timeViz: Timeline Visualization User Guide

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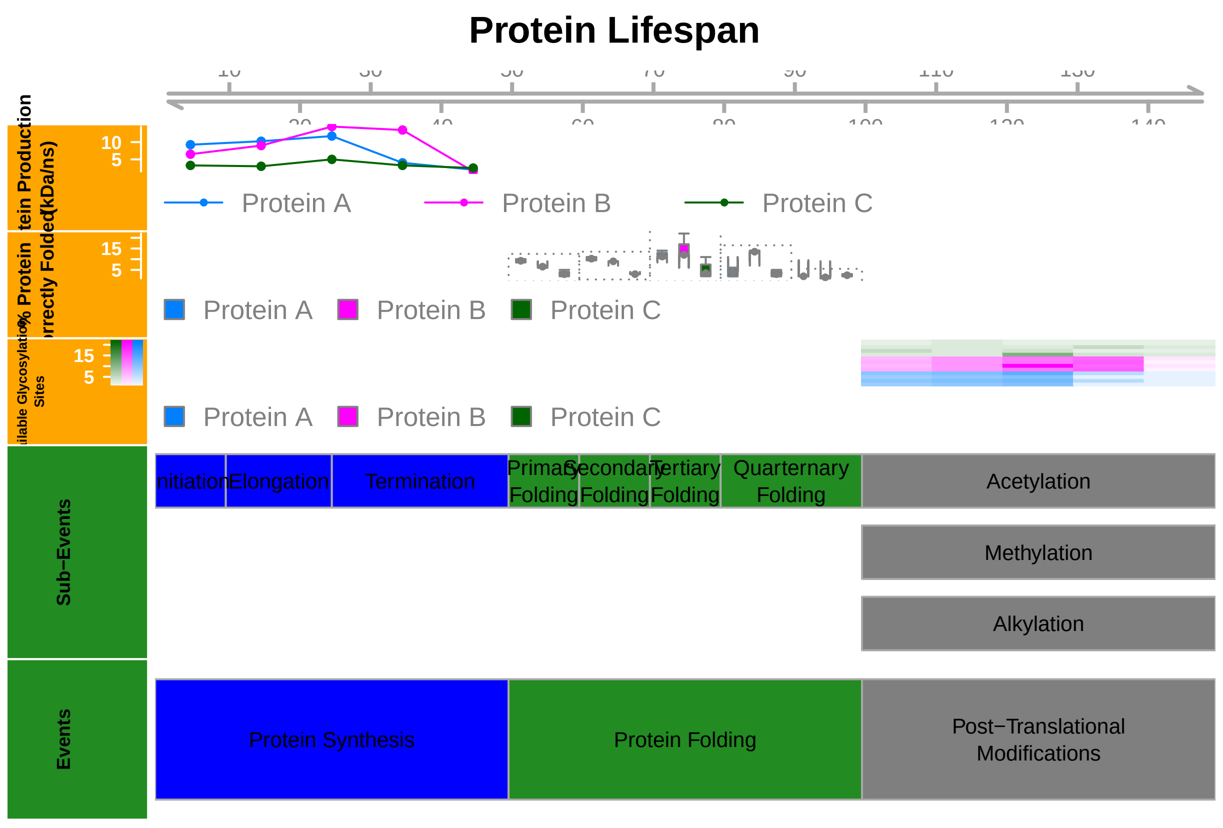
timeViz

timeViz is an R-based software derived from a popular track-based genomic visualization package called Gviz (Hahne & Ivanek, 2016).

This powerful tool will allow users to supply global configuration options and data to plot annotation or data tracks above or below one or more timelines. The user can control the labels, coloring, grouping, shapes, and sizes for several items in each of these tracks.

The following user guide includes basic features of the timeViz tool, example visualizations, and corresponding code.

Visualization Plot: Example 1

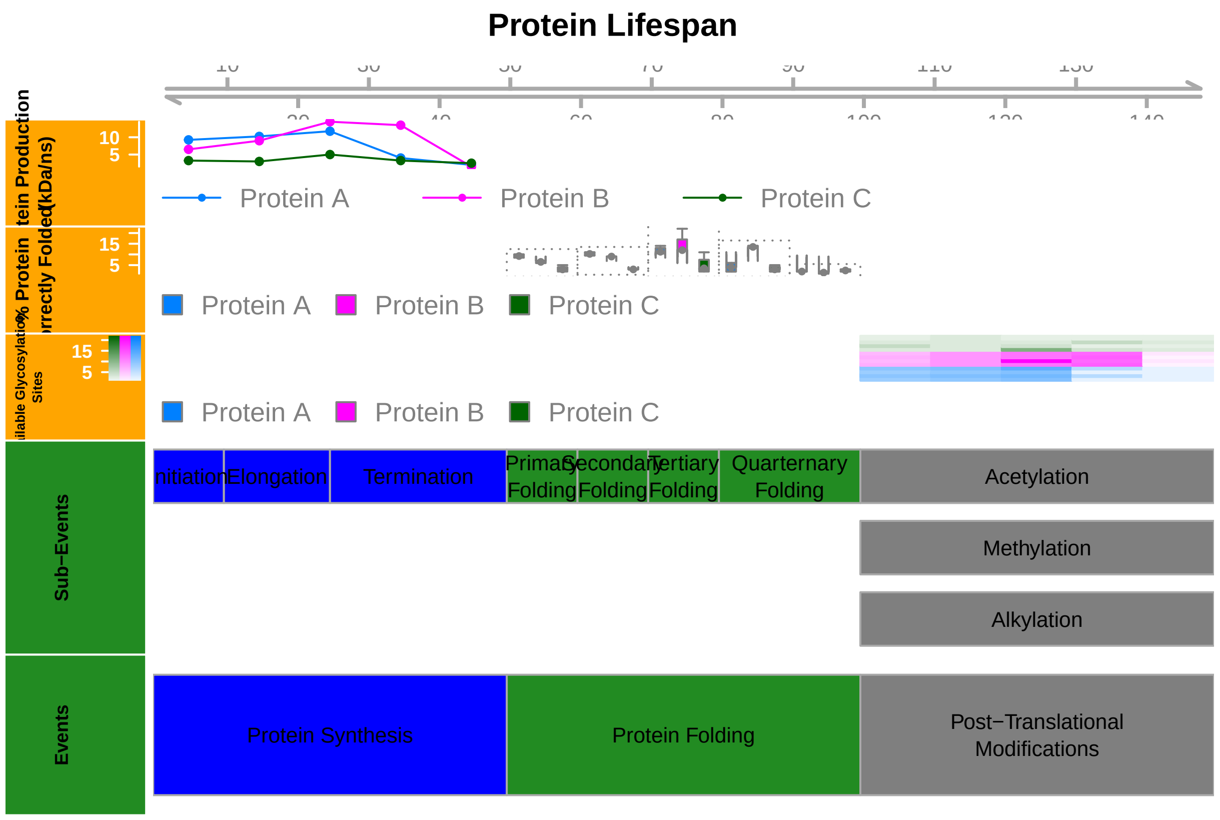


Visualization Code: Example 1

```r
## import XLSX sheet 1 (configuration)
config = read.xlsx("TimevizConfig.xlsx", sheet = "Configuration")

## parse out.file =
## config$Value[config$Variable.Name=='Output PDF']
out.height = as.numeric(config$Value[config$Variable.Name ==
    "Output Height"])
out.width = as.numeric(config$Value[config$Variable.Name ==
    "Output Width"])
main = config$Value[config$Variable.Name == "Main Title"]
main.size = as.numeric(config$Value[config$Variable.Name ==
    "Main Font Size"])
track.width = as.numeric(config$Value[config$Variable.Name ==
    "Track Box Width"])
from.to = as.numeric(unlist(str_split(config$Value[config$Variable.Name ==
    "From To"], ";")))
track.sheet.names = unlist(str_split(config$Value[config$Variable.Name ==
    "Track List"], ";"))
track.types = unlist(str_split(config$Value[config$Variable.Name ==
    "Track Type"], ";"))
track.heights = as.numeric(unlist(str_split(config$Value[config$Variable.Name ==
    "Track Heights"], ";")))
track.names = unlist(str_split(config$Value[config$Variable.Name ==
    "Track Names"], ";"))
track.box.colors = unlist(str_split(config$Value[config$Variable.Name ==
    "Track Box Color"], ";"))
track.bg.color = unlist(str_split(config$Value[config$Variable.Name ==
    "Track Background Color"], ";"))
track.label.colors = unlist(str_split(config$Value[config$Variable.Name ==
    "Track Label Color"], ";"))
track.label.sizes = as.numeric(unlist(str_split(config$Value[config$Variable.Name ==
    "Track Label Size"], ";")))
data.types = unlist(str_split(config$Value[config$Variable.Name ==
    "Data Type"], ";"))
data.groups = unlist(str_split(config$Value[config$Variable.Name ==
    "Data Groups"], ";"))
data.aggs = unlist(str_split(config$Value[config$Variable.Name ==
    "Data Aggregate"], ";"))

## initilize plot list object and other variables
plot.list = list()
data.count = 1

## for each track do
for (i in 1:length(track.types)) {
    track.type = track.types[i]
    track.sheet.name = track.sheet.names[i]
    track.name = gsub("\\\\n", "\n", track.names[i])
    track.box.color = track.box.colors[i]
    track.label.color = track.label.colors[i]
    track.label.size = track.label.sizes[i]
```

```r
## determine track type and append track to list
## object
if (track.type == "time") {

    ## initialize an axis track and add to plot list
    ## object
    plot.list[[i]] = GenomeAxisTrack(name = track.name,
        background.title = track.box.color, background.panel = track.bg.color,
        fontcolor.title = track.label.color, cex.title = track.label.size)

    ## Data track
} else if (track.type == "data") {
    data.type = data.types[data.count]
    data.group = unlist(str_split(data.groups[data.count],
        ","))
    data.agg = data.aggs[data.count]

    ## Import sheet to get label
    config.data = read.xlsx("TimevizConfig.xlsx",
        sheet = track.sheet.name)

    ## determine starts and stops
    starts = as.numeric(unlist(lapply(str_split(config.data$Time.Ranges,
        ";"), function(x) {
        x[1]
    })))
    ends = as.numeric(unlist(lapply(str_split(config.data$Time.Ranges,
        ";"), function(x) {
        x[2]
    })))

    ## pull in a dummy data-set from the examples in the
    ## user guide
    config.data.granges = GRanges(seqnames = "chrX",
        strand = rep("*", length(starts)), ranges = IRanges(start = starts,
            end = ends), mcols = config.data[,
            2:ncol(config.data)])

    ## Is there any grouping?

    if (any(nchar(data.group) == 0)) {
        ## plot a data track without grouping
        dTrack <- DataTrack(config.data.granges,
            name = track.name, type = data.type,
            background.title = track.box.color,
            background.panel = track.bg.color,
            fontcolor.title = track.label.color,
            cex.title = track.label.size)

    } else {

        ## Aggregate data on the mean?
        if (data.agg == "NULL") {
            ## plot a data track with grouping no aggregate
            plot.list[[i]] = DataTrack(config.data.granges,
              name = track.name, groups = data.group,
              type = data.type, background.title = track.box.color,
              background.panel = track.bg.color,
              fontcolor.title = track.label.color,
              cex.title = track.label.size)
        } else {
            ## plot a data track with and aggregate
            plot.list[[i]] = DataTrack(config.data.granges,
              name = track.name, groups = data.group,
              type = data.type, aggregateGroups = TRUE,
              background.title = track.box.color,
              background.panel = track.bg.color,
              fontcolor.title = track.label.color,
              cex.title = track.label.size)
        }
    }

    ## advance counter
    data.count = data.count + 1

    ## annotation Track
} else if (track.type == "annotation") {

    ## Import sheet to get label
    config.annot = read.xlsx("TimevizConfig.xlsx",
        sheet = track.sheet.name)

    ## determine starts and stops
    starts = as.numeric(unlist(lapply(str_split(config.annot$Time.Ranges,
        ";"), function(x) {
        x[1]
    })))
    ends = as.numeric(unlist(lapply(str_split(config.annot$Time.Ranges,
        ";"), function(x) {
        x[2]
    })))

    ## get grouping factor
    group.factor = as.numeric(as.factor(config.annot$Annotation.Name))

    ## plot an annotation track plot annotation label
    ## above/below/on box,
    plot.list[[i]] = AnnotationTrack(start = starts,
        end = ends, chromosome = "chrX", strand = rep("*",
            length(starts)), id = gsub("\\\\n",
            "\n", config.annot$Annotation.Name),
        name = track.name, shape = "box", featureAnnotation = "id",
        group = group.factor, stacking = "squish",
        fontcolor.feature = config.annot$Annotation.Label.Color,
        cex.feature = config.annot$Annotation.Label.Size,
        fill = config.annot$Annotation.Color, background.title = track.box.color,
            background.panel = track.bg.color, fontcolor.title = track.label.color,
            cex.title = track.label.size)

    } else {
        ## invalid imput track type -- exit with non-zero
        ## status
        print(paste0("Please provide valid track type.
                     The given track type is not valid: ",
            track.type))
        quit(status = 3)  ## non 0 exit status
    }
}



## Uncomment code below to plot tracks
## plotTracks(plot.list, from = from.to[1], to =
## from.to[2],
## sizes=track.heights,main=main,cex.main=main.size,
## title.width=track.width)
```

Visualization Plot: Example 2



Visualization Code: Example 2

```r
## import XLSX sheet 1 (configuration)
## if(!file.exists(opt$inFile)){
## print(paste0('Error, ',opt$inFile,' does not
## exist')) q(status=1) }
infile.config = "20211031_TimeVizConfig.xlsx"
config = read.xlsx(infile.config, sheet = "Configuration")

## parse out.file =
## config$Value[config$Variable.Name=='Output PDF']
## out.file = opt$outFile if(file.exists(out.file)){
## print(paste0('Error, ',out.file,' already exists.
## Please use a different file name')) q(status=1) }
out.height = as.numeric(config$Value[config$Variable.Name ==
    "Output Height"])
out.width = as.numeric(config$Value[config$Variable.Name ==
    "Output Width"])
main.title = config$Value[config$Variable.Name == "Main Title"]
main.size = as.numeric(config$Value[config$Variable.Name ==
    "Main Font Size"])
track.width = as.numeric(config$Value[config$Variable.Name ==
    "Track Box Width"])
from.to = as.numeric(unlist(str_split(config$Value[config$Variable.Name ==
    "From To"], ";")))
track.sheet.names = unlist(str_split(config$Value[config$Variable.Name ==
    "Track List"], ";"))
track.types = unlist(str_split(config$Value[config$Variable.Name ==
    "Track Type"], ";"))
track.heights = as.numeric(unlist(str_split(config$Value[config$Variable.Name ==
    "Track Heights"], ";")))
track.names = unlist(str_split(config$Value[config$Variable.Name ==
    "Track Names"], ";"))
track.box.colors = unlist(str_split(config$Value[config$Variable.Name ==
    "Track Box Color"], ";"))
track.bg.color = unlist(str_split(config$Value[config$Variable.Name ==
    "Track Background Color"], ";"))
track.label.colors = unlist(str_split(config$Value[config$Variable.Name ==
    "Track Label Color"], ";"))
track.label.sizes = as.numeric(unlist(str_split(config$Value[config$Variable.Name ==
    "Track Label Size"], ";")))
data.types = unlist(str_split(config$Value[config$Variable.Name ==
    "Data Type"], ";"))
data.groups = unlist(str_split(config$Value[config$Variable.Name ==
    "Data Groups"], ";"))
data.aggs = unlist(str_split(config$Value[config$Variable.Name ==
    "Data Aggregate"], ";"))

## Additional config fields from Seth
main.trackLabelPos = config$Value[config$Variable.Name ==
    "Timeline Track Label Position"]
main.trackDirection = as.numeric(config$Value[config$Variable.Name ==
    "Track Directions"])
```

```r
main.trackTicks = as.numeric(config$Value[config$Variable.Name ==
    "Track Little Ticks"])
main.trackLineWidth = as.numeric(config$Value[config$Variable.Name ==
    "Track Line Width"])
main.trackShowID = as.numeric(config$Value[config$Variable.Name ==
    "Track Show ID"])
main.trackCexID = as.numeric(config$Value[config$Variable.Name ==
    "Track Cex ID"])
main.trackYAxisTicks = config$Value[config$Variable.Name ==
    "Track Y-axis Ticks"]
main.dataBoxRatio = as.numeric(config$Value[config$Variable.Name ==
    "Data Box Ratio"])
main.dataTrackGrid = as.numeric(config$Value[config$Variable.Name ==
    "Data Track Grid"])
main.dataLegend = as.numeric(config$Value[config$Variable.Name ==
    "Data Legend"])
main.trackShape = config$Value[config$Variable.Name ==
    "Shape Annotation"]
main.trackAnnotationGroup = config$Value[config$Variable.Name ==
    "Track Directions"]
main.groupLabel = config$Value[config$Variable.Name ==
    "Group Labels"]
main.trackLineType = as.numeric(config$Value[config$Variable.Name ==
    "Track Line Type"])
main.trackLineWidth = as.numeric(config$Value[config$Variable.Name ==
    "Track Line Width"])
main.showID = config$Value[config$Variable.Name ==
    "Show ID"]

## Validate config Verify all required track lists
## have the same number of elements Use
## track.sheet.names and data.types as the expected
## counts
lenTrackSheetNames = length(track.sheet.names)
lenTrackTypes = length(track.types)
lenTrackHeights = length(track.heights)
lenTrackNames = length(track.names)
lenTrackBoxColors = length(track.box.colors)
lenTrackBGColor = length(track.bg.color)
lenTrackLabelColors = length(track.label.colors)
lenTrackLabelSizes = length(track.label.sizes)
lenDataTypes = length(data.types)
lenDataGroups = length(data.groups)
lenDataAggs = length(data.aggs)
expectTrackLen = lenTrackSheetNames
if (lenTrackTypes != expectTrackLen) {
    cat("track.types should have ")
    cat(expectTrackLen, "values\n")
    q(status = 1)
}

## If any required tracks are of null length, throw
## error
```

```
####################### Prepare Desired Tracks

## initialize plot list object and other variables
plot.list = list()
data.count = 1

## for each track do
for (i in 1:length(track.types)) {
    track.type = track.types[i]
    track.sheet.name = track.sheet.names[i]
    track.name = gsub("\\\\n", "\n", track.names[i])
    track.box.color = track.box.colors[i]
    track.label.color = track.label.colors[i]
    track.label.size = track.label.sizes[i]

    ## determine track type and append track to list
    ## object
    if (track.type == "time") {

        ## initialize an axis track and add to plot list
        ## object wishlist: add ticksAt (minor/major ticks
        ## based on time units), figure out how to add the
        ## title - currently not working
        plot.list[[i]] = GenomeAxisTrack(name = track.name,
            background.title = track.box.color, background.panel = track.bg.color,
            fontcolor.title = track.label.color, cex.title = track.label.size)

        ## Data track
    } else if (track.type == "data") {
        data.type = data.types[data.count]
        data.group = unlist(str_split(data.groups[data.count],
            ","))
        data.agg = data.aggs[data.count]

        ## Import sheet to get label
        config.data = read.xlsx(infile.config, sheet = track.sheet.name)

        ## determine starts and stops
        starts = as.numeric(unlist(lapply(str_split(config.data$Time.Ranges,
            ";"), function(x) {
            x[1]
        })))
        ends = as.numeric(unlist(lapply(str_split(config.data$Time.Ranges,
            ";"), function(x) {
            x[2]
        })))

        ## pull in a dummy data-set from the examples in the
        ## user guide
        config.data.granges = GRanges(seqnames = "chrX",
            strand = rep("*", length(starts)), ranges = IRanges(start = starts,
                end = ends), mcols = config.data[,
                2:ncol(config.data)])
        ## Is there any grouping?  wishlist: Add group
        ## specific color coding, color coding for y-axis
        ## (default to white right now)
        if (any(nchar(data.group) == 0)) {
            ## plot a data track without grouping
            dTrack <- DataTrack(config.data.granges,
                name = track.name, type = data.type,
                background.title = track.box.color,
                background.panel = track.bg.color,
                fontcolor.title = track.label.color,
                cex.title = track.label.size)

        } else {

            ## Aggregate data on the mean?
            if (data.agg == "NULL") {
                ## plot a data track with grouping no aggregate
                plot.list[[i]] = DataTrack(config.data.granges,
                  name = track.name, groups = data.group,
                  type = data.type, aggregateGroups = FALSE,
                  background.title = track.box.color,
                  background.panel = track.bg.color,
                  fontcolor.title = track.label.color,
                  cex.title = track.label.size)
            } else {
                ## plot a data track with and aggregate
                plot.list[[i]] = DataTrack(config.data.granges,
                  name = track.name, groups = data.group,
                  type = data.type, aggregateGroups = TRUE,
                  background.title = track.box.color,
                  background.panel = track.bg.color,
                  fontcolor.title = track.label.color,
                  cex.title = track.label.size)
            }
        }

        ## advance counter
        data.count = data.count + 1

        ## annotation Track
    } else if (track.type == "annotation") {

        ## Import sheet to get label
        config.annot = read.xlsx(infile.config, sheet = track.sheet.name)

        ## determine starts and stops
        starts = as.numeric(unlist(lapply(str_split(config.annot$Time.Ranges,
            ";"), function(x) {
            x[1]
        })))
        ends = as.numeric(unlist(lapply(str_split(config.annot$Time.Ranges,
            ";"), function(x) {
            x[2]
```

```r
        })))

        ## get grouping factor
        group.factor = as.numeric(as.factor(config.annot$Annotation.Name))

        ## plot an annotation track wishlist: how to stagger
        ## annotations better? input for box shape, ellipse,
        ## arrows...etc, plot annotation label
        ## above/below/on box,
        plot.list[[i]] = AnnotationTrack(start = starts,
            end = ends, chromosome = "chrX", strand = rep("*",
                length(starts)), id = gsub("\\\\n",
                "\n", config.annot$Annotation.Name),
            name = track.name, shape = main.trackShape,
            featureAnnotation = "id", group = group.factor,
            stacking = "squish", fontcolor.feature = config.annot$Annotation.Label.Color,
            cex.feature = config.annot$Annotation.Label.Size,
            fill = config.annot$Annotation.Color, background.title = track.box.color,
            background.panel = track.bg.color, fontcolor.title = track.label.color,
            cex.title = track.label.size)

    } else {
        ## invalid input track type -- exit with non-zero
        ## status
        print(paste0("Please provide valid track type. The given track type is not valid: ",
            track.type))
        quit(status = 3)  ## non 0 exit status
    }
}

####################### Prepare Desired Tracks

# pdf( out.file, height=out.height,
# width=out.width)

## Uncomment code below to plot tracks plotTracks(
## plot.list, from = from.to[1], to = from.to[2],
## sizes=track.heights, main=main.title,
## cex.main=main.size, title.width=track.width)

# dev.off()
```

Time Track Parameters

Parameter	Description
out.file	File location and name for output PDF
out.height	Height of the PDF in inches. Default = 8
out.width	Height of the PDF in inches. Default = 8
main	Main title for the plot (top). Default = No Title
main.size	main title font size (expansion factor). Default = 1
track.width	An expansion factor for the width of the track boxes that hold the track labels. Default = 1
from.to	Start position of tracks to end position of tracks in time unit. Can be used to plot only a subset of the total data. Semicolon separated.. Default=min(data);max(data)
track.sheet.names	list of tracks (and the order of the tracks to plot top to bottom). Use the sheet names in this spreadsheet to list tracks. Semicolon separated.
track.types	list of track types - one for each track. Semicolon separated. Options include: data, annotation and time.
track.heights	heights for each track relative to the sum across tracks (ie: 1;3;3 = 1/7th of total height;3/7ths of total height;3/7ths of total height). Semicolon separated. Default = all track heights are equal
track.names	Names to be printed for each track. Semicolon separated. Defaults = sheet names in this spreadsheet
track.box.colors	The color of the box the track title is printed inside of. Semicolon separated. Default = grey
track.bg.color	The color of the track background.
track.label.colors	The color of the track label. Semicolon separated. Default = black
track.label.sizes	The font size (expansion factor) for each title label. Semicolon separated. Default = 1
data.types	For data tracks only, report the type of desired plot. Choose from the following: . Semicolon separated.
data.groups	For data tracks only, report the way samples should be grouped. Semicolon and comma separated. If empty, no grouping performed
data.aggs	Should the data be aggregated on the mean? (only if groups are supplied). Semicolon separated. Default = NULL

Data Track Parameters

Parameter	Description
aggregateGroups	Logical scalar. Aggregate the values within a sample group using the aggregation funnction specified in the aggregationparameter.
aggregation	Function or character scalar. Used to aggregate values in windows or for collapsing overlapping items. The function has to accept a numeric vector as a single input parameter and has to return a numeric scalar with the aggregated value. Alternatively, one of the predefined options mean, median sum, min, max or extreme can be supplied as a character scalar. Defaults to mean.
alpha.confint	Numeric scalar. The transparency for the confidence intervalls in confint-type plots.
amount	Numeric scalar. Amount of jittering in xy-type plots. See panel.xyplot for details.
baseline	Numeric scalar. Y-axis position of an optional baseline. This parameter has a special meaning for mountain-type and polygon-type plots, see the 'Details' section in DataTrack for more information.
box.legend	Logical scalar. Draw a box around a legend.
box.ratio	Numeric scalar. Parameter controlling the boxplot appearance. See panel.bwplot for details.
box.width	Numeric scalar. Parameter controlling the boxplot appearance. See panel.bwplot for details.
cex	Numeric scalar. The default pixel size for plotting symbols.
cex.legend	Numeric scalar. The size factor for the legend text.
cex.sampleNames	Numeric scalar. The size factor for the sample names text in heatmap or horizon plots. Defaults to an automatic setting.
coef	Numeric scalar. Parameter controlling the boxplot appearance. See panel.bwplot for details.
col	Character or integer vector. The color used for all line and symbol elements, unless there is a more specific control defined elsewhere. Unless groups are specified, only the first color in the vector is usually regarded.
col.baseline	Character scalar. Color for the optional baseline, defaults to the setting of col.
col.boxplotFrame	Character scalar. Line color of the frame around grouped boxplots.
col.confint	Character vector. Border colors for the confidence intervals for confint-type plots.
col.histogram	Character scalar. Line color in histogram-type plots.
col.horizon	The line color for the segments in the horizon-type plot. See horizonplot for details.
col.mountain	Character scalar. Line color in mountain-type and polygon-type plots, defaults to the setting of col.
col.sampleNames	Character or integer scalar. The color used for the sample names in heatmap plots.
collapse	Logical scalar. Collapse overlapping ranges and aggregate the underlying data.
degree	Numeric scalar. Parameter controlling the loess calculation for smooth and mountain-type plots. See panel.loess for details.

(continued)

Parameter	Description
do.out	Logical scalar. Parameter controlling the boxplot appearance. See panel.bwplot for details.
evaluation	Numeric scalar. Parameter controlling the loess calculation for smooth and mountain-type plots. See panel.loess for details.
factor	Numeric scalar. Factor to control amount of jittering in xy-type plots. See panel.xyplot for details.
family	Character scalar. Parameter controlling the loess calculation for smooth and mountain-type plots. See panel.loess for details.
fill.confint	Character vector. Fill colors for the confidence intervals for confint-type plots.
fill.histogram	Character scalar. Fill color in histogram-type plots, defaults to the setting of fill.
fill.horizon	The fill colors for the segments in the horizon-type plot. This should be a vector of length six, where the first three entries are the colors for positive changes, and the latter three entries are the colors for negative changes. Defaults to a red-blue color scheme. See horizonplot for details.
fill.mountain	Character vector of length 2. Fill color in mountain-type and polygon-type plots.
fontcolor.legend	Integer or character scalar. The font color for the legend text.
fontface.legend	Integer or character scalar. The font face for the legend text.
fontfamily.legend	Integer or character scalar. The font family for the legend text.
fontsize.legend	Numeric scalar. The pixel size for the legend text.
gradient	Character vector. The base colors for the gradient plotting type or the heatmap type with a single group. When plotting heatmaps with more than one group, the col parameter can be used to control the group color scheme, however the gradient will always be from white to 'col' and thus does not offer as much flexibility as this gradient parameter.
grid	Logical vector. Draw a line grid under the track content.
groups	Vector coercable to a factor. Optional sample grouping. See 'Details' section in DataTrack for further information.
horizon.origin	The baseline relative to which changes are indicated on the horizon-type plot. See horizonplot for details.
horizon.scale	The scale for each of the segments in the horizon-type plot. Defaults to 1/3 of the absolute data range. See horizonplot for details.
jitter.x	Logical scalar. Toggle on jittering on the x axis in xy-type plots. See panel.xyplot for details.
jitter.y	Logical scalar. Toggle off jittering on the y axis in xy-type plots. See panel.xyplot for details.
legend	Boolean triggering the addition of a legend to the track to indicate groups. This only has an effect if at least two groups are present.
levels.fos	Numeric scalar. Parameter controlling the boxplot appearance. See panel.bwplot for details.
lineheight.legend	Numeric scalar. The line height for the legend text.
lty.baseline	Character or numeric scalar. Line type of the optional baseline, defaults to the setting of lty.
lty.mountain	Character or numeric scalar. Line type in mountain-type and polygon-type plots, defaults to the setting of lty.

(continued)

Parameter	Description
lwd.baseline	Numeric scalar. Line width of the optional baseline, defaults to the setting of lwd.
lwd.mountain	Numeric scalar. Line width in mountain-type and polygon-type plots, defaults to the setting of lwd.
min.distance	Numeric scalar. The mimimum distance in pixel below which to collapse ranges.
missingAsZero	Logical scalar. Defines how the missing values are treated in the aggregation procedure with running window. Setting it to TRUEfills empty positions with zeros, which is default. FALSE fills empty positions with NA.
na.rm	Boolean controlling whether to discard all NA values when plotting or to keep empty spaces for NAs
ncolor	Integer scalar. The number of colors for the 'gradient' plotting type
notch	Logical scalar. Parameter controlling the boxplot appearance. See panel.bwplot for details.
notch.frac	Numeric scalar. Parameter controlling the boxplot appearance. See panel.bwplot for details.
pch	Integer scalar. The type of glyph used for plotting symbols.
separator	Numeric scalar. Number of pixels used to separate individual samples in heatmap- and horizon-type plots.
showColorBar	Boolean. Indicate the data range color mapping in the axis for 'heatmap' or 'gradient' types.
showSampleNames	Boolean. Display the names of the individual samples in a heatmap or a horizon plot.
span	Numeric scalar. Parameter controlling the loess calculation for smooth and mountain-type plots. See panel.loess for details.
stackedBars	Logical scalar. When there are several data groups, draw the histogram-type plots as stacked barplots or grouped side by side.
stats	Function. Parameter controlling the boxplot appearance. See panel.bwplot for details.
transformation	Function. Applied to the data matrix prior to plotting or when calling the score method. The function should accept exactly one input argument and its return value needs to be a numeric vector which can be coerced back into a data matrix of identical dimensionality as the input data.
type	Character vector. The plot type, one or several in p,l, b, a, a_confint, s, g, r, S, confint, smooth, histogram, mountain, polygon, h, bo See 'Details' section in DataTrack for more information on the individual plotting types.
varwidth	Logical scalar. Parameter controlling the boxplot appearance. See panel.bwplot for details.
window	Numeric or character scalar. Aggregate the rows values of the data matrix to window equally sized slices on the data range using the method defined in aggregation. If negative, apply a running window of size windowSize using the same aggregation method. Alternatively, the special value auto causes the function to determine the optimal window size to avoid overplotting, and fixed uses fixed-size windows of size windowSize.
windowSize	Numeric scalar. The size of the running window when the value of window is negative.

(continued)

Parameter	Description
yTicksAt	Numeric vector. The points at which y-axis tick-marks are to be drawn. By default, when NULL, tickmark locations are computed.
ylim	Numeric vector of length 2. The range of the y-axis scale.

Annotation Track Parameters

Parameter	Description
arrowHeadMaxWidth	Numeric scalar. The maximum width of the arrow head in pixels if shape is arrow.
arrowHeadWidth	Numeric scalar. The width of the arrow head in pixels if shape is fixedArrow.
cex	Numeric scalar. The font expansion factor for item identifiers.
cex.group	Numeric scalar. The font expansion factor for the group-level annotation.
col	Character or integer scalar. The border color for all track items.
col.line	Character scalar. The color used for connecting lines between grouped items. Defaults to a light gray, but if set to NULL the same color as for the first item in the group is used.
featureAnnotation	Character scalar. Add annotation information to the individual track elements. This can be a value in id, group or feature. Defaults to id. Only works if showFeatureId is not FALSE.
fill	Character or integer scalar. The fill color for untyped items. This is also used to connect grouped items. See grouping for details.
fontcolor.group	Character or integer scalar. The font color for the group-level annotation.
fontcolor.item	Character or integer scalar. The font color for item identifiers.
fontface.group	Numeric scalar. The font face for the group-level annotation.
fontfamily.group	Character scalar. The font family for the group-level annotation.
fontsize.group	Numeric scalar. The font size for the group-level annotation.
groupAnnotation	Character scalar. Add annotation information as group labels. This can be a value in id, group or feature. Defaults to group. Only works if showId is not FALSE.
just.group	Character scalar. the justification of group labels. Either left, right, above or below.
lex	Numeric scalar. The line expansion factor for all track items. This is also used to connect grouped items. See grouping for details.
lineheight	Numeric scalar. The font line height for item identifiers.
lty	Character or integer scalar. The line type for all track items. This is also used to connect grouped items. See grouping for details.
lwd	Integer scalar. The line width for all track items. This is also used to connect grouped items. See grouping for details.
mergeGroups	Logical scalar. Merge fully overlapping groups if collapse==TRUE.
min.height	Numeric scalar. The minimum range height in pixels to display. All ranges are expanded to this size in order to avoid rendering issues. See collapsing for details. For feathered bars indicating the strandedness of grouped items this also controls the height of the arrow feathers.
min.width	Numeric scalar. The minimum range width in pixels to display. All ranges are expanded to this size in order to avoid rendering issues. See collapsing for details.
rotation	Numeric scalar. The degree of text rotation for item identifiers.
rotation.group	Numeric scalar. The degree of text rotation for group labels.
rotation.item	Numeric scalar. The degree of text rotation for item identifiers.

(continued)

Parameter	Description
shape	Character scalar. The shape in which to display the track items. Currently only box, arrow, fixedArrow, ellipse, and smallArrow are implemented.
showFeatureId	Logical scalar. Control whether to plot the individual track item identifiers.
showId	Logical scalar. Control whether to annotate individual groups.
showOverplotting	Logical scalar. Use a color gradient to show the amount of overplotting for collapsed items. This implies that collapse==TRUE