

Package ‘TnT’

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Title Interactive Visualization for Genomic Features

Version 1.2.0

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.

| | |
|----------------|------------------------|
| range-TnTTrack | <i>Range of Tracks</i> |
|----------------|------------------------|

Description

Range of Tracks

Usage

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

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

Arguments

x A TnTTrack object.
 ..., with.revmap, ignore.strand, na.rm
 Passed to [range, GenomicRanges-method](#).

Value

Returns a GRanges object.

| | |
|---------|--|
| saveTnT | <i>Save a TnTBoard to an HTML file</i> |
|---------|--|

Description

A simple wrapper of [saveWidget](#), which saves a TnTBoard/TnTGenome object to an HTML file (e.g. for sharing with others).

Usage

```
saveTnT(tntdef, file, selfcontained = TRUE, libdir = NULL,
        background = "white", knitrOptions = list())
```

Arguments

tntdef A TnTBoard/TnTGenome object to save.
 file, selfcontained, libdir, background, knitrOptions
 Passed to [saveWidget](#).

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

```
if (interactive() && require(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())
    })
  }
  shinyApp(ui = ui, server = server)
}
```

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 | <i>Access Track Tooltips</i> |
|---------|------------------------------|

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)
```

| | |
|--------------------|---------------------------|
| track-constructors | <i>Track Constructors</i> |
|--------------------|---------------------------|

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(gr1, label = deparse(substitute(gr1)),
  tooltip = mcols(gr1), names = base::names(gr1), 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 <code>i</code> 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)))
trackData(track) # track data of block track is an object that inherits GRanges.
ctrack <- merge(track, track)
trackData(ctrack) # track data of composite track is a list of tracks
```

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 | <i>Convert a TnTBoard to htmlwidget</i> |
|-------------|---|

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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