUE),
                      pair = sample(letters, size = N, replace = TRUE))

grl <- split(gr, values(gr)$pair)

## default gap.geom is 'chevron'
p1 <- autoplot(grl, group.selfish = TRUE)
p2 <- autoplot(grl, group.selfish = TRUE, main.geom = "arrowrect", gap.geom = "segment")
tracks(p1, p2)
```

```r
library(IRanges)
set.seed(1)
lambda <- c(rep(0.001, 4500), seq(0.001, 10, length = 500),
             seq(10, 0.001, length = 500))

## @knitr create
xVector <- rpois(1e4, lambda)
xRle <- Rle(xVector)
xRle
```
### code chunk number 19: rle-bin
```r
p1 <- autoplot(xRle)
p2 <- autoplot(xRle, nbin = 80)
p3 <- autoplot(xRle, geom = "heatmap", nbin = 200)
tracks('nbin = 30' = p1, "nbin = 80" = p2, "nbin = 200(heatmap)" = p3)
```

### code chunk number 20: rle-id
```r
p1 <- autoplot(xRle, stat = "identity")
p2 <- autoplot(xRle, stat = "identity", geom = "point", color = "red")
tracks('line' = p1, "point" = p2)
```

### code chunk number 21: rle-slice
```r
p1 <- autoplot(xRle, type = "viewMaxs", stat = "slice", lower = 5)
p2 <- autoplot(xRle, type = "viewMaxs", stat = "slice", lower = 5, geom = "heatmap")
tracks('bar' = p1, "heatmap" = p2)
```

### code chunk number 22: rlel-simul
```r
xRleList <- RleList(xRle, 2L * xRle)
xRleList
```

### code chunk number 23: rlel-bin
```r
p1 <- autoplot(xRleList)
p2 <- autoplot(xRleList, nbin = 80)
p3 <- autoplot(xRleList, geom = "heatmap", nbin = 200)
tracks('nbin = 30' = p1, "nbin = 80" = p2, "nbin = 200(heatmap)" = p3)
```

### code chunk number 24: rlel-id
```r
p1 <- autoplot(xRleList, stat = "identity")
p2 <- autoplot(xRleList, stat = "identity", geom = "point", color = "red")
tracks('line' = p1, "point" = p2)
```

### code chunk number 25: rlel-slice
```r
p1 <- autoplot(xRleList, type = "viewMaxs", stat = "slice", lower = 5)
p2 <- autoplot(xRleList, type = "viewMaxs", stat = "slice", lower = 5, geom = "heatmap")
tracks('bar' = p1, "heatmap" = p2)
```
library(TxDb.Hsapiens.UCSC.hg19.knownGene)
data(genesymbol, package = "biovizBase")
txdb <- TxDb.Hsapiens.UCSC.hg19.knownGene

p1 <- autoplot(txdb, which = genesymbol["ALDOA"], names.expr = "tx_name:::gene_id")
p2 <- autoplot(txdb, which = genesymbol["ALDOA"], stat = "reduce", color = "brown", fill = "brown")
tracks(full = p1, reduce = p2, heights = c(5, 1)) + ylab("")

library(EnsDb.Hsapiens.v75)
ensdb <- EnsDb.Hsapiens.v75

p1 <- autoplot(ensdb, which=GenenameFilter("ALDOA"), names.expr="gene_name")
p2 <- autoplot(ensdb, which=GenenameFilter("ALDOA"), stat="reduce", color="brown", fill="brown")
tracks(full = p1, reduce = p2, heights = c(5, 1)) + ylab("")

## Alternatively, we can specify a GRangesFilter and display all genes
## that are (partially) overlapping with that genomic region:
gr <- GRanges(seqsnames=16, IRanges(30768000, 30770000), strand="+")
autoplot(ensdb, GRangesFilter(gr, "overlapping"), names.expr="gene_name")

## Just submitting the GRanges object also works.
autoplot(ensdb, gr, names.expr="gene_name")

## Or genes encoded on both strands.
gr <- GRanges(seqsnames=16, IRanges(30768000, 30770000), strand="*")
autoplot(ensdb, GRangesFilter(gr, "overlapping"), names.expr="gene_name")

## Also, we can specify directly the gene ids and plot all transcripts of these
## genes (not only those overlapping with the region)
autoplot(ensdb, GeneidFilter(c("ENSG00000196118", "ENSG00000156873")))

library(GenomicAlignments)
data("genesymbol", package = "biovizBase")
bamfile <- system.file("extdata", "SRR027894subRBM17.bam", package="biovizBase")
which <- keepStandardChromosomes(genesymbol["RBM17"])

param = ScanBamParam(which = which), use.names = TRUE)

ga <- readGAlignments(bamfile, param = ScanBamParam(which = which), use.names = TRUE)
```r
# code chunk number 29: ga-exp
pl <- autoplot(ga)
pl2 <- autoplot(ga, geom = "rect")
pl3 <- autoplot(ga, geom = "line", stat = "coverage")
tracks(default = pl, rect = pl2, coverage = pl3)
```

```r
# code chunk number 30: bf-load (eval = FALSE)
library(Rsamtools)
bamfile <- "./wgEncodeCaltechRnaSeqK562R1x75dAlignsRep1V2.bam"
bf <- BamFile(bamfile)
```

```r
# code chunk number 31: bf-est-cov (eval = FALSE)
data(genesymbol, package = "biovizBase")
bf <- BamFile(bamfile)
autoplot(bf, which = c("chr1", "chr2"))

library(BSgenome.Hsapiens.UCSC.hg19)
autoplot(bf, stat = "mismatch", which = genesymbol["ALDOA"], bsgenome = Hsapiens)
```

```r
# code chunk number 32: char-bam (eval = FALSE)
bamfile <- "./wgEncodeCaltechRnaSeqK562R1x75dAlignsRep1V2.bam"
autoplot(bamfile)
```

```r
# code chunk number 33: char-gr
library(rtracklayer)
test_path <- system.file("tests", package = "rtracklayer")
test_bed <- file.path(test_path, "test.bed")
autoplot(test_bed, aes(fill = name))
```

```r
# matrix
volcano <- volcano[20:70, 20:60] - 150
autoplot(volcano)
autoplot(volcano, xlab = "xlab", main = "main", ylab = "ylab")
```
autoplot(volcano, geom = "raster")+scale_fill_fold_change()

## when a matrix has colnames and rownames label them by default
colnames(volcano) <- sort(sample(1:300, size = ncol(volcano), replace = FALSE))
autoplot(volcano)+scale_fill_fold_change()

rownames(volcano) <- letters[sample(1:24, size = nrow(volcano), replace = TRUE)]
autoplot(volcano)

## even with row/col names, you could also disable it and just use numeric index
autoplot(volcano, colnames.label = FALSE)
autoplot(volcano, rownames.label = FALSE, colnames.label = FALSE)

## don’t want the axis has label??
autoplot(volcano, axis.text.x = FALSE)
autoplot(volcano, axis.text.y = FALSE)

# or totally remove axis
colnames(volcano) <- lapply(letters[sample(1:24, size = ncol(volcano), replace = TRUE)],
  function(x){
    paste(rep(x, 7), collapse = "")
  })

## Oops, overlapped
autoplot(volcano)

## tweak with it.
autoplot(volcano, axis.text.angle = -45, hjust = 0)

## when character is the value
x <- sample(c(letters[1:3], NA), size = 100, replace = TRUE)
mx <- matrix(x, nrow = 5)
autoplot(mx)

## tile gives you a white margin
rownames(mx) <- LETTERS[1:5]
autoplot(mx, color = "white")
colnames(mx) <- LETTERS[1:20]
autoplot(mx, color = "white")
autoplot(mx, color = "white", size = 2)

## weird in aes(), though works
## default tile is flexible
autoplot(mx, aes(width = 0.6, height = 0.6))
autoplot(mx, aes(width = 0.6, height = 0.6), na.value = "white")
autoplot(mx, aes(width = 0.6, height = 0.6)) + theme_clear()

###################################################
### Views
###################################################

lambda <- c(rep(0.001, 4500), seq(0.001, 10, length = 500),
  seq(10, 0.001, length = 500))
xVector <- dnorm(1:5e3, mean = 1e3, sd = 200)
xRle <- Rle(xVector)
v1 <- Views(xRle, start = sample(.4e3:.6e3, size = 50, replace = FALSE), width =1000)
autoplot(v1)

names(v1) <- letters[sample(1:24, size = length(v1), replace = TRUE)]
autoplot(v1)
autoplot(v1, geom = "tile", aes(width = 0.5, height = 0.5))
autoplot(v1, geom = "line")
autoplot(v1, geom = "line", aes(color = row)) + theme(legend.position = "none")
autoplot(v1, geom = "line", facets = NULL)
autoplot(v1, geom = "line", facets = NULL, alpha = 0.1)

########################################################################
### ExpressionSet
########################################################################
library(Biobase)
data(sample.ExpressionSet)
sample.ExpressionSet
set.seed(1)
## select 50 features
idx <- sample(seq_len(dim(sample.ExpressionSet)[1]), size = 50)
eset <- sample.ExpressionSet[idx,]
eset
autoplot(as.matrix(pData(eset)))

## default heatmap
p1 <- autoplot(eset)
p2 <- p1 + scale_fill_fold_change()
p2
autoplot(eset, geom = "tile", color = "white", size = 2)
autoplot(eset, geom = "tile", aes(width = 0.6, height = 0.6))

autoplot(eset, pheno.plot = TRUE)
idx <- order(pData(eset)[,1])
eset2 <- eset[,idx]
autoplot(eset2, pheno.plot = TRUE)

## parallel coordainte plot
autoplot(eset, type = "pcp")

## boxplot
autoplot(eset, type = "boxplot")

## scatterplot.matrix
## slow, be carefull
## autoplot(eset[, 1:7], type = "scatterplot.matrix")

## mean-sd
autoplot(eset, type = "mean-sd")

########################################################################
### RangedSummarizedExperiment
########################################################################
library(SummarizedExperiment)
nrows <- 200; ncols <- 6
counts <- matrix(runif(nrows * ncols, 1, 1e4), nrows)
counts2 <- matrix(runif(nrows * ncols, 1, 1e4), nrows)
rowRanges <- GRanges(rep(c("chr1", "chr2"), c(50, 150)),
                   IRanges(floor(runif(200, 1e5, 1e6)), width=100),
                   strand=sample(c("+", "-"), 200, TRUE))
colData <- DataFrame(Treatment=rep(c("ChIP", "Input"), 3),
                      row.names=LETTERS[1:6])
sset <- SummarizedExperiment(assays=SimpleList(counts=counts,
                                          counts2 = counts2),
                          rowRanges=rowRanges, colData=colData)
autoplot(sset) + scale_fill_fold_change()
autoplot(sset, pheno.plot = TRUE)

###############################################################
### pcp
###############################################################
autoplot(sset, type = "pcp")

###############################################################
### boxplot
###############################################################
autoplot(sset, type = "boxplot")

###############################################################
### scatterplot matrix
###############################################################
autoplot(sset, type = "scatterplot.matrix")

###############################################################
### vcf
###############################################################
# Not run:
library(VariantAnnotation)
vccfile <- system.file("extdata", "chr22.vcf.gz", package="VariantAnnotation")
vcf <- readVcf(vccfile, "hg19")
## default use type 'geno'
## default use genome position
autoplot(vcf)
## or disable it
autoplot(vcf, genome.axis = FALSE)
## not transpose
autoplot(vcf, genome.axis = FALSE, transpose = FALSE, rownames.label = FALSE)
autoplot(vcf)
## use
autoplot(vcf, assay.id = "DS")
## equivalent to
autoplot(vcf, assay.id = 2)
## doesn't work when assay.id cannot find
autoplot(vcf, assay.id = "NO")
## use AF or first
autoplot(vcf, type = "info")
## geom bar
autoplot(vcf, type = "info", aes(y = THETA))
autoplot(vcf, type = "info", aes(y = THETA, fill = VT, color = VT))
geom_alignment

Alignment geoms for GRanges object

Description

Show interval data as alignment.

Usage

```r
# S4 method for signature 'GRanges'
geom_alignment(data, ..., xlab, ylab, main, facets = NULL, stat = c("stepping", "identity"), range.geom = c("rect", "arrowrect"), gap.geom = c("chevron", "arrow", "segment"), rect.height = NULL, group.selfish = TRUE, label = TRUE)

# S4 method for signature 'TxDbOREnsDb'
geom_alignment(data, ..., which, columns = c("tx_id", "tx_name", "gene_id"), names.expr = "tx_name", facets = NULL, truncate.gaps = FALSE, truncate.fun = NULL, ratio = 0.0025)
```
geom_alignment

## S4 method for signature 'GRangesList'
geom_alignment(data, ..., which = NULL,
               cds.rect.h = 0.25,
               exon.rect.h = cds.rect.h,
               utr.rect.h = cds.rect.h/2,
               xlab, ylab, main,
               facets = NULL, geom = "alignment",
               stat = c("identity", "reduce"),
               range.geom = "rect",
               gap.geom = "arrow",
               utr.geom = "rect",
               names.expr = NULL,
               label = TRUE,
               label.color = "gray40",
               arrow.rate = 0.015,
               length = unit(0.1, "cm"))

## S4 method for signature 'OrganismDb'
geom_alignment(data, ..., which,
               columns = c("TXNAME", "SYMBOL", "TXID", "GENEID"),
               names.expr = "SYMBOL",
               facets = NULL,
               truncate.gaps = FALSE,
               truncate.fun = NULL, ratio = 0.0025)

Arguments

data A GRanges, data.frame, TxDb or EnsDb object.
... Extra parameters such as aes() passed.
which GRanges object to subset the TxDb or EnsDb object. For EnsDb: can also be a single, or a list of, filter object(s) extending BasicFilter-class.
cds.rect.h cds heights.
exon.rect.h exon heights.
utr.rect.h utr heights.
label.color label color.
arrow.rate arrow rate.
length arrow length.
columns columns to get from object.
xlab Label for x
ylab Label for y
main Title for plot.
facets Faceting formula to use.
stat For GRanges: Character vector specifying statistics to use. "stepping" with randomly assigned stepping levels as y varialbe. "identity" allow users to specify y value in aes.
For TxDb: defualt "identity" give full gene model and "reduce" for reduced model.
geom_alignment

gap.geom Geom for 'gap’ computed from the data you passed based on the group information.
rect.height Half height of the arrow body.
group.selfish Passed to addStepping, control whether to show each group as unique level or not. If set to FALSE, if two groups are not overlapped with each other, they will probably be layout in the same level to save space.
truncate.gaps logical value indicate to truncate gaps or not.
truncate.fun shrinkage function. Please see shrinkagefun in package biovizBase.
ratio used in maxGap.
geom geometric object. only support "gene" now.
range.geom geom for main intervals or exons.
utr.geom geom for utr region.
names.expr expression for showing y label.
label logical value. Whether to label the intervals with names specified by argument names.expr.

Value
A 'Layer'.

Author(s)
Tengfei Yin

Examples

```r
set.seed(1)
N <- 100
require(GenomicRanges)
## ======================================================================
## simmulated GRanges
## ======================================================================
gr <- GRanges(seqnames =
sample(c("chr1", "chr2", "chr3"),
    size = N, replace = TRUE),
IRanges(  start = sample(1:300, size = N, replace = TRUE),
    width = sample(70:75, size = N,replace = TRUE)),
strand = sample(c("+", "-", "*"), size = N,
    replace = TRUE),
value = rnorm(N, 10, 3), score = rnorm(N, 100, 30),
sample = sample(c("Normal", "Tumor"),
    size = N, replace = TRUE),
pair = sample(letters, size = N,
    replace = TRUE))
## ======================================================================
## default
## ======================================================================
ggplot(gr) + geom Alignment()
## or
```

ggplot() + geom_alignment(gr)

### facetting and aesthetics
### geomarch
ggplot(gr) + geom_alignment(facets = sample ~ seqnames, aes(color = strand, fill = strand))

### stat:stepping
### geomarch
ggplot(gr) + geom_alignment(stat = "stepping", aes(group = pair))

### group.selfish controls when
### geomarch
ggplot(gr) + geom_alignment(stat = "stepping", aes(group = pair), group.selfish = FALSE)

### main/gap geom
### geomarch
ggplot(gr) + geom_alignment(range.geom = "arrowrect", gap.geom = "chevron")

### For TxDb
### geomarch
library(TxDb.Hsapiens.UCSC.hg19.knownGene)
data(genesymbol, package = "biovizBase")
txdb <- TxDb.Hsapiens.UCSC.hg19.knownGene
## made a track comparing full/reduce stat.
ggbio() + geom_alignment(data = txdb, which = genesymbol["RBM17"])
p1 <- ggplot(txdb) + geom_alignment(which = genesymbol["RBM17"])
p1
p2 <- ggplot(txdb) + geom_alignment(which = genesymbol["RBM17"], stat = "reduce")
tracks(full = p1, reduce = p2, heights = c(3, 1))
tracks(full = p1, reduce = p2, heights = c(3, 1)) + theme_tracks_sunset()
tracks(full = p1, reduce = p2, heights = c(3, 1)) +
  theme_tracks_sunset(axis.line.color = NA)

### change y labels
### geomarch
ggplot(txdb) + geom_alignment(which = genesymbol["RBM17"], names.expr = "tx_id:::gene_id")

---

**geom_arch**

*Arch geoms for GRanges object*

**Description**

Show interval data as arches.

**Usage**

## S4 method for signature 'data.frame'
geom_arch(data, ..., n = 25, max.height = 10)
## geom_arch

### S4 method for signature 'GRanges'

```r
geom_arch(data, ..., xlab, ylab, main, facets = NULL,
          rect.height = 0, n = 25, max.height = 10)
```

### Arguments

- **data**: A GRanges or data.frame object.
- **...**: Extra parameters passed to autoplot function, aes mapping support height, x, xend.
  - `xstart` of the arches
  - `xend` end of the arches
  - `height` height of arches
- **xlab**: Label for x
- **ylab**: Label for y
- **main**: Title for plot.
- **n**: Integer values at which interpolation takes place to create 'n' equally spaced points spanning the interval ['min(x)', 'max(x)'].
- **facets**: Faceting formula to use.
- **rect.height**: When data is GRanges, this padding the arches from original y value to allow users putting arches 'around' the interval rectangles.
- **max.height**: Max height of all arches.

### Details

To draw a interval data as arches, we need to provide a special geom for this purpose. Arches is popular in gene viewer or genomoe browser, when they try to show isoforms or gene model. `geom_arch`, just like any other geom_* function in ggplot2, you can pass aes() to it to map variable to height of arches.

### Value

A 'Layer'.

### Author(s)

Tengfei Yin

### Examples

```r
set.seed(1)
N <- 100
library(GenomicRanges)

## Simulated GRanges
gr <- GRanges(seqnames = sample(c("chr1", "chr2", "chr3"),
                               size = N, replace = TRUE),
              IRanges(
                     start = sample(1:300, size = N, replace = TRUE),
                     width = sample(70:75, size = N, replace = TRUE)),
```

```r
```
geom_arrow

comedate

strand = sample(c("+", "-", "x"), size = N, replace = TRUE),
value = rnorm(N, 10, 3), score = rnorm(N, 100, 30),
sample = sample(c("Normal", "Tumor"), size = N, replace = TRUE),
pair = sample(letters, size = N, replace = TRUE))

## default
## ---------------------------------------------

ggplot(gr) + geom_arch()
# or
ggplot() + geom_arch(gr)

## facetting and aesthetics
## ---------------------------------------------

ggplot(gr) + geom_arch(aes(color = value, height = value, size = value),
alpha = 0.2, facets = sample ~ seqnames)

describe

Description

Show interval data as arrows.

Usage

## S4 method for signature 'GRanges'
geom_arrow(data, ..., xlab, ylab, main,
angle = 30, length = unit(0.12, "cm"), type = "open",
stat = c("stepping", "identity"), facets = NULL,
arrow.rate = 0.03, group.selfish = TRUE)

Arguments

data A GRanges object.
...
Extra parameters such as aes() passed.
xlab Label for x
ylab Label for y
main Title for plot.
angle The angle of the arrow head in degrees (smaller numbers produce narrower,
pointier arrows). Essentially describes the width of the arrow head.
length A unit specifying the length of the arrow head (from tip to base).
type One of "open" or "closed" indicating whether the arrow head should be a closed
triangle.
**geom_arrow**

**stat**  Character vector specifying statistics to use. "stepping" with randomly assigned stepping levels as y variable. "identity" allow users to specify y value in aes.

**facets**  Faceting formula to use.

**arrow.rate**  Arrow density of the arrow body.

**group.selfish**  Passed to addStepping, control whether to show each group as unique level or not. If set to FALSE, if two groups are not overlapped with each other, they will probably be layout in the same level to save space.

**Value**

A 'Layer'.

**Author(s)**

Tengfei Yin

**Examples**

```r
set.seed(1)
N <- 100
require(GenomicRanges)

## simmulated GRanges
gr <- GRanges(seqnames = sample(c("chr1", "chr2", "chr3"), size = N, replace = TRUE),
             IRanges(start = sample(1:300, size = N, replace = TRUE),
                     width = sample(70:75, size = N, replace = TRUE),
                     strand = sample(c("+", "-", "*"), size = N,replace = TRUE),
                     value = rnorm(N, 10, 3), score = rnorm(N, 100, 30),
                     sample = sample(c("Normal", "Tumor"),
                                     size = N, replace = TRUE),
                     pair = sample(letters, size = N, replace = TRUE))

## default
ggplot(gr) + geom_arrow()

## facetting and aesthetics
ggplot(gr) + geom_arrow(facets = sample ~ seqnames, aes(color = strand, fill = strand))
```

```r
## stat:identity
ggplot(gr) + geom_arrow(stat = "identity", aes(y = value))
```
## stat:stepping

ggplot(gr) + geom_arrow(stat = "stepping", aes(y = value, group = pair))

## group:selfish

ggplot(gr) + geom_arrow(stat = "stepping", aes(y = value, group = pair), group.selfish = FALSE)

## other options to control arrow angle, density, ...

library(grid)
ggplot(gr) + geom_arrow(stat = "stepping", aes(y = value, group = pair),
  arrow.rate = 0.01, length = unit(0.3, "cm"), angle = 45,
  group.selfish = FALSE)

---

**geom_arrowrect**  
*Arrowrect geoms for GRanges object*

### Description

Show interval data as rectangle with a arrow head.

### Usage

```r
## S4 method for signature 'GRanges'
geom_arrowrect(data, ..., xlab, ylab, main,
  facets = NULL, stat = c("stepping", "identity"),
  rect.height = NULL, arrow.head = 0.06,
  arrow.head.rate = arrow.head, arrow.head.fix = NULL,
  group.selfish = TRUE)
```

### Arguments

- **data**: A GRanges object.
- **...**: Extra parameters such as aes() passed.
- **xlab**: Label for x
- **ylab**: Label for y
- **main**: Title for plot.
- **facets**: Faceting formula to use.
- **stat**: Character vector specifying statistics to use. "stepping" with randomly assigned stepping levels as y variable. "identity" allow users to specify y value in aes.
- **rect.height**: Half height of the arrow body.
**geom_arrowrect**

arrow.head Arrow head to body ratio.
arrow.head.rate Arrow head to body ratio. same with arrow.head.
arrow.head.fix fixed length of arrow head.
group.selfish Passed to addStepping, control whether to show each group as unique level or not. If set to FALSE, if two groups are not overlapped with each other, they will probably be layout in the same level to save space.

**Value**

A 'Layer'.

**Author(s)**

Tengfei Yin

**Examples**

```r
set.seed(1)
N <- 100
require(GenomicRanges)
## ======================================================================
## simmulated GRanges
## ======================================================================
gr <- GRanges(seqnames = sample(c("chr1", "chr2", "chr3"),
   size = N, replace = TRUE),
IRanges(
   start = sample(1:300, size = N, replace = TRUE),
   width = sample(70:75, size = N,replace = TRUE)),
strand = sample(c("+", "-", "*"), size = N,
   replace = TRUE),
value = rnorm(N, 10, 3), score = rnorm(N, 100, 30),
sample = sample(c("Normal", "Tumor"),
   size = N, replace = TRUE),
pair = sample(letters, size = N,
   replace = TRUE))

## ======================================================================
## default
## ======================================================================
ggplot(gr) + geom_arrowrect()
## or
ggplot() + geom_arrowrect(gr)

## ======================================================================
## facetting and aesthetics
## ======================================================================
ggplot(gr) + geom_arrowrect(facets = sample ~ seqnames, aes(color = strand, fill = strand))

## ======================================================================
## stat:identity
## ======================================================================
ggplot(gr) + geom_arrowrect(stat = "identity", aes(y = value))
```
## geom_bar

### Example

```r
ggplot(gr) + geom_arrowrect(stat = "stepping", aes(y = value, group = pair))

ggplot(gr) + geom_arrowrect(gr, stat = "stepping", aes(y = value, group = pair), group.selfish = FALSE)
```

---

**geom_bar**  
Segment geoms for GRanges object

---

**Description**

Show interval data as vertical bar, width equals to interval width and use 'score' or specified 'y' as y scale.

**Usage**

```r
## S4 method for signature 'ANY'
geom_bar(data, ...)
## S4 method for signature 'GRanges'
geom_bar(data,..., xlab, ylab, main)
```

**Arguments**

- `data`  
  Typically a GRanges or data.frame object.
- `...`  
  Extra parameters such as aes() or color, size passed.
- `xlab`  
  Label for x
- `ylab`  
  Label for y
- `main`  
  Title for plot.

**Details**

Useful for showing bed like files, when imported as GRanges, have a extra 'score' column, use it as default y, you could also specify y by using aes(y = ).

**Value**

A 'Layer'.

Examples

```r
## load
library(GenomicRanges)

## simul
set.seed(123)
gr.b <- GRanges(seqnames = "chr1", IRanges(start = seq(1, 100, by = 10),
    width = sample(4:9, size = 10, replace = TRUE),
    score = rnorm(10, 10, 3), value = runif(10, 1, 100))
gr.b2 <- GRanges(seqnames = "chr2", IRanges(start = seq(1, 100, by = 10),
    width = sample(4:9, size = 10, replace = TRUE),
    score = rnorm(10, 10, 3), value = runif(10, 1, 100))
gr.b <- c(gr.b, gr.b2)
## default use score as y
## bar
ggplot(gr.b) + geom_bar(aes(fill = value))
## or
ggplot() + geom_bar(gr.b, aes(fill = value))
ggplot(gr.b) + geom_bar(aes(y = value))
## equal to
autoplot(gr.b, geom = "bar")
```

---

**geom_chevron**

Chevron geoms for GRanges object

Description

Break normal intervals stored in GRanges object and show them as chevron, useful for showing model or splice summary.

Usage

```r
## S4 method for signature 'GRanges'
geom_chevron(data, ..., xlab, ylab, main,
    offset = 0.1,
    facets = NULL,
    stat = c("stepping", "identity"),
    chevron.height.rescale = c(0.1, 0.8),
    group.selfish = TRUE)
```

Arguments

- `data` A GRanges object.
- `...` Extra parameters passed to autoplot function.
- `xlab` Label for x
- `ylab` Label for y
- `main` Title for plot.
offset A numeric value or characters. If it’s numeric value, indicate how much you want the chevron to wiggle, usually the rectangle for drawing GRanges is of height unit 1, so it’s better between -0.5 and 0.5 to make it nice looking. Unless you specify offset as one of those columns, this will use height of the chevron to indicate the columns. Of course you could use size of the chevron to indicate the column variable easily, please see the examples.

facets faceting formula to use.

stat character vector specifying statistics to use. ”stepping” with randomly assigned stepping levels as y varialbe. ”identity” allow users to specify y value in aes.

detailechevron.height.rescale A numeric vector of length 2. When the offset parameters is a character which is one of the data columns, this parameter rescale the offset.
group.selfish Passed to addStepping, control whether to show each group as unique level or not. If set to FALSE, if two groups are not overlapped with each other, they will probably be layout in the same level to save space.

Details

To draw a normal GRanges as Chevron, we need to provide a special geom for this purpose. Chevron is popular in gene viewer or genomoe browser, when they try to show isoforms or gene model.geom_chevron, just like any other geom_* function in ggplot2, you can pass aes() to it to use height of chevron or width of chevron to show statistics summary.

Value

A 'Layer'.

Author(s)

Tengfei Yin

Examples

set.seed(1)
N <- 100
require(GenomicRanges)

## simmulated GRanges

#simulated GRanges

gr <- GRanges(seqnames = sample(c("chr1", "chr2", "chr3"), size = N, replace = TRUE),
IRanges(
start = sample(1:300, size = N, replace = TRUE),
width = sample(70:75, size = N,replace = TRUE)),
strand = sample(c("+", "-", "x"), size = N,
replace = TRUE),
value = rnorm(N, 10, 3), score = rnorm(N, 100, 30),
sample = sample(c("Normal", "Tumor"),
size = N, replace = TRUE),
pair = sample(letters, size = N,
replace = TRUE))
# geom_chevron

---

### default
```
ggplot(gr) + geom_chevron()
```

### or
```
ggplot() + geom_chevron(gr)
```

### facetting and aesthetics
```
ggplot(gr) + geom_chevron(facets = sample ~ seqnames, aes(color = strand))
```

---

### stat:identity
```
ggplot(gr) + geom_chevron(stat = "identity", aes(y = value))
```

---

### stat:stepping
```
ggplot(gr) + geom_chevron(stat = "stepping", aes(group = pair))
```

---

### group.selfish controls when
```
ggplot(gr) + geom_chevron(stat = "stepping", aes(group = pair), group.selfish = FALSE, xlab = "xlab", ylab = "ylab", main = "main")
```

---

### offset
```
p <- qplot(x = mpg, y = cyl, data = mtcars)
```

---

```r
gr2 <- GRanges("chr1", IRanges(c(1, 10, 20), width = 5))
gr2.p <- gaps(gr2)
```

```r
gr2.p <- resize(gr2.p, fix = "center", width = width(gr2.p)+2)
note the rectangle height is 0.8
```

```r
offset = 0 just like a line
ggplot(gr2) + geom_rect() + geom_chevron(gr2.p, offset = 0)
```

---

```r
## equal height
```
```
ggplot(gr2) + geom_rect() + geom_chevron(gr2.p, offset = 0.4)
```
## chevron.height

```r
values(gr2.p)$score <- c(100, 200)

ggplot(gr2) + geom_rect() + geom_chevron(gr2.p, offset = "score")

ggplot(gr2) + geom_rect() + geom_chevron(gr2.p, offset = "score",
chevron.height.rescale = c(0.4, 10))
```

### Description

Show interval data as rectangle.

### Usage

```r
## S4 method for signature 'ANY'
geom_rect(data, ...)

## S4 method for signature 'GRanges'
geom_rect(data, ..., xlab, ylab, main,
  facets = NULL, stat = c("stepping", "identity"),
  rect.height = NULL,
  group.selfish = TRUE)
```

### Arguments

- **data**: Typically a GRanges or data.frame object. When it's data.frame, it's simply calling ggplot2::geom_rect.
- **...**: Extra parameters such as aes() or color, size passed.
- **xlab**: Label for x
- **ylab**: Label for y
- **main**: Title for plot.
- **facets**: Faceting formula to use.
- **stat**: Character vector specifying statistics to use. "stepping" with randomly assigned stepping levels as y variable. "identity" allow users to specify y value in aes.
- **rect.height**: Half height of the arrow body.
- **group.selfish**: Passed to addStepping, control whether to show each group as unique level or not. If set to FALSE, if two groups are not overlapped with each other, they will probably be layout in the same level to save space.

### Value

A 'Layer'.

### Author(s)

Tengfei Yin
Examples

```r
set.seed(1)
N <- 100
require(GenomicRanges)

# simmulated GRanges
gr <- GRanges(seqnames = sample(c("chr1", "chr2", "chr3"), size = N, replace = TRUE),
             IRanges(start = sample(1:300, size = N, replace = TRUE),
                     width = sample(70:75, size = N, replace = TRUE),
                     strand = sample(c("+", "-", "*"), size = N, replace = TRUE),
                     value = rnorm(N, 10, 3), score = rnorm(N, 100, 30),
                     sample = sample(c("Normal", "Tumor"), size = N, replace = TRUE),
                     pair = sample(letters, size = N, replace = TRUE))
```

```r
ggplot() + geom_rect(data = mtcars, aes(xmin = mpg, ymin = wt, xmax = mpg + 10, ymax = wt + 0.2, fill = cyl))
```

```r
ggplot(gr) + geom_rect()
# or
ggplot() + geom_rect(gr)
```

```r
ggplot(gr) + geom_rect(facets = sample ~ seqnames, aes(color = strand, fill = strand))
```

```r
ggplot(gr) + geom_rect(stat = "identity", aes(y = value))
```

```r
ggplot(gr) + geom_rect(stat = "stepping", aes(y = value, group = pair))
```
# geom_segment

## ----------------------------------
## group.selfish controls when
## ----------------------------------

ggplot(gr) + geom_rect(stat = "stepping", aes(y = value, group = pair), group.selfish = FALSE)

---

**geom_segment**

Segment geoms for GRanges object

### Description

Show interval data as segments.

### Usage

```r
## S4 method for signature 'ANY'
geom_segment(data, ...)

## S4 method for signature 'GRanges'
geom_segment(data, ..., xlab, ylab, main,
  facets = NULL, stat = c("stepping", "identity"),
  group.selfish = TRUE)
```

### Arguments

- `data` A GRanges or data.frame object.
- `...` Extra parameters such as aes() or color, size passed.
- `xlab` Label for x
- `ylab` Label for y
- `main` Title for plot.
- `facets` Faceting formula to use.
- `stat` Character vector specifying statistics to use. "stepping" with randomly assigned stepping levels as y varialbe. "identity" allow users to specify y value in aes.
- `group.selfish` Passed to addStepping, control whether to show each group as unique level or not. If set to FALSE, if two groups are not overlapped with each other, they will probably be layout in the same level to save space.

### Value

A 'Layer'.

### Author(s)

Tengfei Yin
Examples

```r
set.seed(1)
N <- 100
require(GenomicRanges)

## simmulated GRanges
gr <- GRanges(seqnames = sample(c("chr1", "chr2", "chr3"),
                               size = N, replace = TRUE),
              IRanges(
                     start = sample(1:300, size = N, replace = TRUE),
                     width = sample(70:75, size = N, replace = TRUE),
                     strand = sample(c("+", "-", "*"), size = N,
                                     replace = TRUE),
                     value = rnorm(N, 10, 3),
                     score = rnorm(N, 100, 30),
                     sample = sample(c("Normal", "Tumor"),
                                     size = N, replace = TRUE),
                     pair = sample(letters, size = N,
                                   replace = TRUE))

## data.frame call ggplot2::geom_segment
ggplot() + geom_segment(data = mtcars, aes(x = mpg, y = wt, xend = mpg + 10, yend = wt + 0.2,
                                           fill = cyl))

## default

## facetting and aesthetics
ggplot(gr) + geom_segment(facets = sample ~ seqnames, aes(color = strand, fill = strand))

## stat:identity
ggplot(gr) + geom_segment(stat = "identity", aes(y = value))

## stat:stepping
```
ggplot(gr) + geom_segment(stat = "stepping", aes(y = value, group = pair))

## ======================================================================
## group.selfish controls when
## ======================================================================

ggplot(gr) + geom_segment(stat = "stepping", aes(y = value, group = pair), group.selfish = FALSE)

---

**GGbio**

*a sub class of ggplot and gg class defined in ggplot2 package, used for ggbio specific methods.*

**Usage**

\[
\text{GGbio}(\text{ggplot} = \text{NULL}, \text{data} = \text{NULL}, \text{fetchable} = \text{FALSE}, \text{blank} = \text{FALSE}, \ldots)
\]

**Arguments**

- **ggplot**
  - A ggplot or gg object.
- **data**
  - Raw data.
- **fetchable**
  - Logical value, default FALSE, is there any fetch method available.
- **blank**
  - Logical value, default FALSE, is this plot a blank plot.
- **...**
  - More properties passed to class like Cache.

**Details**

This class is defined to facilitate the ggbio-specific visualization method, especially when using \text{ggplot} to construct ggbio supported object, that will return a ggbio class. And internals tricks will help a lazy evaluation for following + method.

**Value**

- A ggbio object.

**Author(s)**

Tengfei Yin

**See Also**

- \text{ggplot}

**Examples**

\[
p1 \leftarrow \text{qplot}()
g1 \leftarrow \text{ggbio}(p1)
\text{class}(g1)
\]
ggplot methods

Description

These methods extend ggplot to support several types of Bioconductor objects, as well as some base types like matrix. They return a ggbio object, which stores the original data object. Please check the corresponding method for mold to see how an object is coerced into a data.frame.

Usage

```r
## S3 method for class 'Vector'
ggplot(data, mapping = aes(), ..., 
       environment = parent.frame())

## S3 method for class 'Seqinfo'
ggplot(data, mapping = aes(), ..., 
       environment = parent.frame())

## S3 method for class 'ExpressionSet'
ggplot(data, mapping = aes(), ..., 
       environment = parent.frame())

## S3 method for class 'RsamtoolsFile'
ggplot(data, mapping = aes(), ..., 
       environment = parent.frame())

## S3 method for class 'TxDbOREnsDb'
ggplot(data, mapping = aes(), ..., 
       environment = parent.frame())

## S3 method for class 'BSgenome'
ggplot(data, mapping = aes(), ..., 
       environment = parent.frame())

## S3 method for class 'matrix'
ggplot(data, mapping = aes(), ..., 
       environment = parent.frame())

## S3 method for class 'character'
ggplot(data, mapping = aes(), ..., 
       environment = parent.frame())

## S3 method for class 'SummarizedExperiment'
ggplot(data, mapping = aes(), 
       assay.id = 1L, ..., environment = parent.frame())

## S3 method for class 'GAlignments'
ggplot(data, mapping = aes(), ..., 
       environment = parent.frame())

## S3 method for class 'VCF'
ggplot(data, mapping = aes(), ..., 
       environment = parent.frame())
```

Arguments

data          original data object.
mapping       the aesthetic mapping.
...            other arguments passed to specific methods.
environment  fall-back environment for evaluation of aesthetic symbols
assay.id     index of assay you are using when multiple assays exist.

Details

The biggest difference for objects returned by `ggplot` in ggbio from ggplot2, is we always keep
the original data copy, this is useful because in ggbio, our starting point is not always data.frame,
many special statistical transformation is computed upon original data objects instead of coerced
data.frame. This is a hack to follow ggplot2's API while allow our own defined components to trace
back to original data copy and do the transformation. For objects supported by mold we transform
them to data.frame stored along the original data set, for objects which not supported by mold
method, we only store the original copy for ggbio specific graphics.

`ggplot()` is typically used to construct a plot incrementally, using the `+` operator to add layers to the
existing `ggplot` object. This is advantageous in that the code is explicit about which layers are added
and the order in which they are added. For complex graphics with multiple layers, initialization with
`ggplot` is recommended. You can always call `qplot` in package ggplot2 or `autoplot` in ggbio for
convenient usage.

There are three common ways to invoke `ggplot`:

- `ggplot(df, aes(x, y, <other aesthetics>))`
- `ggplot(df)`
- `ggplot()`

The first method is recommended if all layers use the same data and the same set of aesthetics,
although this method can also be used to add a layer using data from another data frame. The
second method specifies the default data frame to use for the plot, but no aesthetics are defined
up front. This is useful when one data frame is used predominantly as layers are added, but the
aesthetics may vary from one layer to another. The third method initializes a skeleton `ggplot`
object which is fleshed out as layers are added. This method is useful when multiple data frames
are used to produce different layers, as is often the case in complex graphics.

The examples below illustrate how these methods of invoking `ggplot` can be used in constructing
a graphic.

Value

a return ggbio object, which is a subclass of `ggplot` defined in ggplot2 package, but that’s more, a
`.data` list entry is stored with the returned object.

Author(s)

Tengfei Yin

See Also

mold, ggbio

Examples

```r
set.seed(1)
N <- 100
library(GenomicRanges)
## GRanges
gr <- GRanges(seqnames =
```
sample(c("chr1", "chr2", "chr3"),
    size = N, replace = TRUE),
IRanges(
    start = sample(1:300, size = N, replace = TRUE),
    width = sample(70:75, size = N, replace = TRUE),
    strand = sample(c("+", "-", "*"), size = N, replace = TRUE),
    value = rnorm(N, 10, 3),
    score = rnorm(N, 100, 30),
    sample = sample(c("Normal", "Tumor"), size = N, replace = TRUE),
    pair = sample(letters, size = N, replace = TRUE))

## automatically facetting and assign y
## this must mean geom_rect support GRanges object
ggplot(gr) + geom_rect()

## use pure ggplot2's geom_rect, no auto facet
ggplot(gr) + ggplot2::geom_rect(aes(xmin = start, ymin = score,
    xmax = end, ymax = score + 1))

### GRangesList
grl <- split(gr, values(gr)$pair)

### IRanges
ir <- ranges(gr)

### Seqinfo
seqlengths(gr) <- c(400, 500, 420)

### matrix
mx <- matrix(1:12, nrow = 3)

### Views
## ExpressionSet

```r
library(Biobase)
data(sample.ExpressionSet)
sample.ExpressionSet
set.seed(1)
## select 50 features
idx <- sample(seq_len(dim(sample.ExpressionSet)[1]), size = 50)
eset <- sample.ExpressionSet[idx,]

ggplot(eset) + geom_tile(aes(x = x, y = y, fill = value))
```

## please check autoplot, matrix method which gives you more control

```r
ggplot(eset) + geom_tile(aes(x = x, y = y, fill = sex))
ggplot(eset) + geom_tile(aes(x = x, y = y, fill = type))
```

## Rle

```r
library(IRanges)
lambda <- c(rep(0.001, 4500), seq(0.001, 10, length = 500),
            seq(10, 0.001, length = 500))
xVector <- rpois(1e4, lambda)
xRle <- Rle(xVector)
ggplot(xRle) + geom_tile(aes(x = x, y = y, fill = value))
```

## RleList

```r
xRleList <- RleList(xRle, 2L * xRle)
xRleList

```r
ggplot(xRleList) + geom_tile(aes(x = x, y = y, fill = value)) +
facet_grid(group~.)
```

```r
names(xRleList) <- c("a", "b")
ggplot(xRleList) + geom_tile(aes(x = x, y = y, fill = value)) +
facet_grid(group~.)
```

## RangedSummarizedExperiment

```r
library(SummarizedExperiment)
nrows <- 200; ncols <- 6
counts <- matrix(runif(nrows * ncols, 1, 1e4), nrows)
counts2 <- matrix(runif(nrows * ncols, 1, 1e4), nrows)
rowRanges <- GRanges(rep(c("chr1", "chr2"), c(50, 150)),
                      IRanges(floor(runif(200, 1e5, 1e6)), width=100),
                      strand=sample(c("+", "-"), 200, TRUE))
colData <- DataFrame(Treatment=rep(c("ChIP", "Input"), 3),
                      row.names=LETTERS[1:6])
sset <- SummarizedExperiment(assays=SimpleList(counts=counts,
counts2 = counts2),
rowRanges=rowRanges, colData=colData)
ggplot(sset) + geom_raster(aes(x = x, y = y, fill = value))
```
ggsave

Save a ggplot object or tracks with sensible defaults

Description

ggsave is a convenient function for saving a plot. It defaults to saving the last plot that you displayed, and for a default size uses the size of the current graphics device. It also guesses the type of graphics device from the extension. This means the only argument you need to supply is the filename.

Usage

ggsave(filename, plot = last_plot(),
device = default_device(filename), path = NULL,
scale = 1, width = par("din")[1],
height = par("din")[2], units = c("in", "cm", "mm"),
dpi = 300, limitsize = TRUE, ...)

Arguments

filename  file name/filename of plot
plot  plot to save, defaults to last plot displayed
device  device to use, automatically extract from file name extension
path  path to save plot to (if you just want to set path and not filename)
scale  scaling factor
width  width (defaults to the width of current plotting window)
height  height (defaults to the height of current plotting window)
units  units for width and height when either one is explicitly specified (in, cm, or mm)
dpi  dpi to use for raster graphics
limitsize  when TRUE (the default), ggsave will not save images larger than 50x50 inches, to prevent the common error of specifying dimensions in pixels.
...  other arguments passed to graphics device

Details

ggsave currently recognises the extensions eps/ps, tex (pictex), pdf, jpeg, tiff, png, bmp, svg and wmf (windows only).
Description

'Grob' class is a container for 'grob' based object defined with grid system. Generic function `Grob` gets grob object supported by grid system, and make an instance of subclass of class 'Grob'.

'GrobList' is a container of list of 'Grob' object.

Usage

```r
## S4 method for signature 'gg'
Grob(x)
## S4 method for signature 'gtable'
Grob(x)
## S4 method for signature 'trellis'
Grob(x)
## S4 method for signature 'lattice'
Grob(x)
## S4 method for signature 'GGbio'
Grob(x)
```

Arguments

- `x` object of class: gg, gtable, trellis, lattice, GGbio.

Value

A Grob object.

Author(s)

Tengfei Yin

Ideogram

Plot single chromosome with cytoband

Description

Plot single chromosome with cytoband.

Usage

```r
plotIdeogram(obj, subchr = NULL, zoom.region = NULL, which = NULL, xlab, ylab, main, xlabel = FALSE, color = "red", fill = "red", alpha = 0.7, zoom.offset = 0.2, size = 1, cytoband = TRUE, aspect.ratio = 1/20, genome)
```
Ideogram

## constructor

Ideogram(obj, subchr = NULL, which = NULL, xlabel = FALSE, cytoband = TRUE, color = "red", fill = "red", alpha = 0.7, zoom.region = NULL, zoom.offset = 0.2, size = 1, aspect.ratio = 1/20, ..., genome)

### Arguments

- **obj** A GenomicRanges object, which include extra information about cytoband, check biovizBase::isIdeogram.
- **subchr** A single character of chromosome names to show.
- **which** GRanges object to subset and highlight the ideogram.
- **zoom.region** A numeric vector of length 2 indicating zoomed region.
- **xlab** Label for x
- **ylab** Label for y
- **main** Title for plot.
- **xlabel** A logical value. Show the x label or not.
- **color** color for highlight region.
- **fill** fill color for highlight region.
- **alpha** alpha for highlight regio.
- **zoom.offset** zoomed highlights region offset around chromosome plotting region.
- **size** size for zoomed region rectangle boundary.
- **cytoband** If FALSE, plot just blank chromosome without cytoband. default is TRUE. es
- **aspect.ratio** aspect ratio for the chromosome ideogram plot, default is NULL.
- **genome** genome character passed to getIdeogram
- ... passed to ggbio constructor.

### Details

User could provide the whole ideogram and use subchr to point to particular chromosome.

### Value

A ggplot object.

### Author(s)

Tengfei Yin

### Examples

```
## Not run:
library(biovizBase)
p.ideo <- Ideogram(genome = "hg19")
p.ideo
library(GenomicRanges)
p.ideo + xlim(GRanges("chr2", IRanges(1e8, 1e8+10000)))
Ideogram(genome = "hg19", xlabel = TRUE)
## End(Not run)
```
Create a circle layout.

Usage

## S4 method for signature 'GRanges'
layout_circle(data, ..., geom = c("point", "line", "link", "ribbon", "rect", "bar", "segment", "hist", "scale", "heatmap", "ideogram", "text"), linked.to, radius = 10, trackWidth = 5, space.skip = 0.015, direction = c("clockwise", "anticlockwise"), link.fun = function(x, y, n = 30) bezier(x, y, evaluation = n), rect.inter.n = 60, rank, ylim = NULL, scale.n = 60, scale.unit = NULL, scale.type = c("M", "B", "sci"), grid.n = 5, grid.background = "gray70", grid.line = "white", grid = FALSE, chr.weight = NULL)

## S4 method for signature 'missing'
layout_circle(data, ...) circle(...)

Arguments

data          A GRanges object.
...
geom          The geometric object to use display the data.
linked.to     Character indicates column that specifying end of the linking lines, that column should be a GRanges object.
radius        Numeric value indicates radius. Default is 10.
trackWidth     Numeric value indicates the track width.
space.skip     Numeric value indicates the ratio of skipped region between chunks(chromosomes in GRanges) to the whole track space.
direction      Space layout orders.
link.fun       Function used for interpolate the linking lines. Default is Hmisc::bezier.
rect.inter.n   n passed to interpolate function in rectangle transformation(from a rectangle) to a section in circular view.
rank           For default equal trackWidth, use rank to specify the circle orders.
ylim           Numeric range to control y limits.
scale.n        Approximate number of ticks you want to show on the whole space. used when scale.unit is NULL.
scale.unit     Unit used for computing scale. Default is NULL,
scale.type     Scale type used for
layout_circle

grid logical value indicate showing grid background for track or not.
grid.n integer value indicate horizontal grid line number.
grid.background grid background color.
grid.line grid line color.
chr.weight numeric vectors which sum to <1, the names of vectors has to be matched with seqnames in seqinfo, and you can only specify part of the seqnames, other lengths of chromosomes will be assined proportionally to their seqlengths, for example, you could specify chr1 to be 0.5, so the chr1 will take half of the space and other chromosomes squeezed to take left of the space.

Value
A 'Layer'.

Author(s)
Tengfei Yin

Examples
N <- 100
library(GenomicRanges)
## ======================================================================
## simmulated GRanges
## ======================================================================
gr <- GRanges(seqnames =
sample(c("chr1", "chr2", "chr3"),
   size = N, replace = TRUE),
IRanges(
   start = sample(1:300, size = N, replace = TRUE),
   width = sample(70:75, size = N, replace = TRUE)),
strand = sample(c("+", "-", "*"), size = N,
   replace = TRUE),
value = rnorm(N, 10, 3), score = rnorm(N, 100, 30),
sample = sample(c("Normal", "Tumor"),
   size = N, replace = TRUE),
pair = sample(letters, size = N,
   replace = TRUE))

seqlengths(gr) <- c(400, 500, 700)
values(gr)$to.gr <- gr[sample(1:length(gr), size = length(gr))]
## more formal API

## doesn’t pass gr to the ggplot
ggplot() + layout_circle(gr, geom = "ideo", fill = "gray70", radius = 7, trackWidth = 3) +
   layout_circle(gr, geom = "bar", radius = 10, trackWidth = 4, aes(fill = score, y = score)) +
   layout_circle(gr, geom = "point", color = "red", radius = 14,
   trackWidth = 3, grid = TRUE, aes(y = score)) +
   layout_circle(gr, geom = "link", linked.to = "to.gr", radius = 6,
   trackWidth = 1)

## more formal API

ggplot(gr) + layout_circle(geom = "ideo", fill = "gray70", radius = 7, trackWidth = 3) +
   layout_circle(geom = "bar", radius = 10, trackWidth = 4, aes(fill = score, y = score)) +
layout_karyogram

Create a karyogram layout

Description

Create a karyogram layout.

Usage

## S4 method for signature 'GRanges'
layout_karyogram(data, ..., xlab, ylab, main,
   facets = seqnames ~ ., cytoband = FALSE, geom = "rect",
   stat = NULL, ylim = NULL, rect.height = 10)

Arguments

data
   a GRanges object, which could contain extra information about cytoband. If you want an accurate genome mapping, please provide seqlengths with this GRanges object, otherwise it will emit a warning and use data space to estimate the chromosome space which is very rough.

... Extra parameters such as aes() or arbitrary color and size.

xlab character vector or expression for x axis label.
ylab character vector or expression for y axis label.
main character vector or expression for plot title.
facets faceting formula to use.
cytoband logical value indicate to show the cytobands or not.
geom The geometric object to use display the data.
stat character vector specifying statistics to use.
ylim limits for y axis, usually the chromosome spaces y limits are from 0 to rect.height, which 10, so if you want to stack some data on top of it, you can set limits to like c(10, 20).
rect.height numeric value indicate half of the rectangle ploting region, used for alignment of multiple layers.

Value

A 'Layer'.

Author(s)

Tengfei Yin
Examples

### R code from vignette source 'karyogram.Rnw'

```r
library(ggbio)
data(hg19IdeogramCyto, package = "biovizBase")
head(hg19IdeogramCyto)
## default pre-set color stored in
getOption("biovizBase")$cytobandColor
```

```r
library(GenomicRanges)
library(biovizBase)
```

```r
## it's a 'ideogram'
biovizBase::isIdeogram(hg19)
```

```r
## set to FALSE
autoplot(hg19, layout = "karyogram", cytoband = FALSE, aes(fill = gieStain)) +
  scale_fill_giemsa()
```

```r
library(GenomicRanges)
dn <- darned_hg19_subset500
```

```r
## add seqlengths
## we have seqlengths information in another data set
data(hg19Ideogram, package = "biovizBase")
seqlengths(dn) <- seqlengths(hg19Ideogram)[names(seqlengths(dn))]
```

```r
## now we have seqlengths
head(dn)
```

```r
## then we change order
dn <- keepSeqlevels(dn, paste0("chr", c(1:22, "X")))
```

```r
autoplot(dn, layout = "karyogram")
```

```r
## this equivalent to
```
## autoplot(seqinfo(dn))

### code chunk number 6: load-RNAediting-color

```r
# since default is geom rectangle, even though it’s looks like segment
# we still use both fill/color to map colors
autoplot(dn, layout = "karyogram", aes(color = exReg, fill = exReg))
```

### code chunk number 7: load-RNAediting-color-NA

```r
# since default is geom rectangle, even though it’s looks like segment
# we still use both fill/color to map colors
autoplot(dn, layout = "karyogram", aes(color = exReg, fill = exReg)) +
scale_color_discrete(na.value = "brown")
```

### code chunk number 8: load-RNAediting-color-fake

```r
dn2 <- dn
seqlengths(dn2) <- rep(max(seqlengths(dn2)), length(seqlengths(dn2)) )
autoplot(dn2, layout = "karyogram", aes(color = exReg, fill = exReg))
```

### code chunk number 9: plotKaryogram (eval = FALSE)

```r
# plotKaryogram(dn)
# plotKaryogram(dn, aes(color = exReg, fill = exReg))
```

### code chunk number 10: low-default

```r
# plot ideogram
p <- ggplot(hg19) + layout_karyogram(cytoband = TRUE)
p
# equivalent autoplot(hg19, layout = "karyogram", cytoband = TRUE)
```

### code chunk number 11: low-default-addon

```r
p <- p + layout_karyogram(dn, geom = "rect", ylim = c(11, 21), color = "red")
# commented line below won’t work
# the cytoband fill color has been used already.
# p <- p + layout_karyogram(dn, aes(fill = exReg, color = exReg), geom = "rect")
p
```

### code chunk number 12: edit-space
### Plot class

genealize a graphic object to a Plot object.

#### Usage

```
## S4 method for signature 'gg'
Plot(x)
## S4 method for signature 'trellis'
Plot(x, mutable = FALSE)
## S4 method for signature 'GGbio'
Plot(x)
## S4 method for signature 'Ideogram'
Plot(x)
```

#### Arguments

- **x**: object of gg, GGbio, trellis, Ideogram.
- **mutable**: whether a plot response to + method or not.

#### Value

A Plot object.

#### Author(s)

Tengfei Yin
plotFragLength  

Plot estimated fragment length for paired-end RNA-seq data

Description

Plot estimated fragment length for paired-end RNA-seq data against single reduced data model.

Usage

```r
## S4 method for signature 'character,GRanges'
plotFragLength(data, model,
               gap.ratio = 0.0025,
               geom = c("segment", "point", "line"),
               type = c("normal", "cut"),
               heights = c(400, 100),
               annotation = TRUE)
```

Arguments

- `data` A character indicate the bam file.
- `model` A reduced model to compute estimated fragment length. please see details.
- `gap.ratio` When type is set to "cut", it will provide a compact view, which cut the common gaps in a certain ratio.
- `geom` One or all three geoms could be drawn at the same time. y value of "point" and "line" indicate the estimated fragment length. and if geom is set to "segment", the segment is from the left most position to paired right most position, should be equal to "isize".
- `type` "normal" return a uncut view, loose but the coordinate is true genomic coordinates. "cut" cut the view in a compact way.
- `heights` Numeric vector indicate the heights of tracks.
- `annotation` A logical value. TRUE shows model, and FALSE shows only fragment length with labels.

Details

We use a easy way to define this estimated fragment length, we collect all paired reads and model, reduce model first, then find common gaps, remove common gaps between paired-end reads, and compute the new estimated fragment length.

Value

A ggplot object when annotation = FALSE and a frame grob if annotation = TRUE

Author(s)

Tengfei Yin
Examples

## Not run:
```
data(genesymbol)
bamfile <- system.file("extdata", "SRR027894subRBM17.bam", package="biovizBase")
library(TxDb.Hsapiens.UCSC.hg19.knownGene)
txdb <- TxDb.Hsapiens.UCSC.hg19.knownGene
model <- exonsBy(txdb, by = "tx")
model.new <- subsetByOverlaps(model, genesymbol["RBM17"])
exons.rbm17 <- subsetByOverlaps(exons(txdb), genesymbol["RBM17"])
exons.new <- reduce(exons.rbm17)
plotFragLength(bamfile, exons.new, geom = "line")
plotFragLength(bamfile, exons.new, geom = c("point","segment"))
plotFragLength(bamfile, exons.new, geom = c("point","segment"), annotation = FALSE)
plotFragLength(bamfile, exons.new, geom = c("point","segment"), type = "cut",
              gap.ratio = 0.001)
## End(Not run)
```

Description

A Manhattan plot is a special scatter plot used to visualize data with a large number of data points, with a distribution of some higher-magnitude values. For example, in GWAS (genome-wide association studies). Here we mainly focus on GWAS Manhattan plots. X-axis is genomic coordinates and Y-axis is negative logarithm of the associated P-value for each single nucleotide polymorphism. So higher the value, more stronger the association they are.

Usage

```
plotGrandLinear(obj, ..., facets, space.skip = 0.01, geom = NULL,
                cutoff = NULL, cutoff.color = "red", cutoff.size = 1,
                legend = FALSE, xlim, ylim, xlab, ylab, main,
                highlight.gr = NULL, highlight.name = NULL,
                highlight.col = "red", highlight.label = TRUE,
                highlight.label.size = 5, highlight.label.offset =
                0.05, highlight.label.col = "black", spaceline = FALSE)
```

Arguments

- **obj**: GRanges object which contains extra p-value, before users pass this object, they need to make sure the p-value has been changed to -log10(p).
- **...**: extra arguments passed, such as color, size, alpha.
- **facets**: facets formula, such as group ~ .
- **space.skip**: numeric value for skip ratio, between chromosome spaces. default is 0.01.
- **geom**: geometric object, default is "point".
- **cutoff**: A numeric vector which used as cutoff for Manhattan plot.
plotGrandLinear

cutoff.color  A character specifying the color used for cutoff. Default is "red".
cutoff.size   A numeric value which used as cutoff line size.
legend        A logical value indicate whether to show legend or not. Default is FALSE which disabled the legend.
xlim          limits for x scale.
ylim          limits for y scale.
xlab          Label for xscale.
ylab          Label for yscale.
main          title.
highlight.gr  a GRanges object, this will highlight overlapped region with provided intervals.
highlight.name if NULL, using rownames of GRanges object provided by argument highlight.gr, otherwise use character to indicate column used as labeled names.
highlight.col highlight colors.
highlight.label logical value, label the highlighted region of not.
highlight.label.size highlight label size.
highlight.label.offset highlight label offset.
highlight.label.col highlight label color.
spaceline     show line between chromosomes.

Details
Please use seqlengths of the object and space.skip arguments to control the layout of the coordiant genome transformation.
aes(y = ...) is required.
aes(color = ) is used to mapping to data variables, if just pass "color" without aes(), then will recycle the color to represent each chromosomes. please see the example below.

Value
Return a ggplot object.

Author(s)
Tengfei Yin

Examples
## load
library(ggbio)
data(hg19IdeogramCyto, package = "biovizBase")
data(hg19Ideogram, package = "biovizBase")
library(GenomicRanges)

## simul_gr
library(biovizBase)
```r
gr <- GRanges(rep(c("chr1", "chr2"), each = 5),
               IRanges(start = rep(seq(1, 100, length = 5), times = 2),
                      width = 50))
autoplot(gr)

## coord: genome
autoplot(gr, coord = "genome")
gr.t <- transformToGenome(gr)
head(gr.t)

## is
is_coord_genome(gr.t)
metadata(gr.t)$coord

## simul_snp
chrs <- as.character(levels(seqnames(hg19IdeogramCyto)))
seqlths <- seqlengths(hg19Ideogram)[chrs]
set.seed(1)
nchr <- length(chrs)
nsnps <- 100
gr.snp <- GRanges(rep(chrs, each=nsnps),
                   IRanges(start =
                        do.call(c, lapply(chrs, function(chr){
                                    N <- seqlths[chr]
                                    runif(nsnps,1,N)
                        })),
                   width = 1),
                   SNP=paste("rs",1:(nchr*nsnps), sep=''),
                   pvalue = -log10(runif(nchr*nsnps)),
                   group = sample(c("Normal", "Tumor"), size = nchr*nsnps,
                                   replace = TRUE)
)

## shorter
seqlengths(gr.snp)
nms <- seqnames(seqinfo(gr.snp))
nms.new <- gsub("chr", "", nms)
names(nms.new) <- nms
gr.snp <- renameSeqlevels(gr.snp, nms.new)
seqlengths(gr.snp)

## unorder
autoplot(gr.snp, coord = "genome", geom = "point", aes(y = pvalue), space.skip = 0.01)

## sort
gr.snp <- keepSeqlevels(gr.snp, c(1:22, "X", "Y"))
autoplot(gr.snp, coord = "genome", geom = "point", aes(y = pvalue), space.skip = 0.01)

## with_seq
names(seqlths) <- gsub("chr", "", names(seqlths))
seqlengths(gr.snp) <- seqlths[names(seqlengths(gr.snp))]
autoplot(gr.snp, coord = "genome", geom = "point", aes(y = pvalue), space.skip = 0.01)

## line
autoplot(gr.snp, coord = "genome", geom = "line", aes(y = pvalue, group = seqnames,
```
plotRangesLinkedToData

## plotGrandLinear
plotGrandLinear(gr.snp, aes(y = pvalue))

## morecolor
plotGrandLinear(gr.snp, aes(y = pvalue, color = seqnames))
plotGrandLinear(gr.snp, aes(y = pvalue), color = c("green", "deepskyblue"))
plotGrandLinear(gr.snp, aes(y = pvalue), color = c("green", "deepskyblue", "red"))
plotGrandLinear(gr.snp, aes(y = pvalue), color = "red")

## cutoff
plotGrandLinear(gr.snp, aes(y = pvalue), cutoff = 3, cutoff.color = "blue", cutoff.size = 4)

## cutoff-low
plotGrandLinear(gr.snp, aes(y = pvalue)) + geom_hline(yintercept = 3, color = "blue", size = 4)

## longer
## let's make a long name
nms <- seqnames(seqinfo(gr.snp))
nms.new <- paste("chr00000", nms, sep = "")
names(nms.new) <- nms
gm.snp <- renameSeqlevels(gr.snp, nms.new)
seqlengths(gr.snp)

## rotate
plotGrandLinear(gr.snp, aes(y = pvalue)) + theme(axis.text.x=element_text(angle=-90, hjust=0))

## sessionInfo
sessionInfo()

---

plotRangesLinkedToData

*Plot Ranges Linked with Data*

### Description

Plot GRanges object structure and linked to a even spaced paralell coordinates plot which repesenting the data in elementeMetadata.

### Usage

```r
## S4 method for signature 'RangedSummarizedExperiment'
plotRangesLinkedToData(data, ..., 
      stat.y = seq_len(ncol(data)), stat.ylab = names(assays(data)[stat.assay]),
      stat.assay = 1L)

## S4 method for signature 'GenomicRangesORGRangesList'
plotRangesLinkedToData(data, ..., 
      stat.y = seq_len(ncols(data))),
      stat.ylab, sig, sig.col = c("black", "red"),
```
stat.coord.trans = coord_trans(),
annotation = list(), width.ratio = 0.8,
theme.stat = theme_gray(), theme.align = theme_gray(),
linetype = 3, heights)

Arguments

data  GRanges object with a DataFrame as elementMetadata.
... Parameters passed to control lines in top plot.
stat.y  integer (variable position starting in DataFrame of data, start from 1) or strings (variable names) which indicate the column names.
stat.ylab  y label for stat track (the top track).
stat.assay  default 1L, element of assays.
sig  a character of element meta data column of logical value, indicates which row is significant. and will be shown in link lines and rectangle.
sig.col  colors for significant, valid when you specify "sig" argument, the first color indicates FALSE, non-significant, the second color indicates TRUE.
stat.coord.trans  transformation used for top plot.
annotation  A list of ggplot object.
width.ratio  Control the segment length of statistic layer.
theme.stat  top plot theme.
theme.align  alignment themes.
linetype  linetype
heights  Heights of each track.

Details

Inspired by some graphics produced in some other packages, for example in package DEXseq, the author provides graphics with gene models and linked to an even spaced statistics summary. This is useful because we always plot everything along the genomic coordinates, but genomic features like exons are not evenly distributed, so we could actually treat the statistics associated with exons like categorical data, and show them as “Parallel Coordinates Plots”. This is one special layout which represent the data in a nice manner and also keep the genomic structure information. With ability of tracks, it’s possible to generate such type of a graphic along with other annotations.

The data we want is a normal GRanges object, and make sure the intervals are not overlaped with each other (currently), and you may have multiple columns which store the statistics for multiple samples, then we produce the graphic we introduced above and users could pass other annotation track in the function which will be shown below the main linked track.

The reason you need to pass annotation into the function instead of binding them by tracks later is because binding manually with annotation tracks is tricky and this function doesn’t return a ggplot object.

Value

return a frame grob; side-effect (plotting) if plot=T.
plotSpliceSum

Plot Splice Summary from RNA-seq data

Description

Plot splice summary by simply counting overlaped junction read in weighted way or not.

Usage

## For character,GRangesList
## S4 method for signature 'character,GRangesList'
plotSpliceSum(data, model, ..., weighted = TRUE)

## For character,TxDB
## S4 method for signature 'character,TxDB'
plotSpliceSum(data, model, which, ...
, weighted = TRUE)

## For character,EnsDb
## S4 method for signature 'character,EnsDb'
plotSpliceSum(data, model, which, ...
, weighted = TRUE)

Examples

library(TxDB.Hsapiens.UCSC.hg19.knownGene)
library(ggbio)
data(genesymbol, package = "biovizBase")
txdb <- TxDb.Hsapiens.UCSC.hg19.knownGene
model <- exonsBy(txdb, by = "tx")
model17 <- subsetByOverlaps(model, genesymbol["RBM17"])
exons <- exons(txdb)
exon17 <- subsetByOverlaps(exons, genesymbol["RBM17"])
## reduce to make sure there is no overlap
## just for example
exon.new <- reduce(exon17)
## suppose
values(exon.new)$sample1 <- rnorm(length(exon.new), 10, 3)
values(exon.new)$sample2 <- rnorm(length(exon.new), 10, 10)
values(exon.new)$score <- rnorm(length(exon.new))
values(exon.new)$significant <- sample(c(TRUE,FALSE), size = length(exon.new),replace = TRUE)

plotRangesLinkedToData(exon.new, stat.y = c("sample1", "sample2"))
plotRangesLinkedToData(exon.new, stat.y = 1:2)
plotRangesLinkedToData(exon.new, stat.y = 1:2, size = 3, linetype = 4)
plotRangesLinkedToData(exon.new, stat.y = 1:2, size = 3, linetype = 4,
sig = "significant")
plotRangesLinkedToData(exon.new, stat.y = 1:2, size = 3, linetype = 4,
 sig = "significant", sig.col = c("gray90","red"))
plotSpliceSum

Arguments

data  A character specifying the bam file path of RNA-seq data.

model  A GRangesList which representing different isoforms, a TxDb or an EnsDb object. For the latter cases, users need to pass "which" argument which, for TxDb, is a GRanges object to specify the region and for EnsDb can be a GRanges object, a filter extending the BasicFilter-class class or a list thereof. And we get canonical model internally.

which  A GRanges object specifying the region you want to get model from the TxDb object. For EnsDb: a GRanges object or a single or list of filter object(s) extending BasicFilter-class.

weighted  If TRUE, weighted by simply add 1/cases matched to each model and if FALSE, simply add 1 to every case.

...  Extra arguments passed to qplot function, such as, offset which control the height of chevron.

Details

Internally we use biovizBase:::spliceSummary for simple counting, but we encourage users to use their own robust way to make slicing summary and store it as GRangesList, then plot the summary by qplot function.

Value

A ggplot object.

Author(s)

Tengfei Yin

See Also

qplot

Examples

```r
## Not run:
bamfile <- system.file("extdata", "SRR027894subRBM17.bam", package="biovizBase")
library(TxDb.Hsapiens.UCSC.hg19.knownGene)
txdb <- TxDb.Hsapiens.UCSC.hg19.knownGene
data(genesymbol)
exons <- exonsBy(txdb, by = "tx")
exons.rbm17 <- subsetByOverlaps(exons, genesymbol["RBM17"])  
plotSpliceSum(bamfile, exons.rbm17)
plotSpliceSum(bamfile, exons.rbm17, weighted = FALSE, offset = 0.01)
plotSpliceSum(bamfile, txdb, which = genesymbol["RBM17"])  
plotSpliceSum(bamfile, txdb, which = genesymbol["RBM17"], offset = 0.01)
plotSpliceSum(bamfile, txdb, which = genesymbol["RBM17"],
  show.label = TRUE,
  label.type = "count")
## End(Not run)
```
Description

Plot stacked overview for genome with or without cytoband. It’s a wrapper around layout_karyogram.

Usage

```r
plotStackedOverview(obj, ..., xlab, ylab, main, geom = "rect",
                     cytoband = FALSE, rescale = TRUE,
                     rescale.range = c(0, 10))
```

```r
plotKaryogram(obj, ..., xlab, ylab, main, geom = "rect",
               cytoband = FALSE, rescale = TRUE,
               rescale.range = c(0, 10))
```

Arguments

- `obj`: a GRanges object, which could contain extra information about cytoband. If it's missing, will ask user to provide species information and download proper data set from UCSC. If you want an accurate genome mapping, please provide seqlengths with this GRanges object, otherwise it will emit a warning and use data space to estimate the chromosome space which is very rough.

- `...`: arguments passed to graphic functions to control aesthetics. For example, if you use geom "point", you need to provide "y" in aes(), and if can also pass color, fill, size etc. to control graphics.

- `xlab`: label for x

- `ylab`: label for y

- `main`: title for plot.

- `geom`: geom plotted on the stacked layout. Default is "rect", which showing interval data as rectangles. It automatically figures out boundary so you don’t have to provide information in aes, users could specify other supported geom works for data.frame.

- `cytoband`: logical value. Default is FALSE. If TRUE, plotting cytoband, this require your data have arbitrary column as name and gieStain. the easiest way is to use getIdeogram to get your data. Notice for this function, when cytoband is TRUE, it will only plot cytoband without overlaying your data. If you really need to overlay extra data on cytoband, please plus layout_karyogram for that purpose.

- `rescale`: logical value. Default is TRUE, which rescale your data into the rescale.range, this make sure your data will not be plotted outside the stacked overview box.

- `rescale.range`: Numeric range of length 2. Default is (0, 10), because stacked layout draws a white background as chromosome space and this space is of height 10. We hide the y-axis since we don’t need it for stacked overview. Sometime users may want to leave some margin for their data, they can use this arguments to control the rescale.
Details

Stacked overview is just an arbitrary layout for karyogram layout, it use facets seqnaems ~ . as default to stack the genome. For accurate mapping, you need to provide seqlengths information in your GRanges object. Otherwise, data space will be computed for stacked overview chromosome background, this is _NOT_ the actual chromosome space!.

Value

A ggplot object.

Author(s)

Tengfei Yin

Examples

```r
## Not run:
library(biovizBase)
data(hg19IdeogramCyto, package = "biovizBase")
library(GenomicRanges)

## you can also get ideogram by biovizBase::getIdeogram

## make shorter and clean labels
old.chrs <- seqnames(seqinfo(hg19IdeogramCyto))
new.chrs <- gsub("chr", "", old.chrs)
## lst <- as.list(new.chrs)
names(new.chrs) <- old.chrs
new.ideo <- renameSeqlevels(hg19IdeogramCyto, new.chrs)
new.ideo <- keepSeqlevels(new.ideo, c(as.character(1:22), "X", "Y"))
new.ideo

## sample data
data(darned_hg19_subset500, package = "biovizBase")
idx <- is.na(values(darned_hg19_subset500)$exReg)
values(darned_hg19_subset500)$exReg[idx] <- "unknown"

## you need to add seqlengths for accurate mapping
chrnames <- unique(as.character(seqnames(darned_hg19_subset500)))
data(hg19Ideogram, package = "biovizBase")
seqlengths(darned_hg19_subset500) <- seqlengths(hg19Ideogram)[sort(chrnames)]

dn <- darned_hg19_subset500
values(dn)$score <- rnorm(length(dn))

## plotStackedOverview is a simple wrapper around this functions to
## create a stacked layout
plotStackedOverview(new.ideo, cytoband = TRUE)
plotStackedOverview(dn)
plotStackedOverview(dn, aes(color = exReg, fill = exReg))
## this will did the trick for you to rescale the space
plotStackedOverview(dn, aes(x = midpoint, y = score), geom = "line")
plotStackedOverview(dn, aes(x = midpoint, y = score), geom = "line", rescale.range = c(4, 6))
```
## no rescale

plotStackedOverview(dn, aes(x = midpoint, y = score), geom = "line", rescale = FALSE, xlab = "xlab", ylab = "ylab", main = "main") + ylab("ylab")

## no object? will ask you for species and query the data on the fly
plotStackedOverview()
plotStackedOverview(cytoband = TRUE)

## End(Not run)

### rescale

#### rescale ggplot object

**Description**

Rescale a numeric vector or ggplot object, could be used for static zoom-in in ggbio.

**Usage**

```r
## S4 method for signature 'numeric'
rescale(x, to = c(0, 1),
        from = range(x, na.rm = TRUE))
```

```r
## S4 method for signature 'ggplot'
rescale(x, xlim, ylim, sx = 1, sy = 1)
## S4 method for signature 'gg'
rescale(x, xlim, ylim, sx = 1, sy = 1)
```

**Arguments**

- **x**: A numeric object or ggplot object to be rescaled.
- **to**: For numeric object. it’s a vector of two numeric values, specifying the range to be rescale.
- **from**: Range of x.
- **xlim**: For ggplot object. This specify the new limits on x-scale.
- **ylim**: For ggplot object. This specify the new limits on y-scale.
- **sx**: Scale fold for x-scale. Default is 1, no change.
- **sy**: Scale fold for y-scale. Default is 1, no change.

**Details**

When x is numeric value, it’s just call scales::rescale, please refer to the manual page to check more details. If x is ggplot object, it first try to estimate current x limits and y limits of the ggplot object, then rescale based on those information.

**Value**

Return the object of the same class as x after rescaling.
Author(s)
Tengfei Yin

Examples

```r
library(ggbio)
head(mtcars)
range(mtcars$mpg)
p <- qplot(data = mtcars, x = mpg, y = disp, geom = "point")
p.new <- rescale(p, xlim = c(20, 25))
p.new
```

Description

In biology, lots of data are scaled to value around 0, and people like to show them as blue-white-red scale color, where negative value are blue, 0 is white and positive value is red, and they are scaled for continuous variables.

Usage

`scale_fill_fold_change()`

Value

a list.

Author(s)

Tengfei Yin

Examples

```r
p1 <- autoplot(volcano - 150)
p1
p1 + scale_fill_fold_change()
```
scale_fill_giemsa  

scale filled color to customized giemsa color.

Description
scale filled color to customized giemsa color.

Usage
scale_fill_giemsa(fill = getOption("biovizBase")$cytobandColor)

Arguments
fill  a character vector to indicate colors, and names of vector mapped to gieStain name.

Value
a list.

Author(s)
Tengfei Yin

Examples
getOption("biovizBase")$cytobandColor
library(biovizBase)
data(hg19 IdeogramCyto)
p1 <- autoplot(hg19 IdeogramCyto, layout = "karyogram", aes(fill = gieStain))
p1
p1 + scale_fill_giemsa()

scale_x_sequnit  

scale x by unit

Description
scale x by unit 'Mb', 'kb', 'bp'.

Usage
scale_x_sequnit(unit = c("Mb", "kb", "bp"), append = NULL)

Arguments
unit  unit to scale x. Default is Mb.
append  default NULL. If pass a character, it disalbe unit and arbitrarily append a text behind the original x scale numbers.
Value

'position_c'

Author(s)

Tengfei Yin

Examples

```r
library(ggplot2)

p <- qplot(x = seq(1, to = 10000, length.out = 40), y = rnorm(40), geom = "point")
## default mb
p + scale_x_sequnit()  

p + scale_x_sequnit("kb")

p + scale_x_sequnit("bp")
```

**stat_aggregate**

Generates summaries on the specified windows

### Description

Generates summaries on the specified windows

### Usage

```r
## S4 method for signature 'GRanges'
stat_aggregate(data, ..., xlab, ylab, main, by, FUN, 
maxgap=0L, minoverlap=1L, 
type=c("any", "start", "end", "within", "equal"), 
select=c("all", "first", "last", "arbitrary"), 
y = NULL, window = NULL, facets = NULL, 
method = c("mean", "median", "max", "min", "sum", "count", "identity"), 
geom = NULL)
```

### Arguments

- **data** 
  A GRanges or data.frame object.
- **...** 
  Arguments passed to plot function. such as `aes()` and `color`.
- **xlab** 
  Label for x
- **ylab** 
  Label for y
- **main** 
  Title for plot.
- **by** 
  An object with 'start', 'end', and 'width' methods. Passed to `aggregate`.
- **FUN** 
  The function, found via `match.fun`, to be applied to each window of 'x'. Passed to `aggregate`.
maxgap, minoverlap
It passed to findOverlaps.
Intervals with a separation of maxgap or less and a minimum of minoverlap overlapping positions, allowing for maxgap, are considered to be overlapping. maxgap should be a scalar, non-negative, integer. minoverlap should be a scalar, positive integer.

type
It passed to findOverlaps.
By default, any overlap is accepted. By specifying the type parameter, one can select for specific types of overlap. The types correspond to operations in Allen’s Interval Algebra (see references). If type is start or end, the intervals are required to have matching starts or ends, respectively. While this operation seems trivial, the naive implementation using outer would be much less efficient. Specifying equal as the type returns the intersection of the start and end matches. If type is within, the query interval must be wholly contained within the subject interval. Note that all matches must additionally satisfy the minoverlap constraint described above.
The maxgap parameter has special meaning with the special overlap types. For start, end, and equal, it specifies the maximum difference in the starts, ends or both, respectively. For within, it is the maximum amount by which the query may be wider than the subject.
select
It passed to findOverlaps.
When select is "all" (the default), the results are returned as a Hits object. When select is "first", "last", or "arbitrary" the results are returned as an integer vector of length query containing the first, last, or arbitrary overlapping interval in subject, with NA indicating intervals that did not overlap any intervals in subject.
If select is "all", a Hits object is returned. For all other select the return value depends on the drop argument. When select != "all" && !drop, an IntegerList is returned, where each element of the result corresponds to a space in query. When select != "all" && drop, an integer vector is returned containing indices that are offset to align with the unlisted query.
y
A character indicate the varialbe column for which aggregation is taken on, same as aes(y = ).
window
Integer value indicate window size.
facets
Faceting formula to use.
method
customized method for aggregating, if FUN is not provided.
geom
The geometric object to use display the data.

Value
A 'Layer'.

Author(s)
Tengfei Yin

Examples
library(GenomicRanges)
set.seed(1)
N <- 1000
## simmulated GRanges

```r
gr <- GRanges(seqnames =
  sample(c("chr1", "chr2", "chr3"),
  size = N, replace = TRUE),
IRanges(
  start = sample(1:300, size = N, replace = TRUE),
  width = sample(70:75, size = N, replace = TRUE),
  strand = sample(c("+", "-", "*"), size = N,
  replace = TRUE),
  value = rnorm(N, 10, 3), score = rnorm(N, 100, 30),
  sample = sample(c("Normal", "Tumor"),
  size = N, replace = TRUE),
pair = sample(letters, size = N,
  replace = TRUE))
```

```r
ggplot(gr) + stat_aggregate(aes(y = value))
## or
## ggplot(gr) + stat_aggregate(y = "value")
ggplot(gr) + stat_aggregate(aes(y = value), window = 36)
ggplot(gr) + stat_aggregate(aes(y = value), select = "first")
## Not run:
## no hits
## ggplot(gr) + stat_aggregate(aes(y = value), select = "first", type = "within")
## End(Not run)
ggplot(gr) + stat_aggregate(aes(y = value), fill = "gray40", geom = "bar")
ggplot(gr) + stat_aggregate(aes(y = value), geom = "boxplot")
```

```r
ggplot(gr) + stat_aggregate(aes(y = value), window = 30, geom = "boxplot", windows = 60)
ggplot(gr) + stat_aggregate(aes(y = value), geom = "boxplot", win = 30, facets = sample ~ seqnames)
## FIXME:
## autoplot(gr, stat = "aggregate", aes(y = value), window = 36)
## autoplot(gr, stat = "aggregate", geom = "boxplot", aes(y = value), window = 36)
```

---

### stat_bin

**Binning method**

<table>
<thead>
<tr>
<th>Description</th>
<th>Usage</th>
</tr>
</thead>
</table>
| Binning method especially for Rle and RleList. For data.frame it is just calling `ggplot2::stat_bin`. | `## S4 method for signature 'ANY'
stat_bin(data, ...)`
| | `## S4 method for signature 'Rle'` |
stat_bin(data, ..., binwidth, nbin = 30, xlab, ylab, main, geom = c("bar", "heatmap"), type = c("viewSums", "viewMins", "viewMaxs", "viewMeans"))

## S4 method for signature 'RleList'
stat_bin(data, ..., binwidth, nbin = 30, xlab, ylab, main, indName = "sample", geom = c("bar", "heatmap"), type = c("viewSums", "viewMins", "viewMaxs", "viewMeans"))

Arguments

data Typically a data.frame or Rle or RleList object.
... arguments passed to aesthetics mapping.
binwidth width of the bins.
nbin number of bins.
xlab x label.
 ylab y label.
main title.
indName when faceted by a RleList, name used for labeling faceted factor. Default is 'sample'.
geom geometric types.
type statistical summary method used within bins, shown as bar height or heatmap colors.

Value
a ggplot object.

Author(s)
Tengfei Yin

Examples
library(IRanges)
lambda <- c(rep(0.001, 4500), seq(0.001, 10, length = 500),
  seq(10, 0.001, length = 500))
xVector <- rpois(1e4, lambda)
xRle <- Rle(xVector)
xRleList <- RleList(xRle, 2L * xRle)

ggplot() + stat_bin(xRle)
ggplot(xRle) + stat_bin()
ggplot(xRle) + stat_bin(nbin = 100)
ggplot(xRle) + stat_bin(binwidth = 200)

p1 <- ggplot(xRle) + stat_bin(type = "viewMeans")
p2 <- ggplot(xRle) + stat_bin(type = "viewSums")
## y scale are different.
Calculate coverage.

Usage

# for GRanges
## S4 method for signature 'GRanges'
stat_coverage(data, ..., xlim, xlab, ylab, main,
facets = NULL, geom = NULL)

# for GRangesList
## S4 method for signature 'GRangesList'
stat_coverage(data, ..., xlim, xlab, ylab, main,
facets = NULL, geom = NULL)

# for Bamfile
## S4 method for signature 'BamFile'
stat_coverage(data, ..., maxBinSize = 2^14,
xlim, which, xlab, ylab,
main, facets = NULL, geom = NULL,
method = c("estimate", "raw"),
space.skip = 0.1, coord = c("linear", "genome"))

Arguments

data A GRanges or data.frame object.

... Extra parameters such as aes() passed to geom_rect, geom_alignment, or geom_segment.

xlim Limits for x.

xlab Label for x
stat_coverage

ylabel  Label for y
main    Title for plot.
facets  Faceting formula to use.
geom    The geometric object to use display the data.
maxBinSize maxBinSize.
method 'estimate’ for parsing estimated coverage(fast), 'raw’ is slow and parse the accurate coverage.
which  GRanges which defines region to subset the results.
space.skip  used for coordinate genome, skip between chromosomes.
coord  coordinate system.

Value
A 'Layer'.

Author(s)
Tengfei Yin

Examples
library(ggbio)
### ==============================================================
### simulates GRanges
### ==============================================================
set.seed(1)
N <- 1000
library(GenomicRanges)
gr <- GRanges(seqnames =
sample(c("chr1", "chr2", "chr3"),
        size = N, replace = TRUE),
    IRanges(  start = sample(1:300, size = N, replace = TRUE),
        width = sample(70:75, size = N, replace = TRUE)),
    strand = sample(c("+", "-", "*"), size = N, replace = TRUE),
    value = rnorm(N, 10, 3), score = rnorm(N, 100, 30),
    sample = sample(c("Normal", "Tumor"), size = N, replace = TRUE),
    pair = sample(letters, size = N, replace = TRUE))

ggplot(gr) + stat_coverage()
ggplot() + stat_coverage(gr)

ggplot(gr) + stat_coverage(geom = "point")
ggplot(gr) + stat_coverage(geom = "area")
ggplot(gr) + stat_coverage(aes(y = ..coverage..), geom = "bar")
ggplot(gr) + stat_coverage(aes(y = ..coverage..)) + geom_point()

## for bam file
## TBD
stat_gene

Calculate gene structure

Description

Calculate gene structure.

Usage

## S4 method for signature 'TxDb'
stat_gene(data, ...)

Arguments

data A GRanges or data.frame object.
...
Extra parameters such as aes() passed to geom_alignment.

Value

A 'Layer'.

Author(s)

Tengfei Yin

See Also

gem_alignment

Examples

## Not run:
## loading package
## Deprecated
library(TxDb.Hsapiens.UCSC.hg19.knownGene)
data(genesymbol, package = "biovizBase")
txdb <- TxDb.Hsapiens.UCSC.hg19.knownGene

## made a track comparing full/reduce stat.
p1 <- ggplot() + geom_alignment(txdb, which = genesymbol["RBM17"])
p1 <- ggplot() + stat_gene(txdb, which = genesymbol["RBM17"])## or
p1 <- ggplot(txdb) + stat_gene(which = genesymbol["RBM17"])## ggplot(txdb) + geom_alignment(which = genesymbol["RBM17"], stat = "reduce")
p2 <- ggplot(txdb) + stat_gene(\什麼 = genesymbol["RBM17"], stat = "reduce")## ggplot(txdb) + geom_alignment(\什麼 = genesymbol["RBM17"] + stat_reduce())## ggplot(txdb) + geom_alignment(\什麼 = genesymbol["RBM17"])
tracks(full = p1, reduce = p2, heights = c(3, 1))

## change y labels
stat_identity

Transform the data to a data.frame and for multiple geoms.

Description

Transform the data to a suitable data.frame and then one could use multiple geom or even stat to re-plot the data.

Usage

```r
## S4 method for signature 'ANY'
stat_identity(data, ...)

## S4 method for signature 'GRanges'
stat_identity(data, ..., geom = NULL)

## S4 method for signature 'Rle'
stat_identity(data, ..., xlab, ylab, main, geom = NULL)

## S4 method for signature 'RleList'
stat_identity(data, ..., xlab, ylab, main,
             geom = NULL, indName = "sample")
```

Arguments

- `data`: Typically a GRanges or data.frame object.
- `...`: Extra parameters such as aes() passed to geom_rect, geom_alignment, or geom_segment.
- `geom`: The geometric object to use display the data.
- `xlab`: x label.
- `ylab`: y label.
- `main`: title of graphic..
- `indName`: sample name.

Value

A 'Layer'.

Author(s)

Tengfei Yin
Examples

```r
## load
set.seed(1)
N <- 50
require(GenomicRanges)

## simul
## simmulated GRanges
gr <- GRanges(
  seqnames = sample(c("chr1", "chr2", "chr3"), size = N, replace = TRUE),
  IRanges(
    start = sample(1:300, size = N, replace = TRUE),
    width = sample(70:75, size = N, replace = TRUE),
    strand = sample(c("+", "-", "*"), size = N, replace = TRUE),
    value = rnorm(N, 10, 3), score = rnorm(N, 100, 30),
    sample = sample(c("Normal", "Tumor"), size = N, replace = TRUE),
    pair = sample(letters, size = N, replace = TRUE))

## geom_point_start
ggplot() + stat_identity(gr, aes(x = start, y = value), geom = "point")
## or more formal
ggplot(gr) + stat_identity(aes(x = start, y = value), geom = "point")

## geom_point_midpoint
ggplot(gr) + stat_identity(aes(x = midpoint, y = value), geom = "point")

## geom_rect_all
ggplot(gr) + stat_identity(aes(xmin = start, xmax = end, y = value), geom = "rect")

## geom_rect_y
ggplot(gr) + stat_identity(aes(y = value), geom = "rect")

## geom_line
ggplot(gr) + stat_identity(aes(x = start, y = value), geom = "line")

## geom_segment
ggplot(gr) + stat_identity(aes(y = value), geom = "segment")

## Rle/RleList
library(IRanges)
lambda <- c(rep(0.001, 4500), seq(0.001, 10, length = 500),
  seq(10, 0.001, length = 500))
xVector <- rpois(1e4, lambda)
xRle <- Rle(xVector)
xRleList <- RleList(xRle, 2L * xRle)

ggplot(xRle) + stat_identity(geom = "point")
ggplot(xRleList) + stat_identity(geom = "point")
```
stat_mismatch  Calculate mismatch summary

Description
Calculate mismatch summary

Usage
```
## for GRanges
## S4 method for signature 'GRanges'
stat_mismatch(data, ..., bsgenome,
  xlab, ylab, main,
  geom = c("segment", "bar"),
  show.coverage = TRUE)
## for BamFile
## S4 method for signature 'BamFile'
stat_mismatch(data, ..., bsgenome, which,
  xlab, ylab, main,
  geom = c("segment", "bar"),
  show.coverage = TRUE)
```

Arguments
- `data`: A GRanges or BamFile object.
- `...`: Extra parameters such as `aes()` passed to `geom_rect`, `geom_alignment`, or `geom_segment`.
- `bsgenome`: BSgenome object.
- `which`: GRanges object to subset the data.
- `xlab`: Label for x
- `ylab`: Label for y
- `main`: Title for plot.
- `geom`: The geometric object to use display the data.
- `show.coverage`: Whether to show coverage as background or not.

Value
A 'Layer'.

Author(s)
Tengfei Yin
stat_reduce

Reduce an object.

Description
Reduce GRanges, IRanges or TxDb object.

Usage

## S4 method for signature 'GRanges'
stat_reduce(data, ...,
  xlab, ylab, main,
  drop.empty.ranges = FALSE,
  min.gapwidth = 1L,
  facets = NULL, geom = NULL)

## S4 method for signature 'IRanges'
stat_reduce(data, ...,
  xlab, ylab, main,
  drop.empty.ranges = FALSE,
  min.gapwidth = 1L,
  with.inframe.attrib=FALSE,
  facets = NULL, geom = NULL)

## S4 method for signature 'TxDbOREnsDb'
stat_reduce(data, ...)

Arguments

data GRanges, IRanges or TxDb object.
...
  passed to aesthetics mapping.
xlab x label.
ylab y label.
main title.
drop.empty.ranges
  pass to reduce function.
min.gapwidth pass to reduce function.
with.inframe.attrib pass to reduce function.
facets pass to reduce function.
geom geometric type.

Value
a ggplot object.

Author(s)
Tengfei Yin
See Also

reduce.

Examples

```r
set.seed(1)
N <- 1000
library(GenomicRanges)

gr <- GRanges(seqnames =
  sample(c("chr1", "chr2", "chr3"),
     size = N, replace = TRUE),
IRanges(
     start = sample(1:300, size = N, replace = TRUE),
     width = sample(70:75, size = N,replace = TRUE),
     strand = sample(c("+", "-", "*"), size = N,
                    replace = TRUE),
     value = rnorm(N, 10, 3), score = rnorm(N, 100, 30),
     sample = sample(c("Normal", "Tumor"),
                    size = N, replace = TRUE),
     pair = sample(letters, size = N,
                  replace = TRUE))

ggplot(gr) + stat_reduce()
autoplot(gr, stat = "reduce")
strand(gr) <- "*"
  ggplot(gr) + stat_reduce()

library(TxDb.Hsapiens.UCSC.hg19.knownGene)
data(genesymbol, package = "biovizBase")
txdb <- TxDb.Hsapiens.UCSC.hg19.knownGene
## made a track comparing full/reduce stat.
  ggplot(txdb) + stat_reduce(which = genesymbol["RBM17"])
```

**stat_slice**

Slice Rle/RleList to view them as bar or heatmap.

Description

Slice Rle/RleList to different view by set lower or other parameters, then view summary for all those viewed region.

Usage

```r
## S4 method for signature 'Rle'
stat_slice(data, ...,
  xlab, ylab, main,
  na.rm = FALSE,
  geom = NULL,
  lower=-Inf, upper=Inf,
  includeLower=TRUE, includeUpper=TRUE,
  rangesOnly = FALSE,
```
stat_slice

type = c("viewSums", "viewMins",
"viewMaxs", "viewMeans")

## S4 method for signature 'RleList'
stat_slice(data, ..., xlab, ylab, main,
indName = "sample",
na.rm = FALSE,
geom = NULL,
lower=-Inf, upper=Inf,
includeLower=TRUE, includeUpper=TRUE,
rangesOnly = FALSE,
type = c("viewSums", "viewMins",
"viewMaxs", "viewMeans"))

Arguments

data a data.frame or Rle or RleList object.
...
arguments passed to aesthetics mapping.
xlab x label.
ylab y label.
main title.
indName when faceted by a RleList, name used for labeling faceted factor. Default is 'sample'.
geom geometric types.
type statistical summary method used within bins, shown as bar height or heatmap colors.
na.rm logical value, default FALSE, passed to function like viewMaxs for statistical summary computation.
lower passed to slice.
upper passed to slice.
includeLower passed to slice.
includeUpper passed to slice.
rangesOnly passed to slice.

Value

a ggplot object.

Author(s)

Tengfei Yin

See Also

slice
Examples

```r
library(IRanges)
lambda <- c(rep(0.001, 4500), seq(0.001, 10, length = 500),
            seq(10, 0.001, length = 500))
xVector <- rpois(1e4, lambda)
xRle <- Rle(xVector)
xRleList <- RleList(xRle, 2L * xRle)

ggplot(xRle) + stat_slice(lower = 5)
ggplot(xRle) + stat_slice(lower = 5, geom = "bar")
ggplot(xRle) + stat_slice(lower = 5, geom = "heatmap")

p1 <- ggplot(xRle) + stat_slice(type = "viewMeans", lower = 5,
                           geom = "bar")
p2 <- ggplot(xRle) + stat_slice(type = "viewSums", lower = 5,
                           geom = "bar")
## y scale are different.
tracks(viewMeans = p1, viewSums = p2)

ggplot(xRleList) + stat_slice(lower = 5)
ggplot(xRleList) + stat_slice(lower = 5, geom = "bar")
ggplot(xRleList) + stat_slice(lower = 5, geom = "heatmap")

p1 <- ggplot(xRleList) + stat_slice(type = "viewMeans", lower = 5,
                           geom = "bar")
p2 <- ggplot(xRleList) + stat_slice(type = "viewSums", lower = 5,
                           geom = "bar")
## y scale are different.
tracks(viewMeans = p1, viewSums = p2)
```

stat_stepping

Calculate stepping levels

Description

Calculate stepping levels.

Usage

```r
## S4 method for signature 'GRanges'
stat_stepping(data, ..., xlab, ylab, main,
              facets = NULL,
              geom = c("rect", "alignment", "segment"))
```

Arguments

- `data`: A GRanges or data.frame object.
- `...`: Extra parameters such as aes() passed to geom_rect, geom_alignment, or geom_segment.
- `xlab`: Label for x
- `ylab`: Label for y
- `main`: Title for plot.
facets

Faceting formula to use.

geom

The geometric object used to display the data. For 'stepping', could be one of 'rect', 'alignment', 'segment'.

Value

A 'Layer'.

Author(s)

Tengfei Yin

Examples

```r
set.seed(1)
N <- 50

require(GenomicRanges)
## simul
## ---------------------------------------------------------------
## simmulated GRanges
## ---------------------------------------------------------------
gr <- GRanges(seqnames = sample(c("chr1", "chr2", "chr3"), size = N, replace = TRUE),
  IRanges(
    start = sample(1:300, size = N, replace = TRUE),
    width = sample(70:75, size = N, replace = TRUE),
    strand = sample(c("+", "-", "*"), size = N,
    replace = TRUE),
    value = rnorm(N, 10, 3), score = rnorm(N, 100, 30),
    sample = sample(c("Normal", "Tumor"),
    size = N, replace = TRUE),
    pair = sample(letters, size = N, replace = TRUE))

## default
ggplot(gr) + stat_stepping()
## or
ggplot() + stat_stepping(gr)

## facet_aes
ggplot(gr) + stat_stepping(aes(color = strand, fill = strand),
  facets = sample ~ seqnames)

## geom_segment
ggplot(gr) + stat_stepping(aes(color = strand),
  geom = "segment", xlab = "Genomic coord", ylab = "y", main = "hello")

## geom_alignment
## ggplot(gr) + stat_stepping(geom = "alignment")

## geom_alignment_group
## ggplot(gr) + stat_stepping(aes(group = pair),geom = "alignment")
```
**stat_table**  
Tabulate a GRanges object

**Description**
Tabulate a GRanges object

**Usage**
```
## S4 method for signature 'GRanges'
stat_table(data, ..., xlab, ylab, main,
  geom = NULL, stat = NULL)
## S4 method for signature 'GRangesList'
stat_table(data, ..., xlab, ylab, main,
  facets = NULL, geom = NULL)
```

**Arguments**
- `data`: A GRanges or data.frame object.
- `...`: Extra parameters such as `aes()` passed to `geom_rect`, `geom_alignment`, or `geom_segment`.
- `xlab`: Label for x
- `ylab`: Label for y
- `main`: Title for plot.
- `facets`: Faceting formula to use.
- `geom`: The geometric object to use display the data.
- `stat`: The geometric object to use display the data.

**Value**
A 'Layer'.

**Author(s)**
Tengfei Yin

**Examples**
```
## load
set.seed(1)
N <- 100
require(ggbio)
require(GenomicRanges)
## simul
## ======================================================================
## simmulated GRanges
## ======================================================================
gr <- GRanges(seqnames =
  sample(c("chr1", "chr2", "chr3"),
  size = N, replace = TRUE),
```
IRanges(
    start = sample(1:300, size = N, replace = TRUE),
    width = sample(70:75, size = N, replace = TRUE),
    strand = sample(c("+", "-", "*"), size = N,
    replace = TRUE),
    value = rnorm(N, 10, 3), score = rnorm(N, 100, 30),
    sample = sample(c("Normal", "Tumor"),
    size = N, replace = TRUE),
    pair = sample(letters, size = N,
    replace = TRUE))

gr <- c(gr[seqnames(gr) == "chr1"])[sample(1:10, size = 1e4, replace = TRUE)], gr)

## default
ggplot(gr) + stat_table()

## double
ggplot(gr) + stat_table(geom = "segment", aes(y = ..score.., color = ..score..))

## single
ggplot(gr) + stat_table(aes(color = score))

---

theme

theme in ggbio

Description

Theme defined in ggbio for plot or tracks.

Usage

theme_null()
theme_noexpand()
theme_alignment(ylabel = FALSE, base_size = 12, base_family = "",
    axis = TRUE, border = TRUE, grid = TRUE)
theme_pack_panels(strip.bg = FALSE, strip.text.y = TRUE)
theme_clear(grid.y = FALSE, grid.x.minor = FALSE, grid.x.major = FALSE,
    panel.background.fill = "white", panel.border.color = NA,
    axis.ticks.x = FALSE, axis.ticks.y = TRUE, grid.color = "gray95",
    axis.line.color = "gray80")
theme_tracks_sunset(bg = "#fffedb", alpha = 1, ...)
theme_genome()

Arguments

alpha alpha blending from 0(transparent) to 1(solid).
axis logical value, show axis or not.
axis.line.color color for axis line.
axis.ticks.x show x ticks or not.
axis.ticks.y show y ticks or not.
base_family family for font.
base_size size for font.
bg background color for tracks.
border logical value, show border or not.
grid logical value, show background grid or not.
grid.color grid line color.
grid.x.major show x major grid line or not.
grid.x.minor show x minor grid line or not.
grid.y show y grid or not.
panel.background.fill panel background fill color.
panel.border.color panel border color.
strip.bg if strip background is removed.
strip.text.y if strip text is removed.
ylabel logical value. Show labels or not.
... passed to theme_clear.

Details
Themes specially designed for tracks, are named following naming schema theme_tracks_ *

Value
Return a theme.

Author(s)
Tengfei Yin

Examples
```r
## load
library(ggbio)
p <- qplot(data = mtcars, x = mpg, y = wt, facets = cyl ~ .)
p + theme_null()
p + theme_clear()
p + theme_pack_panels()
p + theme_alignment()
p1 <- qplot(data = mtcars, x = mpg, y = wt)
tracks(p1 = p, p2 = p1)
tracks(p1 = p, p2 = p1) + theme_tracks_sunset()
```

Tracked

Description
Create a tracked object, designed for tracks function.

Usage
```r
Tracked(mutable = TRUE, fixed = FALSE, labeled = TRUE,
        hasAxis = FALSE, bgColor = "white", height = unit(1, "null"))
```
tracks

Arguments

mutable: logical value, default TRUE. To control whether a track is updatable by applying + on it.

fixed: logical value, default FALSE. To control whether the scale response to a xlim change or not.

labeled: logical value, default TRUE. To control whether to label it all not.

hasAxis: logical value, default FALSE. To control whether to show axis for that track or not.

bgColor: character to control background color of a track.

height: unit, to control track height.

Value

a Tracked object.

Author(s)

Tengfei Yin

tracks

Tracks for genomic graphics

Description

tracks is a convenient constructor for bindind graphics as trakcs. You don’t have to worry about adjusting different graphics, tracks did that for you. It’s NOT just limited to bind genomic tracks, you can use this function to bind any tracks with the same defination of x axis, for example, sets of time series plots you made.

Tracks view is most common way to viewing genome features and annotation data and widely used by most genome browsers. Our assumption is that, most graphics you made with ggbio or by yourself using ggplot2, are almost always sitting on the genomic coordinates or the same x axis. And to compare annotation information along with genome features, we need to align those plots on exactly the same x axis in order to form your hypothesis. This function leaves you the flexibility to construct each tracks separately with worrying your alignments later.

Usage

tracks(..., heights, xlim, xlab = NULL, main = NULL, title = NULL, theme = NULL, track.plot.color = NULL, track.bg.color = NULL, main.height = unit(1.5, "lines"), scale.height = unit(1, "lines"), xlab.height = unit(1.5, "lines"), padding = unit(-1, "lines"), label.bg.color = "white", label.bg.fill = "gray80", label.text.color = "black", label.text.cex = 1, label.text.angle = 90, label.width = unit(2.5, "lines"))
Arguments

... plots of class ggplot, generated from ggplot2 or ggbio.
heights numeric vector of the same length of passed graphic object to indicate the ratio of each track.
xlim limits on x. could be IRanges, GRanges, numeric value
xlab label for x axis.
main title for the tracks.
title title for the tracks, alias like main.
theme theme object used for building tracks, this will set to default, which could be reseted later.
track.plot.color Vector of characters of length 1 or the same length of passed plots, background color for each track, default is white.
track.bg.color background color for the whole tracks.
main.height unit. Height to control the title track height.
scale.height unit. Height to control the scale track height.
xlab.height unit. Height to control the xlab track height.
padding single numeric value or unit, if numeric value, the unit would be "lines" by default.
label.bg.color track labeling background rectangle border color.
label.bg.fill track labeling background fill color.
label.text.color track labeling text color.
label.text.cex track labeling text size.
label.text.angle angle to rotate the track labels.
label.width track labeling size.

Details

tracks did following modification for passed plots.

• remove x-axis, ticks, xlab and tile for each track and add scales at bottom. We suppose a new xlab and title would be provided by the tracks function for the whole tracks, but we still keep individual’s y axis.
• align x-scale limits to make sure every plots sitting on exactly the same x scale.
• squeezing plots together to some extent.
• labeling tracks if names are provided, please check utilities section about labeled method.
• return a track object. This would allow many features introduced in this manual.

Value

A Tracks object.
tracks

Track class

constructor tracks will return a Tracks object, which has following slots.

grobs a ggplotGrobList object contains a list of ggplot object, which is our passed graphics.
backup a backup of all the slots for holding the original tracks, so users could edit it and reset it back at any time later, and backup method will reset the backpped copy.
ylim y limits for each plot.
labeled vector of logical value indicates whether a track is labeled or not, for labeled attributes please check utilities section.
mutable vector of logical value indicates whether a track is mutable for theme editing or not, for mutable attributes please check utilities section.
hasAxis vector of logical value indicates whether a track has axis or not, for hasAxis attributes please check utilities section.
heights, xlim, xlab, main, title, theme, fixed, track.plot.color, track.bg.color, main.height, scale.height, xlab.height, padding, label.bg.color, label.bg.fill, label.text.color, label.text.cex, label.text.angle, label.width those slots are described in arguments section for constructor.

Utilities

Please check examples for usage.

summary(object) summary information about tracks object.

fixed(x), fixed(x) <- value x is the ggplot object, this controls if a track has a fixed x scale or not, if the fixed attributes is TRUE, then when you pass this plot to a tracks, this plot won’t be re-aligned with other tracks and will keep the original x-axis, this allow you to pass some plot like ideogram. fixed function will return a logical value
labeled(x), labeled(x) <- value x is the ggplot object, if you pass named graphics into tracks, it will create the labels on the left for you. Several ways supported to name it. You can pass a list of graphics with names. Or you can use tracks('name1' = p1, 'name 2' = p2, ...) with quotes for complicated words or simply tracks(part1 = p1, part = p2, ...).
mutable(x), mutable(x) <- value x is the ggplot object, this controls whether a plot in the tracks mutable to theme changing or not, when you use + method for Tracks object, add-on edit will only be applied to the the mutable plots.
bgColor(x), bgColor(x) <- value x is the ggplot object, this change the background color for single plot shown in the tracks.

xlim(x), xlim(x) <- value when x is the numeric value, it calls ggplot2::coord_cartesian(xlim = ...) method, we doesn’t use ggplot2::xlim() for the reason it will cut data outside the range, and we believe the best behavior would be zoom-in/out like most browser. when x is IRanges, GRanges, it get the range and passed to ggplot2::coord_cartesian function.

when x is Tracks object, xlim(x) will return x limits for that tracks. xlim(x) <- value replace method only works for Tracks object. value could be numeric, IRanges, GRanges object. This will change the x limits associated with tracks.

+ xlim(obj):obj is the numeric range, or IRanges, GRanges object.
+ coord_cartesian(): please read manual in ggplot2, this controls both xlim an ylim, only accept numerical range.

+ The most nice features about Tracks object is the one inherited from ggplot2’s components additive features, with + method you can use any theme object and utilities in ggplot2 package, to add them on a Tracks object, for example, if x is our Tracks object, x + theme would apply theme to any plots in the tracks except those are immutable.
Backup and reset

reset(obj) obj is the Tracks object, this reset the tracks back to original or backuped version.
backup(obj) obj is the Tracks object, this clear previous backup and use current setting for a new backup.

Author(s)
Tengfei Yin

See Also
align.plots

Examples

```r
## make a simulated time series data set
df1 <- data.frame(time = 1:100, score = sin((1:100)/20)*10)
p1 <- qplot(data = df1, x = time, y = score, geom = "line")
df2 <- data.frame(time = 30:120, score = sin((30:120)/20)*10, value = rnorm(120-30 + 1))
p2 <- ggplot(data = df2, aes(x = time, y = score)) + geom_line() + geom_point(size = 4, aes(color = value))
## check p2
p1
## check p2
p2

## binding
tracks(p1, p2)

## or
tks <- tracks(p1, p2)
tks

## combine
c(tks, tks)
tks + tks
cbind(tks, tks)
rbind(tks, tks) ## different wth c()!
library(grid)
x <- ggbio:::get_gtable(tks)
grid.draw(cbind(x, x))

## labeling: default labeling a named graphic
## simply pass a name with it
tracks(time1 = p1, time2 = p2)
## or pass a named list with it
lst <- list(time1 = p1, time2 = p2)
tracks(lst)

## more complicated case please use quotes
tracks(time1 = p1, "second time" = p2)

## set heights
tracks(time1 = p1, time2 = p2, heights = c(1, 3))
```
## if you want to disable label arbitrarily
## default label is always TRUE
labeled(p2)
labeled(p2) <- FALSE
## set labeled to FALSE, remove label even the plot has a name
tracks(time1 = p1, time2 = p2)
labeled(p2) <- TRUE

## fix a plot, not synchronize with other plots
p3 <- p1
## default is always FALSE
fixed(p3)
## set to TRUE
fixed(p3) <- TRUE
fixed(p3)

tracks(time1 = p1, time2 = p2, "time3(fixed)" = p3)

fixed(p3) <- FALSE
## otherwise you could run

## control axis
hasAxis(p1)
hasAxis(p1) <- TRUE
# ready for weird looking
tracks(time1 = p1, time2 = p2)
# set it back
hasAxis(p1) <- FALSE

## mutable
mutable(p1)
tracks(time1 = p1, time2 = p2) + theme_bw()
mutable(p1) <- FALSE
# mutable for "+" method
tracks(time1 = p1, time2 = p2) + theme_bw()
mutable(p1) <- TRUE

## bgColor
bgColor(p1)
tracks(time1 = p1, time2 = p2)
bgColor(p1) <- "brown"
# mutable for "+" method
tracks(time1 = p1, time2 = p2)
# set it back
bgColor(p1) <- "white"

## apply a theme to each track
tks <- tracks(time1 = p1, time2 = p2) + theme_bw()
tks
reset(tks)
## store it with tracks

tks <- tracks(time1 = p1, time2 = p2, theme = theme_bw())
tks

tks <- tks + theme_gray()
tks

## reset will be introduced later
reset(tks)

## apply a pre-defined theme for tracks!
tracks(time1 = p1, time2 = p2) + theme_tracks_sunset()

## change limits
tracks(time1 = p1, time2 = p2) + xlim(c(1, 40))
tracks(time1 = p1, time2 = p2) + xlim(1, 40)
tracks(time1 = p1, time2 = p2) + coord_cartesian(xlim = c(1, 40))

# change y
tracks(time1 = p1, time2 = p2) + ylim(1, 40) + ylim(0, 10)

library(GenomicRanges)
gr <- GRanges("chr", IRanges(1, 40))
# GRanges
tracks(time1 = p1, time2 = p2) + xlim(gr)
# IRanges
tracks(time1 = p1, time2 = p2) + xlim(ranges(gr))
tks <- tracks(time1 = p1, time2 = p2)

xlim(tks) <- c(1, 35)
xlim(tks) <- gr
xlim(tks) <- ranges(gr)

## xlab, title
tracks(time1 = p1, time2 = p2, xlab = "time")
tracks(time1 = p1, time2 = p2, main = "title")
tracks(time1 = p1, time2 = p2, title = "title")
tracks(time1 = p1, time2 = p2, xlab = "time", title = "title") + theme_tracks_sunset()

## backup and restore

tks <- tracks(time1 = p1, time2 = p2)
tks

tks <- tks + xlim(1, 40)
tks
reset(tks)
tks <- tks + xlim(1, 40)
tks
reset(tks)
tks <- backup(tks)
tks <- tks + theme_bw()
tks
reset(tks)

## padding (need to be fixed for more delicate control)
tracks(time1 = p1, time2 = p2, padding = 2)

## track color
tracks(time1 = p1, time2 = p2, track.bg.color = "yellow")
tracks(time1 = p1, time2 = p2, track.plot.color = c("yellow", "brown"))
Simple navigation for ggbio object.

Description
A set of simple navigation API apply to ggbio object, let you move along the genome and zoom in/out.

Usage
```
zoom(fac = 1/2)
zoom_in(fac = 1/2)
zoom_out(fac = 2)
nextView(unit = c("view", "gene", "exon", "utr"))
prevView(unit = c("view", "gene", "exon", "utr"))
```

Arguments
- **fac**: numeric value to indicate zoom factor, multiple of current view width. If it’s smaller than 1, then it’s zoom-in operation; if it’s bigger than 1, then it’s zoom-out operation.
- **unit**: only support 'view' unit now.

Details
- `zoom_in` and `zoom_out` are just simple wrapper around `zoom` function.
- For more convenient, gene features based jumpting we will support it in the future.

Value
A special class of navigation.

Author(s)
Tengfei Yin
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