

Package ‘TnT’

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Title Interactive Visualization for Genomic Features

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Description A R interface to the TnT javascript library (<https://github.com/tntvis>) to provide interactive and flexible visualization of track-based genomic data.

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| | |
|-----------------|------------------------|
| composite-track | <i>Composite Track</i> |
|-----------------|------------------------|

Description

Two or more arbitrary tracks can be used to create a composite track, by which different features can be shown in the same track.

Usage

```
## S4 method for signature 'TnTTrack,TnTTrack'
merge(x, y, ...)
```

```
## S4 method for signature 'TnTTrack,missing'
merge(x, y, ...)
```

Arguments

`x, y, ...` Track constructed with [track-constructors](#) or composite track.

Value

Returns a "CompositeTrack" object.

See Also

<http://tnt.marlin.pub/articles/examples/track-CompositeTrack.html>

Examples

```
gr <- GRanges("chr1", IRanges(c(11000, 20000, 60000), width = 2000))
gpos <- GRanges("chr1", IRanges(c(12000, 21000, 61000), width = 1), value = c(1, 2, 3))
btrack <- BlockTrack(gr, label = "Block Track", tooltip = as.data.frame(gr), color = "lightblue4")
ptrack <- PinTrack(gpos, label = "Pin Track", tooltip = as.data.frame(gpos), background = "beige")

ctrack <- merge(btrack, ptrack)
## Not run:
TnTBoard(ctrack)

## End(Not run)
```

knit_print.TnTBoard *Printing TnTBoard in Rmarkdown*

Description

S3 method to automatically render a TnTBoard with knitr.

Usage

```
## S3 method for class 'TnTBoard'
knit_print(x, ..., options = NULL)
```

Arguments

x A TnTBoard or TnTGenome object.
..., options Passed to `htmlwidget::knit_print.htmlwidget`.

Value

`htmlwidget::knit_print.htmlwidget` invisibly returns a character vector with "browsable_html" S3 class.

References

[knit_print](#)

Examples

```
track <- BlockTrack(GRanges("chr12", IRanges(c(100, 400, 700), width = 100)),
                    color = c("green", "red", "blue"))
tntboard <- TnTGenome(track)
## Not run:
knitr::knit_print(tntboard)

## End(Not run)
```

| | |
|--------|--|
| mapcol | <i>Scale Qualitative Values to Color</i> |
|--------|--|

Description

A simple util function that scales a factor to color based on the palette function.

Usage

```
mapcol(value, palette.fun = grDevices::rainbow, ...)
```

Arguments

| | |
|-------------|--|
| value | A factor or character vector that may have n unique values. |
| palette.fun | The palette function to generate colors. For example, terrain.colors . |
| ... | Extra arguments passed to the palette function. |

Value

A character vector as colors, with the same length of value. Same values in value will have the same color.

Examples

```
mapcol(iris$Species)
```

| | |
|------------------------|--------------------------|
| range, TnTBoard-method | <i>Range of TnTBoard</i> |
|------------------------|--------------------------|

Description

Get combined range of all tracks in a TnTBoard, used internally.

Usage

```
## S4 method for signature 'TnTBoard'
range(x, ..., with.revmap = FALSE, ignore.strand = FALSE, na.rm = FALSE)
```

Arguments

| | |
|--|---|
| x | TnTBoard. |
| ..., with.revmap, ignore.strand, na.rm | Passed to range, GenomicRanges-method . |

Value

GRanges.

Value

Return NULL.

Examples

```
data <- GRanges("chr2", IRanges(c(6,9,42), width = 1),
                value = c(0.3, 0.5, 0.9))
track <- PinTrack(data, label = NULL, background = "green")
genome <- TnTGenome(list(track))
destfile <- tempfile(fileext = ".html")
destfile
saveTnT(genome, destfile)
## Not run:
utils::browseURL(destfile)

## End(Not run)
```

seqinfo

Seqinfo of TnTTrack and TnTBoard

Description

Seqinfo of TnTTrack and TnTBoard

Usage

```
## S4 replacement method for signature 'RangeBasedTrack'
seqinfo(x, new2old = NULL, pruning.mode = c("error", "coarse", "fine", "tidy")) <- value

## S4 method for signature 'RangeBasedTrack'
seqinfo(x)

## S4 method for signature 'RangeBasedTrack'
seqlevelsInUse(x)

## S4 method for signature 'TnTBoard'
seqinfo(x)

## S4 method for signature 'CompositeTrack'
seqinfo(x)

## S4 replacement method for signature 'CompositeTrack'
seqinfo(x, new2old = NULL, pruning.mode = c("error", "coarse", "fine", "tidy")) <- value

## S4 method for signature 'CompositeTrack'
seqlevelsInUse(x)
```

Arguments

x A TnTTrack or TnTBoard object.
new2old, pruning.mode, value
 Passed to seqinfo method for GenomicRanges.

Value

seqinfo returns a SeqInfo object.

Examples

```
btrack1 <- BlockTrack(GRanges("chr1", IRanges(1, 123)))
btrack2 <- BlockTrack(GRanges("chr2", IRanges(3, 599)))
ctrack <- merge(btrack1, btrack2)
board <- TnTBoard(list(btrack1, btrack2))

seqinfo(btrack1)
seqinfo(btrack2)
seqinfo(ctrack)
seqinfo(board)
```

strandlabel

Display Labels with Strand

Description

A simple util function that used internally to generate display labels of GeneTrack and TxTrack.

Usage

```
strandlabel(labels, strands)
```

Arguments

| | |
|---------|--|
| labels | Character vector, names of each feature. |
| strands | Factor or character vector with the same length of labels, can be "+", "-" or "*". |

Value

A character vector that combines the labels with strand information.

Examples

```
strandlabel(c("gene1", "gene2", "gene3"), c("+", "-", "*"))
```

Description

Output and render functions for using TnT within Shiny applications and interactive Rmd documents.

Usage

```
TnTOutput(outputId, width = "100%", height = "auto")
renderTnT(expr, env = parent.frame(), quoted = FALSE)
```

Arguments

| | |
|---------------|--|
| outputId | output variable to read from |
| width, height | Must be a valid CSS unit (like '100%', '400px', 'auto') or a number, which will be coerced to a string and have 'px' appended. |
| expr | An expression that generates a TnTBoard/TnTGenome object. |
| env | The environment in which to evaluate expr. |
| quoted | Is expr a quoted expression (with quote())? This is useful if you want to save an expression in a variable. |

Value

An output or render function that enables the use of the converted htmlwidget within Shiny applications.

Examples

```
library(shiny)

ui <- fluidPage(fluidRow(
  column(width = 2, {
    "A Simple Example Here"
  }),
  column(width = 10, {
    TnTOutput("out")
  })
))
server <- function (input, output) {
  re.btrack <- reactive({
    gr <- GRanges("chr12", IRanges(100, 1000))
    BlockTrack(gr)
  })
  output$out <- renderTnT({
    TnTBoard(re.btrack())
  })
}
## Not run:
shinyApp(ui = ui, server = server)
```



```
## End(Not run)
```

tntboard

TnTBoard

Description

A TnTBoard or TnTGenome object stores a list of tracks and can be automatically shown in an interactive R session or in rmarkdown output.

Usage

```
TnTBoard(
  tracklist,
  view.range = GRanges(),
  coord.range = IRanges(),
  zoom.allow = IRanges(),
  allow.drag = TRUE,
  use.tnt.genome = FALSE
)
```

```
TnTGenome(
  tracklist,
  view.range = GRanges(),
  coord.range = IRanges(),
  zoom.allow = IRanges(),
  allow.drag = TRUE
)
```

Arguments

| | |
|----------------|--|
| tracklist | One track or a list of tracks to view. |
| view.range | Length-one GRanges object, sets the initial view range. |
| coord.range | Length-one IRanges object or length-two numeric vector, sets the coordinate limit of the board (i.e. minimum/maximum possible coordinate). |
| zoom.allow | Length-one IRanges object or length-two numeric vector, sets the minimum and maximum extent of the board (i.e. the limit when zooming in and zooming out). |
| allow.drag | Logical, whether drag should be allowed? Default TRUE. |
| use.tnt.genome | Logical, whether to add axis and location. ‘TnTGenome(...)’ is essentially a wrapper to ‘TnTBoard(..., use.tnt.genome = TRUE)’. |

Value

Returns a TnTBoard or TnTGenome object which has printing method to be rendered as a html-widget.

Examples

```
track <- BlockTrack(GRanges("chr1", IRanges(start = c(100, 300, 500), width = c(10, 100, 200))))
## Not run:
TnTGenome(track)

## End(Not run)
```

tooltip

Access Track Tooltips

Description

Access Track Tooltips

Usage

```
tooltip(x)

tooltip(x) <- value

## S4 method for signature 'TrackData'
tooltip(x)

## S4 method for signature 'TnTTrack'
tooltip(x)

## S4 replacement method for signature 'TrackData,data.frame'
tooltip(x) <- value

## S4 replacement method for signature 'TnTTrack,data.frame'
tooltip(x) <- value
```

Arguments

x A TnTTrack object.

value A data frame to replace, its row number should equal to length of data.

Value

tooltip returns a data frame.

Examples

```
gr <- GRanges("chr12", IRanges(c(6, 69), c(42, 135)), Name = c("my range 1", "my range 2"))
track <- BlockTrack(gr)
tooltip(track)
tooltip(track)$width <- width(gr)
tooltip(track)
```

Description

Track Constructors

Usage

```
BlockTrack(  
  range,  
  label = deparse(substitute(range)),  
  tooltip = mcols(range),  
  color = "blue",  
  background = NULL,  
  height = 30  
)
```

```
VlineTrack(  
  pos,  
  label = deparse(substitute(pos)),  
  tooltip = mcols(pos),  
  color = "green",  
  background = NULL,  
  height = 40  
)
```

```
PinTrack(  
  pos,  
  value = mcols(pos)$value,  
  domain = numeric(),  
  label = deparse(substitute(pos)),  
  tooltip = mcols(pos),  
  color = "red",  
  background = NULL,  
  height = 40  
)
```

```
LineTrack(  
  pos,  
  value = mcols(pos)$value,  
  domain = numeric(),  
  label = deparse(substitute(pos)),  
  color = "yellow",  
  background = NULL,  
  height = 70  
)
```

```
AreaTrack(  
  pos,  
  value = mcols(pos)$value,
```

```
    domain = numeric(),
    label = deparse(substitute(pos)),
    color = "pink",
    background = NULL,
    height = 70
)

GeneTrackFromTxDb(
  txdb,
  seqlevel = seqlevels(txdb),
  label = deparse(substitute(txdb)),
  color = "black",
  background = NULL,
  height = 100
)

FeatureTrack(
  range,
  label = deparse(substitute(range)),
  tooltip = mcols(range),
  names = base::names(range),
  color = "black",
  background = NULL,
  height = 200
)

GroupFeatureTrack(
  grl,
  label = deparse(substitute(grl)),
  tooltip = mcols(grl),
  names = base::names(grl),
  color = "black",
  background = NULL,
  height = 200
)

TxTrackFromTxDb(
  txdb,
  seqlevel = seqlevels(txdb),
  label = deparse(substitute(txdb)),
  color = "red",
  background = NULL,
  height = 300
)

TxTrackFromGRanges(
  gr,
  label = deparse(substitute(gr)),
  color = "red",
  background = NULL,
  height = 300
)
```

Arguments

| | |
|----------------|---|
| range, pos | GRanges or IRanges object. For pos, all the width should be one. |
| label | Character, shown as label of the track on the left, could be NULL. |
| tooltip | A data frame that is parallel to range or pos. |
| color | Character vector or integer vector that sets the color of the features. It can be color names, hexadecimal string or positive integer <i>i</i> meaning <code>palette()[i]</code> , as described in <code>col2rgb</code> . It can be parallel to the data (i.e. have the same length) thus sets colors of each individual feature. |
| background | Length-one character vector that sets background of the track, could be NULL. |
| height | Length-one numeric vector that sets height of the track. |
| value, domain | 'value' is a numeric vector that is parallel to pos, which indicates height of features at each position for PinTrack, LineTrack and AreaTrack. 'domain' is a length-two numeric vector which sets the lower and upper limit of 'value' (i.e. the limit on y-axis). |
| txdb, seqlevel | The TxDb and seqlevel to extract gene or transcript from. |
| names | Character vector with the same length of data, which is used to generate display labels shown together with features when zooming in. |
| gr1 | For 'GroupFeatureTrack' function, a GRangesList object that represents grouped ranges as data source. It is assumed that ranges in each group are on the same strand and do not overlap. |
| gr | For 'TxTrackFromGRanges' function, a GRanges object that represents exons and cds as data source, and will be rendered as transcripts. Two meta-columns ("type", "tx_id") are required, "type" can be "exon" or "cds" by which ranges of "cds" will be filled with color, "tx_id" indicates the grouping. |

Value

Returns an object that extends "TnTTrack" class.

See Also

You can find various examples at <http://tnt.marlin.pub/articles/examples/>, also see `composite-track` on how to create a composite track.

Examples

```
BlockTrack(range = GRanges("chr1", IRanges(199, 4000)),
           color = "green", background = "red", height = 100)
```

trackdata

Access Track Data

Description

Access and modify the track data. `x$name` and `x$name <- value` are just shortcuts for `trackData(x)$name` and `trackData(x)$name <- value`, respectively.

Usage

```

trackData(x)

trackData(x) <- value

## S4 method for signature 'TnTTrack'
x$name

## S4 replacement method for signature 'TnTTrack'
x$name <- value

```

Arguments

| | |
|-------|--|
| x | A TnTTrack object. |
| value | Replaced value. |
| name | Passed to the inner method for track data. |

Value

trackData on all track types except "CompositeTrack" returns an object that inherits GRanges class, which means they should behave like a GRanges. While trackData on "CompositeTrack" returns a list of tracks.

Examples

```

track <- BlockTrack(GRanges("chr1", IRanges(6, 54)))
class(trackData(track)) # track data of block track is an object that inherits GRanges.
#trackData(track)
ctrack <- merge(track, track)
class(trackData(ctrack)) # track data of composite track is a list of tracks
#trackData(ctrack)

```

tracklist

Track List in TnTBoard

Description

The tracks of a TnTBoard are stored as a list which can be accessed or modified with these functions.

Usage

```

tracklist(tntboard)

tracklist(tntboard) <- value

```

Arguments

| | |
|----------|--------------------------------|
| tntboard | A TnTBoard or TnTGenome object |
| value | A list of tracks |

Value

tracklist returns a list of tracks.

Examples

```
bt <- BlockTrack(GRanges("chr21", IRanges(100, 1200)))
li.tracks <- list(bt, bt)
board <- TnTBoard(li.tracks)
tracklist(board)
## Not run:
show(board)

## End(Not run)
tracklist(board) <- list(bt)
## Not run:
show(board)

## End(Not run)
```

trackSpec

Track Spec

Description

Height, background and label are common options of all tracks, use these functions to get and set them.

Usage

```
trackSpec(track, which = c("background", "height", "label"))

trackSpec(track, which = c("background", "height", "label")) <- value
```

Arguments

| | |
|-------|--|
| track | A TnTTrack object. |
| which | Character vector, can be "background", "height" or "label". |
| value | Value to set: background should be character, height should be numeric, label should be character. If length of which is bigger than one, value should be a list with the same length. |

Value

For trackSpec, if length of which equals to one, return a scalar character or numeric, if length of which is bigger than one, return as a list.

Examples

```

track <- BlockTrack(GRanges("chr13", IRanges(6, 9)))
trackSpec(track, "background")
trackSpec(track, c("height", "label"))
trackSpec(track, c("height", "label")) <- list(100, "my range")
trackSpec(track, "background") <- "green"
trackSpec(track)

```

trackWidget

Convert a TnTBoard to htmlwidget

Description

This function is only provided for users who are familiar with the concept of [htmlwidgets-package](#). It explicitly converts a TnTBoard or TnTGenome object to a htmlwidget object. You do not need it in most cases.

Usage

```
trackWidget(tntdef, elementId = NULL)
```

Arguments

| | |
|-----------|--|
| tntdef | A TnTBoard/TnTGenome object or a htmlwidget object. If it is a htmlwidget object, the function will return it as is. |
| elementId | An id for the htmlwidget (random by default). |

Value

The function returns a htmlwidget object.

Examples

```

b <- TnTBoard(BlockTrack(GRanges("chr12", IRanges(1, 123))))
widget <- trackWidget(b)
class(widget)
identical(widget, trackWidget(widget))

```


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