

# Package ‘genoPlotR’

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**Type** Package

**Title** Plot publication-grade gene and genome maps

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**Depends** R (>= 2.10.0), methods, grid, ade4

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**Description** genoPlotR draws gene or genome maps and comparisons between these, in a publication-grade manner. Starting from simple, common files, it will draw postscript or pdf files that can be sent as such to journals

**License** GPL (>= 2)

**LazyLoad** yes

## R topics documented:

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genoPlotR-package    *genoPlotR - a R framework to produce publication-grade maps of genes and genomes.*

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## Description

A R framework to plot comparison of gene stretches or genomes, a la ACT (Artemis Comparison Tool), but with production-grade graphics, and a static interface. Reads directly from tabular files or from wide-spread biological formats such as BLAST and PTT (NCBI).

## Details

Package:	genoPlotR
Type:	Package
Version:	0.1
Date:	2009-12-08
License:	GPL (>=2)
LazyLoad:	yes

The only plotting function is `plot_gene_map`, which produces `link[grid]{grid}` graphics. Data is composed mainly of DNA segments (`dna_seg`) objects, which represent collections of genes or segments of genomes, and of `comparison` objects, which are the pairwise comparisons between the `dna_segs`. Data can be read from files (see `read_functions`) or from R objects like `data.frames` or `lists`, with `dna_seg` and `comparison` conversion functions.

## Author(s)

Lionel Guy

Maintainer: Lionel Guy <lionel.guy@ebc.uu.se>

## See Also

`plot_gene_map` for plotting. `dna_seg` and `comparison` for the base objects and conversion functions. `read_dna_seg_from_tab`, `read_dna_seg_from_ptt`, `read_comparison_from_tab` and `read_comparison_from_blast` to read from files.

## Examples

```
## simple example
## dna segments
## data.frame with several genes
names1 <- c("feat1", "feat2", "feat3")
starts1 <- c(2, 1000, 1050)
ends1 <- c(600, 800, 1345)
strands1 <- c("-", -1, 1)
cols1 <- c("blue", "grey", "red")
df1 <- data.frame(name=names1, start=starts1, end=ends1,
                  strand=strands1, col=cols1)
dna_seg1 <- dna_seg(df1)
is.dna_seg(dna_seg1)
```

```
## with only one gene, or two, and merging
gene2a <- dna_seg(list(name="feat1", start=50, end=900, strand="-", col="blue"))
genes2b <- dna_seg(data.frame(name=c("feat2", "feat3"), start=c(800, 1200),
                               end=c(1100, 1322), strand=c("+", 1),
                               col=c("grey", "red")))

dna_seg2 <- c.dna_seg(gene2a, genes2b)
is.dna_seg(dna_seg2)

## reading from file
dna_seg3_file <- system.file('extdata/dna_seg3.tab', package = 'genoPlotR')
dna_seg3 <- read_dna_seg_from_tab(dna_seg3_file)
is.dna_seg(dna_seg3)

## comparison
## from a data.frame
comparison1 <- as.comparison(data.frame(start1=starts1, end1=ends1,
                                         start2=dna_seg2$start,
                                         end2=dna_seg2$end))

is.comparison(comparison1)

## from a file
comparison2_file <- system.file('extdata/comparison2.tab',
                                package = 'genoPlotR')
comparison2 <- read_comparison_from_tab(comparison2_file,
                                         color_scheme="red_blue")

is.comparison(comparison1)

## plot
plot_gene_map(dna_segs=list(dna_seg1, dna_seg2, dna_seg3),
               comparisons=list(comparison1, comparison2))
```

---

annotation

---

*Annotation class and class functions*


---

## Description

An annotation describes a DNA segment. It has labels attached to positions. Each label can be attached to a single position or to a range.

## Usage

```
annotation(x1, x2 = NA, text, rot = 0, col = "black")
as.annotation(df, x2 = NA, rot = 0, col = "black")
is.annotation(annotation)
```

## Arguments

x1	Numeric. A vector giving the first or only position of the label. Mandatory.
x2	Numeric. A vector of the same length as x1. If a row (or the whole column) is NA, then the annotation(s) will be attached to x0. Else, the annotation will be attached to the range between both positions. NA by default.
text	Character of the same length as x0. Gives the text of the labels. Mandatory.

<code>rot</code>	Numeric of the same length as <code>x0</code> . Gives the rotation, in degrees, of the labels. 0 by default.
<code>col</code>	Vector of the same length as <code>x0</code> . The color of the labels. <code>black</code> by default.
<code>df</code>	A data frame to convert to an annotation object. Should have at least columns <code>x1</code> and <code>text</code> .
<code>annotation</code>	An object to test.

### Details

An `annotation` object is a data frame with columns `x0`, `x1`, `text`, `col` and `rot`. They give, respectively, the first (or only) position, eventually the second position, the text, the color and the rotation of the annotation. When plotted with `plot_gene_map`, it will add an annotation row on top of the first `dna_seg`. Labels for which only one position is given will be centered on that position. Labels for which two positions are given are linked by an horizontal square bracket and the label is plotted in the middle of the positions.

### Value

`annotation` and `as.annotation` return an annotation object. `is.annotation` returns a logical.

### Author(s)

Lionel Guy

### See Also

[plot\\_gene\\_map, middle](#).

### Examples

```
## loading data
data(three_genes)

## Calculating middle positions
mid_pos <- middle(dna_segs[[1]])

# Create first annotation
annot1 <- annotation(x1=mid_pos, text=dna_segs[[1]]$name)
plot_gene_map(dna_segs=dna_segs, comparisons=comparisons, annotations=annot1)

## Exploring options
annot2 <- annotation(x1=c(mid_pos[1], dna_segs[[1]]$end[2]),
                    x2=c(NA, dna_segs[[1]]$end[3]),
                    text=c(dna_segs[[1]]$name[1], "region1"),
                    rot=c(30, 0), col=c("grey", "black"))
plot_gene_map(dna_segs=dna_segs, comparisons=comparisons,
              annotations=annot2, annotation_height=1.3)

## Annotations on all the segments
annots <- lapply(dna_segs, function(x){
  mid <- middle(x)
  annot <- annotation(x1=mid, text=x$name, rot=30)
})
plot_gene_map(dna_segs=dna_segs, comparisons=comparisons,
```

```
annotations=annots, annotation_height=1.8, annotation_cex=1)
```

---

apply\_color\_scheme *Apply a color scheme*

---

## Description

Apply a color scheme to a numeric vector, eventually taking the direction into account.

## Usage

```
apply_color_scheme(x, direction = NULL, color_scheme = "grey",  
decreasing = FALSE, rng = NULL)
```

## Arguments

x	A numeric, that will be used to apply a gradient of colors to a comparison.
direction	If a red-blue scheme is choosen, the vector (composed of -1 and 1 values and of same length as x) giving the direction of the comparison.
color_scheme	Character. One of red_blue, blue_red, grey, gray.
decreasing	Logical. Are the values of the comparisons oriented such as the lower the value, the closer the relationship (e.g. e-values, gaps, mismatches, etc)? FALSE by default.
rng	Numeric of length 2. Gives the higher and lower limit to apply a color scheme.

## Details

A color scale is calculated, with the darker color corresponding to the highest values of x, or the contrary is decreasing is TRUE. For the moment, two schemes (red-blue and grey scale) are used.

For the red-blue scale (as in ACT), the direct comparisons are colored in red hues, and the reversed ones in blue hues.

This is especially useful to replace comparison values (such as BLAST percent identity values) by color hues.

## Value

A character vector of same length as x, representing colors.

## Author(s)

Lionel Guy

## References

Artemis Comparison Tool, <http://www.sanger.ac.uk/Software/ACT/>

## See Also

[comparison](#)

## Examples

```
## Load data
data(three_genes)

## Color schemes
## Greys
comparisons[[1]]$values <- c(70, 80, 90)
comparisons[[1]]$col <- apply_color_scheme(comparisons[[1]]$values,
                                           color_scheme="grey")
plot_gene_map(dna_segs=dna_segs, comparisons=comparisons)
## Red-blue
comparisons[[1]]$col <- apply_color_scheme(comparisons[[1]]$values,
                                           direction=comparisons[[1]]$direction,
                                           color_scheme="red_blue")
plot_gene_map(dna_segs=dna_segs, comparisons=comparisons)
## Decreasing
comparisons[[1]]$col <- apply_color_scheme(comparisons[[1]]$values,
                                           direction=comparisons[[1]]$direction,
                                           color_scheme="red_blue",
                                           decreasing=TRUE)
plot_gene_map(dna_segs=dna_segs, comparisons=comparisons)
## Range
comparisons[[1]]$col <- apply_color_scheme(comparisons[[1]]$values,
                                           direction=comparisons[[1]]$direction,
                                           color_scheme="red_blue",
                                           rng=c(30,100))
plot_gene_map(dna_segs=dna_segs, comparisons=comparisons)
```

---

barto

---

*Comparison of 4 Bartonella genomes*


---

## Description

Comparison of 4 Bartonella genomes by BLAST.

## Usage

```
data(barto)
```

## Format

barto, a list of three dataframes, representing the four genomes and their pairwise comparisons:

- `dna_segs` which is a list of 4 `dna_seg` objects, containing all the protein genes for each genome. Obtained by reading ptt files downloaded from NCBI with `read_dna_seg_from_ptt`.
- `comparisons` which is a list of 3 `comparison` objects, obtained by doing genome-to-genome (fasta files) BLASTs, and then reading the resulting tab files with `read_comparison_from_blast`.
- `rnt_segs` which is a list of 4 `dna_seg` objects, containing all the RNA genes of the four genomes. Obtained by reading rnt files downloaded from NCBI with `read_dna_seg_from_ptt`.

A bash script to obtain the same file as in the dataset is available in the `extdata` folder of the package. Find its location by running `system.file('extdata/barto.sh', package = 'genoPlotR')`.

## References

BLAST: <http://www.ncbi.nlm.nih.gov/blast/>

## Examples

```
data(barto)
plot_gene_map(barto$rnt_segs, barto$comparisons, gene_type="blocks")
```

---

c.dna_seg	<i>Concatenate dna_seg objects</i>
-----------	------------------------------------

---

## Description

Concatenate dna\_seg objects.

## Usage

```
## S3 method for class 'dna\_seg':
c(...)
```

## Arguments

... dna\_segs to be concatenated.

## Value

A dna\_seg object

## Author(s)

Lionel Guy

## See Also

[dna\\_seg](#)

## Examples

```
## load data
data(three_genes)

dna_segs[1:2]
c(dna_segs[[1]], dna_segs[[2]])
```

---

chrY_subseg	<i>Comparisons of subsegments of the Y chromosome in human and chimp</i>
-------------	--

---

### Description

A subsegment of the Y chromosome in Homo sapiens and Pan troglodytes, to illustrate support for exons and introns.

### Usage

```
data(chrY_subseg)
```

### Format

A list of two data frames, representing the Y segment in the two species, and containing:

- `dna_segs` which is a list of two `dna_seg` objects, containing each three rows (or genes).
- `comparison` which is a list of one `comparison` objects.

### Details

Header for the Homo sapiens genbank file: LOCUS NC\_000023 220001 bp DNA linear CON 10-JUN-2009 DEFINITION Homo sapiens chromosome X, GRCh37 primary reference assembly. ACCESSION NC\_000023 REGION: 2600000..2820000 GPC\_000000047

Header for the Pan troglodytes file: LOCUS NC\_006491 220001 bp DNA linear CON 18-SEP-2006 DEFINITION Pan troglodytes chromosome X, reference assembly (based on Pan\_troglodytes-2.1). ACCESSION NC\_006491 REGION: 2620000..2840000

### Examples

```
data(chrY_subseg)
plot_gene_map(chrY_subseg$dna_segs, chrY_subseg$comparison, dna_seg_scale=TRUE,
              scale=FALSE)
```

---

comparison	<i>Comparison class and class functions</i>
------------	---

---

### Description

A comparison is a collection of similarities, representing the comparison between two DNA segments. These functions are class functions to create, convert and test comparison objects.

### Usage

```
comparison(x)
as.comparison(df)
is.comparison(comparison)
```



**Arguments**

<code>x</code>	Can be a <code>list</code> or <code>data.frame</code> object. See the details for the columns in the <code>data.frame</code> .
<code>df</code>	A <code>data.frame</code> object. See details for the required columns.
<code>comparison</code>	Any object to test.

**Details**

Objects (either data frames or lists) should have at least named elements `start1`, `end1`, `start2` and `end2`. In addition, it take use a `col` column to give either a color or a numeric vector that can be used for color-coding.

`comparison` tries to build a comparison object from either a data frame or a list, as `.comparison` accepts only `data.frames`.

`is.comparison` returns `TRUE` if the object tested is a comparison object.

Read functions such as [read\\_comparison\\_from\\_tab](#) and [read\\_comparison\\_from\\_blast](#) also return comparison objects.

**Value**

A comparison object for `comparison` and `as.comparison`. Comparison objects are also of class `data.frame`. They contain the columns `start1`, `end1`, `start2`, `end2`, `direction` and `col` (color).

A logical for `is.comparison`.

**Author(s)**

Lionel Guy

**See Also**

[dna\\_seg](#), [read\\_comparison\\_from\\_tab](#), [read\\_comparison\\_from\\_blast](#), [trim.comparison](#), [reverse.comparison](#).

**Examples**

```
## Get some values
starts1 <- c(2, 1000, 1050)
ends1 <- c(600, 800, 1345)
starts2 <- c(50, 800, 1200)
ends2 <- c(900, 1100, 1322)

## From a data.frame
comparison1 <- as.comparison(data.frame(start1=starts1, end1=ends1,
                                         start2=starts2, end2=ends2))

comparison1
is.comparison(comparison1)
is.data.frame(comparison1)
comparison(data.frame(start1=starts1, end1=ends1,
                      start2=starts2, end2=ends2))

## From a list
comparison(list(start1=starts1, end1=ends1,
                start2=starts2, end2=ends2))
```

```
## From a file
comparison2_file <- system.file('extdata/comparison2.tab',
                                package = 'genoPlotR')
comparison2 <- read_comparison_from_tab(comparison2_file)
```

dna\_seg

*DNA segment (dna\_seg) class and class functions*

## Description

A DNA segment is a collection of genes or elements along a genome, to be represented on a map. These functions are class functions to create, convert and test dna\_seg objects.

## Usage

```
dna_seg(x, ...)
as.dna_seg(df, col = "blue", lty = 1, lwd = 1, pch = 8, cex = 1, gene_type = "ar")
is.dna_seg(dna_seg)
```

## Arguments

x	A data.frame or list that can be coerced to a data frame.
...	Arguments further passed to as.dna_seg (see below).
df	A data frame representing the dna_seg object. See details for necessary columns.
col	Either a color vector of the same length as df or of length one, to be applied to the whole object. Default to blue.
lty	A vector of the same length as df or of length one, giving the line type around the objects.
lwd	Same as lty, giving the line width.
pch	Same as lty, giving the character representing each object. Goes with gene_type points.
cex	Same as lty, giving the character size representing each object. Goes with gene_type points.
gene_type	Vector of the same length as df or of length one, giving the type of representation of each object.
dna_seg	Object to test.

## Details

Objects to be converted needs to have their first 4 columns named name, start, end and strand. Extra columns with names col, lty, lwd, pch, cex, gene\_type will be used in the plotting process. Other extra columns will be kept in the object, but not used.

dna\_seg tries to build a dna\_seg object from a data frame or a list.

as.dna\_seg tries to build a dna\_seg object from a data frame.

Read functions such as [read\\_dna\\_seg\\_from\\_tab](#) and [read\\_dna\\_seg\\_from\\_ptt](#) also return dna\_seg objects.

**Value**

A comparison object for `comparison` and `as.comparison`. DNA seg objects are also of class `data.frame`. They contain the following columns: `name`, `start`, `end`, `strand`, `col`, `lty`, `lwd`, `pch`, `cex`, `gene_type`.

A logical for `is.comparison`.

**Author(s)**

Lionel Guy

**See Also**

[read\\_dna\\_seg\\_from\\_tab](#), [read\\_dna\\_seg\\_from\\_ptt](#), [gene\\_types](#).

**Examples**

```
## generate data
names1 <- c("feat1", "feat2", "feat3")
starts1 <- c(2, 1000, 1050)
ends1 <- c(600, 800, 1345)
strands1 <- c("-", -1, 1)
cols1 <- c("blue", "grey", "red")

## create data.frame
df1 <- data.frame(name=names1, start=starts1, end=ends1,
                  strand=strands1, col=cols1)

## with dna_seg
dna_seg1 <- dna_seg(df1)
dna_seg1
as.dna_seg(df1)

## test
is.dna_seg(dna_seg1)

## directly readable with read_dna_seg_from_tab
## Not run:
write.table(x=dna_seg1, file="dna_seg1.tab", quote=FALSE,
           row.names=FALSE, sep="\t")

## End(Not run)

## with only one gene and with list, or two, and merging with c.dna_seg
gene2a <- dna_seg(list(name="feat1", start=50, end=900, strand="-", col="blue"))
genes2b <- dna_seg(data.frame(name=c("feat2", "feat3"), start=c(800, 1200),
                             end=c(1100, 1322), strand=c("+", 1),
                             col=c("grey", "red")))
dna_seg2 <- c(gene2a, genes2b)

## test
is.dna_seg(dna_seg2)

## reading from file
dna_seg3_file <- system.file('extdata/dna_seg3.tab', package = 'genoPlotR')
dna_seg3 <- read_dna_seg_from_tab(dna_seg3_file)
is.dna_seg(dna_seg3)
```

---

`gene_types`*Gene types*

---

**Description**

Returns a vector containing the available gene types.

**Usage**

```
gene_types(auto = TRUE)
```

**Arguments**

`auto` Logical. Should type "auto" be added?

**Value**

A character vector.

**Author(s)**

Lionel Guy

**See Also**

[plot\\_gene\\_map](#)

**Examples**

```
gene_types()

## Load data
data(barto)
n <- length(gene_types(auto=FALSE))

## Get a small subset from the barto dataset
dna_seg <- barto$dna_segs[[3]][1:n,]
plot_gene_map(list(dna_seg))

# Change gene_types and plot again
dna_seg$gene_type <- gene_types(auto=FALSE)
dna_seg$col <- rainbow(n)
dna_seg_r <- dna_seg
dna_seg_r$strand <- -dna_seg$strand
plot_gene_map(list(dna_seg, dna_seg_r))
```

---

human_nt	<i>Human-readable nucleotide scale</i>
----------	--

---

## Description

Return a human readable list from a nucleotide position or lenght.

## Usage

```
human_nt(nt, signif = FALSE)
```

## Arguments

nt	A nucleotide position
signif	Either a logical or an integer. If FALSE (default), nt is not rounded. Else, it returns signif significant digits.

## Details

Return a nucleotide value in nt, kb, Mb or Gb, according to the value given. This is particularly useful to display nice scales without too many trailing zeros.

## Value

Returns a list with 4 elements

n	A numeric value corresponding to nt divided by mult (see below).
tag	A character, giving the multiplier used in text.
mult	The multiplier used, in numeric value.
text	A character, giving the value in a human readable format.

## Author(s)

Lionel Guy

## Examples

```
human_nt(123456)
human_nt(123456, signif=2)
human_nt(123456890, signif=2)
```

---

mauve\_bbone

*Mauve backbone of 4 Bartonella genomes*


---

### Description

The result of a multiple genome alignment with Mauve.

### Usage

```
data(mauve_bbone)
```

### Format

bbone, a list of two dataframes, representing the regions which are conserved in at least two genomes:

- `dna_segs` which is a list of 4 `dna_seg` objects, containing the mauve blocks for each genome.
- `comparisons` which is a list of 3 comparison objects.

A bash script to obtain the same file as in the data is available in the `extdata` folder of the package. Find its location by running `system.file('extdata/mauve.sh', package = 'genoPlotR')`.

The resulting backbone file can then be read with [read\\_mauve\\_backbone](#).

### References

Mauve: <http://asap.ahabs.wisc.edu/mauve/>

### Examples

```
data(mauve_bbone)
plot_gene_map(bbone$dna_segs, bbone$comparisons)
```

---

middle

*Middles of a dna\_seg*


---

### Description

Returns a vector containing the middle of the genes of a `dna_seg`. Useful to prepare annotations, for example.

### Usage

```
middle(dna_seg)
```

### Arguments

`dna_seg`      A `dna_seg` object.

**Value**

A numeric vector.

**Author(s)**

Lionel Guy

**See Also**

[annotation](#), [dna\\_seg](#)

**Examples**

```
## Load data
data(barto)

## Get middles of the first dna_seg
mid <- middle(barto$dna_segs[[1]])
```

---

plot\_gene\_map

*Plot gene and genome maps*


---

**Description**

This plotting function represents linearly DNA segments and their comparisons. It will plot one line per DNA segment, eventually separated by the comparisons. In addition, a tree can be plotted on the left of the plot, and annotations on the top row. Since this is a grid plot, it can be placed into other graphics, or modified subsequently.

**Usage**

```
plot_gene_map(dna_segs,
              comparisons = NULL,
              tree = NULL,
              tree_width = NULL,
              legend = NULL,
              annotations = NULL,
              annotation_height = 1,
              annotation_cex = 0.8,
              xlims = NULL,
              offsets = NULL,
              limit_to_longest_dna_seg = TRUE,
              main = NULL,
              main_pos = "centre",
              dna_seg_labels = NULL,
              gene_type = NULL,
              arrow_head_len = 200,
              dna_seg_line = TRUE,
              scale = TRUE,
              dna_seg_scale = !scale,
```

```

global_color_scheme = c("auto", "auto", "blue_red"),
override_color_schemes = FALSE,
plot_new=TRUE,
debug = 0
)

```

## Arguments

<code>dna_segs</code>	A list of <code>dna_seg</code> objects. Mandatory.
<code>comparisons</code>	A list of <code>comparison</code> objects. Optional.
<code>tree</code>	A tree, under the form of a <code>phylog</code> object. If specified, takes place at the left of the tags. The tree doesn't need to be ordered as the <code>dna_seg_labels</code> , but a permutation of the tree with that order should exist.
<code>tree_width</code>	Numeric. The width of the tree area in the plot, in inches. By default, takes 20 percent of the total plot.
<code>legend</code>	Yet unimplemented.
<code>annotations</code>	An <code>annotation</code> object or a list of <code>annotation</code> objects. See details. Optional.
<code>annotation_height</code>	Numeric. The height, in lines, of the annotation line. One by default, if <code>annotation</code> is defined.
<code>annotation_cex</code>	Numeric. The <code>cex</code> (i.e. the character expansion) of the annotation line.
<code>xlims</code>	A list with as many elements as there are <code>dna_segs</code> , or <code>NULL</code> . If <code>NULL</code> , the whole segment will be represented. If a list, each element of the list is a numeric vector, representing pairs of left and right limits for each subsegment. See details.
<code>offsets</code>	A list or a vector with as many elements as there are <code>dna_segs</code> , or <code>NULL</code> . If is a numeric vector, gives the offset of the first subsegment. If is a list, each element should have the same length as there are subsegments (see <code>xlims</code> ). Gives then the length of each gap. If <code>NULL</code> , the size of the gaps is optimized to minimize the lengths of the comparisons. See details.
<code>limit_to_longest_dna_seg</code>	A logical. Should the plot be restricted to the longest <code>dna_seg</code> ? If no, the other segments can be extended to better fit comparisons.
<code>main</code>	A character. Main title of the plot.
<code>main_pos</code>	Position of the main title. One of <code>centre</code> , <code>left</code> or <code>right</code> .
<code>dna_seg_labels</code>	A character, same length as <code>dna_segs</code> . The names of the segments. If <code>NULL</code> , the names of <code>dna_segs</code> will be used, if available. Else, no name are plotted. If a <code>tree</code> is given, names must exist either in <code>dna_seg_labels</code> or in the names of <code>dna_segs</code> .
<code>gene_type</code>	A character. Describes the type of representation of genes or <code>dna_seg</code> elements. See details.
<code>arrow_head_len</code>	A numeric. Gives the length of arrow heads for gene type "arrows". The arrow head extends at maximum at half of the gene. Set to <code>Inf</code> to have all arrow heads covering the half of the gene. 200 by default.



<code>dna_seg_line</code>	A vector, either logical or giving colors, of length 1 or of same length as <code>dna_segs</code> . Should the line in the middle of the segments be drawn, and if yes, in what color. TRUE by default, which gives black lines. FALSE (logical, or as a string) results in no plotting.
<code>scale</code>	A logical. Should the scale be displayed on the plot. TRUE by default.
<code>dna_seg_scale</code>	A logical, of length one or of the same length as <code>dna_segs</code> . Should a scale be displayed below each or all dna segments, respectively. <code>!scale</code> by default.
<code>global_color_scheme</code>	A character of length 3. If no <code>col</code> column is present on any comparison or <code>override_color_schemes</code> is set, apply a global color scheme over all comparisons. See below for more details. <code>c("auto", "auto", "blue_red")</code> by default.
<code>override_color_schemes</code>	A logical. If TRUE, apply a global color scheme even if there are comparisons that have <code>col</code> columns. FALSE by default.
<code>plot_new</code>	Logical. Produce a new plot? If TRUE, uses <code>grid.newpage</code> before plotting.
<code>debug</code>	A numeric. If > 0, only that number of element will be plotted for each <code>dna_seg</code> and comparison.

## Details

One line is plotted per `dna_seg`. Eventually, the space between the lines will be filled with the comparisons. A phylogenetic tree (a `phylog` object from package `ade4`) can be drawn at the left of the plot.

A scale, a main title and an annotation row at the top of the plot can also be added.

The format of the elements of `dna_segs` is previously determined in the object or can be globally set by `gene_type`. See the function [gene\\_types](#) to return the available types.

`xlims` allow the user to plot subsegments of a `dna_seg`. `xlims` consists of a list composed of as many numeric vectors as there are segments. Each of these numeric vectors give pairs of left and right borders, and gives the direction. For example, `c(1,2,6,4)` will plot two subsegments, segment 1 to 2 which is plotted left to right and segment 4 to 6, plotted right to left. `-Inf` and `Inf` values are accepted. NULL values will result in plotting the whole segment.

`offsets` allows to user to define the placement of the subsegments. If a list is provided, each element of the list should have as many elements as there are subsegments. It will give the size of the gaps, including the first one from the border of the plot to the first subsegment.

`dna_seg_scale` gives the ability to plot scales on one, some or every segment. `c(TRUE, FALSE, TRUE)` will add scales to the first and third segments.

The three elements of `global_color_scheme` are (i) which column serves as scale to apply the color scheme, or "auto" (default); (ii) if the scale is increasing or decreasing (see `apply_color_scheme` for more details), or "auto" (default); (iii) the color scheme to apply.

## Value

Nothing. A lattice graphic is plotted on the current device.

**Note**

This plotting function has been tested as far as possible, but given its complexity and that the package is young, bugs or strange behaviors are possible. Please report them to the author.

As of 10/3/2010, support for viewing exons/introns is only available using genbank and embl formats, not when importing ptt files.

**Author(s)**

Lionel Guy <lionel.guy@ebc.uu.se>, Jens Roat Kultima

**See Also**

[dna\\_seg](#) and [comparison](#) for the base objects; [read\\_dna\\_seg\\_from\\_tab](#), [read\\_dna\\_seg\\_from\\_ptt](#), [read\\_comparison\\_from\\_tab](#) and [read\\_comparison\\_from\\_blast](#) to read from files; [gene\\_types](#) for gene\_type argument; [apply\\_color\\_scheme](#) for color schemes;

**Examples**

```
old.par <- par(no.readonly=TRUE)
data("three_genes")

## Segments only
plot_gene_map(dna_segs=dna_segs)

## With comparisons
plot_gene_map(dna_segs=dna_segs, comparisons=comparisons)

## Tree
names <- c("A_aaa", "B_bbb", "C_ccc")
names(dna_segs) <- names
tree <- newick2phylog("((A_aaa:4.2,B_bbb:3.9):3.1,C_ccc:7.3):1);")
plot_gene_map(dna_segs=dna_segs, comparisons=comparisons,
              tree=tree)

## Increasing tree width
plot_gene_map(dna_segs=dna_segs, comparisons=comparisons,
              tree=tree, tree_width=3)

## Annotation
## Calculating middle positions
mid_pos <- middle(dna_segs[[1]])

# Create first annotation
annot1 <- annotation(x1=mid_pos, text=dna_segs[[1]]$name)
plot_gene_map(dna_segs=dna_segs, comparisons=comparisons, annotations=annot1)

## Exploring options
annot2 <- annotation(x1=c(mid_pos[1], dna_segs[[1]]$end[2]),
                    x2=c(NA, dna_segs[[1]]$end[3]),
                    text=c(dna_segs[[1]]$name[1], "region1"),
                    rot=c(30, 0), col=c("grey", "black"))
plot_gene_map(dna_segs=dna_segs, comparisons=comparisons,
              annotations=annot2, annotation_height=1.3)

## xlims
```

```

## Just returning a segment
plot_gene_map(dna_segs, comparisons,
              xlims=list(NULL, NULL, c(Inf,-Inf)),
              dna_seg_scale=TRUE)

## Removing one gene
plot_gene_map(dna_segs, comparisons,
              xlims=list(NULL, NULL, c(-Inf,2800)),
              dna_seg_scale=TRUE)

## offsets
offsets <- c(0, 0, 0)
plot_gene_map(dna_segs=dna_segs, comparisons=comparisons, offsets=offsets)
offsets <- c(200, 400, 0)
plot_gene_map(dna_segs=dna_segs, comparisons=comparisons, offsets=offsets)

## main
plot_gene_map(dna_segs=dna_segs, comparisons=comparisons,
              main="Comparison of A, B and C")
plot_gene_map(dna_segs=dna_segs, comparisons=comparisons,
              main="Comparison of A, B and C", main_pos="left")

## dna_seg_labels
plot_gene_map(dna_segs=dna_segs, comparisons=comparisons,
              dna_seg_labels=c("Huey", "Dewey", "Louie"))

## dna_seg_line
plot_gene_map(dna_segs=dna_segs, comparisons=comparisons,
              dna_seg_line=c("FALSE", "red", grey(0.6)))

## gene_type
plot_gene_map(dna_segs=dna_segs, comparisons=comparisons,
              gene_type="side_blocks")

##
## From here on, using a bigger dataset from a 4-genome comparison
##
data("barto")
## Adding a tree
tree <- newick2phylog("(BB:2.5, (BG:1.8, (BH:1, BQ:0.8):1.9):3);")
## Showing only subsegments
xlims1 <- list(c(1380000, 1445000),
               c(10000, 83000),
               c(15000, 98000),
               c(5000, 82000))
plot_gene_map(barto$dna_segs, barto$comparisons, tree=tree,
              xlims=xlims1,
              dna_seg_scale=TRUE)
## Showing several subsegments per genome
xlims2 <- list(c(1445000, 1415000, 1380000, 1412000),
               c( 10000, 45000, 50000, 83000, 90000, 120000),
               c( 15000, 36000, 90000, 120000, 74000, 98000),
               c( 5000, 82000))
plot_gene_map(barto$dna_segs, barto$comparisons, tree=tree,
              xlims=xlims2,
              dna_seg_scale=TRUE)

## dna_seg_scale & global_color_scheme

```

```

plot_gene_map(barto$dna_segs, barto$comparisons, tree=tree, xlims=xlims1,
              dna_seg_scale=c(TRUE, FALSE, FALSE, TRUE), scale=FALSE,
              global_color_scheme=c("e_value", "auto", "grey"))

## Adding annotations for all genomes
annots <- lapply(barto$dna_segs, function(x){
  mid <- middle(x)
  annot <- annotation(xl=mid, text=x$name, rot=30)
  # removing gene names starting with "B" and keeping 1 in 4
  idx <- grep("^[^B]", annot$text, perl=TRUE)
  annot[idx[idx %% 4 == 0],]
})
plot_gene_map(barto$dna_segs, barto$comparisons, tree=tree,
              annotations=annots,
              xlims=xlims2,
              dna_seg_scale=TRUE)
## Allow segments to be placed out of the longest segment
plot_gene_map(barto$dna_segs, barto$comparisons, tree=tree,
              annotations=annots,
              xlims=xlims2,
              limit_to_longest_dna_seg=FALSE,
              dna_seg_scale=TRUE)
## Hand-made offsets: only placement of first segment
offsets1 <- c(10000, 0, 30000, 10000)
plot_gene_map(barto$dna_segs, barto$comparisons, tree=tree,
              annotations=annots,
              xlims=xlims2,
              offsets=offsets1,
              dna_seg_scale=TRUE)
## Hand-made offsets: size of all gaps
offsets2 <- list(c(10000, 10000),
                 c(2000, 2000, 2000),
                 c(10000, 5000, 2000),
                 c(10000))
plot_gene_map(barto$dna_segs, barto$comparisons, tree=tree,
              annotations=annots,
              xlims=xlims2,
              offsets=offsets2,
              dna_seg_scale=TRUE)

##
## Exploring and modifying a gene map plot
##
plot_gene_map(barto$dna_segs, barto$comparisons, tree=tree,
              annotations=annots,
              xlims=xlims2,
              offsets=offsets2,
              dna_seg_scale=TRUE)

## View viewports
current.vpTree()
## Go down to one of the viewports, add an xaxis, go back up to root viewport
downViewport("dna_seg_scale.3.2")
grid.rect()
upViewport(0)
## Get all the names of the objects
grobNames <- getNames()
grobNames

```

```

## Change the color of the scale line
grid.edit("scale.lines", gp=gpar(col="grey"))
## Remove first dna_seg_lines
grid.remove("dna_seg_line.1.1")

##
## Plot genoPlotR logo
##
col <- c("#B2182B", "#D6604D", "#F4A582", "#FDDBC7",
         "#D1E5F0", "#92C5DE", "#4393C3", "#2166AC")
cex <- 2.3
## First segment
start1 <- c(150, 390, 570)
end1 <- c( 1, 490, 690)
genoR <- c(270, 530)
## Second segment
start2 <- c(100, 520, 550)
end2 <- c(240, 420, 650)
Plot <- c(330)
## dna_segs
ds1 <- as.dna_seg(data.frame(name=c("", "", ""),
                             start=start1, end=end1, strand=rep(1, 3),
                             col=col[c(2, 6, 1)], stringsAsFactor=FALSE))
ds_genoR <- as.dna_seg(data.frame(name=c("geno", "R"),
                                    start=genoR, end=genoR, strand=rep(1, 2),
                                    col=c(col[8], "black"),
                                    stringsAsFactor=FALSE), cex=cex, gene_type="text")
ds2 <- as.dna_seg(data.frame(name=c("", "", ""),
                             start=start2, end=end2, strand=rep(1, 3),
                             col=col[c(5, 3, 7)],
                             stringsAsFactor=FALSE))
ds_Plot <- as.dna_seg(data.frame(name="Plot",
                                  start=Plot, end=Plot, strand=1,
                                  col=col[c(1)],
                                  stringsAsFactor=FALSE), cex=cex, gene_type="text")

## comparison
c1 <- as.comparison(data.frame(start1=start1, end1=end1,
                               start2=start2, end2=end2,
                               col=grey(c(0.6, 0.8, 0.5))))

## Generate genoPlotR logo
## Not run:
cairo_pdf("logo.pdf", h=0.7, w=3)

## End(Not run)
par(fin=c(0.7, 3))
plot_gene_map(dna_segs=list(c(ds1, ds_genoR), c(ds2, ds_Plot)),
              comparisons=list(c1), scale=FALSE, dna_seg_scale=FALSE,
              dna_seg_line=grey(0.7), offsets=c(-20,160))

## Not run:
dev.off()

## End(Not run)
par(old.par)

```

## Description

Calculate the range of dna\_seg and comparisons.

## Usage

```
## S3 method for class 'dna\_seg':  
range(x, ...)  
## S3 method for class 'comparison':  
range(x, overall=TRUE, ...)  
## S3 method for class 'annotation':  
range(x, ...)
```

## Arguments

x	Object to calculate the range from.
overall	Logical, TRUE by default. Should the range be calculated over the whole object? If FALSE, a range is calculated on each side of the comparison.
...	Unused.

## Details

Calculate the overall range of a dna\_seg, comparison or an annotation object.

## Value

A numeric of length 2. For comparison, if overall is FALSE, a data frame with two rows and two columns, xlim1 and xlim2.

## Author(s)

Lionel Guy

## See Also

[dna\\_seg](#), [comparison](#), [trim](#) for further examples.

## Examples

```
## Load data  
data(three_genes)  
  
## On dna_seg  
dna_segs[[1]]  
range(dna_segs[[1]])  
  
## On comparison  
comparisons[[2]]  
range(comparisons[[2]])  
range(comparisons[[2]], overall=FALSE)
```

---

read_functions	<i>Reading functions</i>
----------------	--------------------------

---

## Description

Functions to parse dna\_seg objects from tab, embl, genbank, ptt files or from mauve backbone files, and comparison objects from tab or blast files.

## Usage

```
read_dna_seg_from_tab(file, header = TRUE, ...)
read_dna_seg_from_file(file, tagsToParse=c("CDS"), fileType = "detect",
                      meta_lines = 2, gene_type = "auto", header = TRUE, ...)
read_dna_seg_from_embl(file, tagsToParse=c("CDS"), ...)
read_dna_seg_from_genbank(file, tagsToParse=c("CDS"), ...)
read_dna_seg_from_ptt(file, meta_lines = 2, header = TRUE, ...)
read_comparison_from_tab(file, header = TRUE, ...)
read_comparison_from_blast(file, sort_by = "per_id",
                          filt_high_evalue = NULL,
                          filt_low_per_id = NULL,
                          filt_length = NULL,
                          color_scheme = NULL, ...)
read_mauve_backbone(file, ref = 1, gene_type = "side_blocks",
                    header = TRUE, filter_low = 0, ...)
```

## Arguments

file	Path to file to load. URL are accepted.
header	Logical. Does the tab file has headers (column names)?
tagsToParse	Character vector. Tags to parse in embl or genbank files. Common tags are 'CDS', 'gene', 'misc_feature'.
fileType	Character string. Select file type, could be 'detect' for automatic detection, 'embl' for embl files, 'genbank' for genbank files or 'ptt' for ptt files.
meta_lines	The number of lines in the ptt file that represent "meta" data, not counting the header lines. Standard for NCBI files is 2 (name and length, number of proteins. Default is also 2.
gene_type	Determines how genes are visualized. If 'auto' genes will appear as arrows in there are no introns and as blocks if there are introns. Can also be set to for example 'blocks' or 'arrows'. Do note, currently introns are not supported in the ptt file format. Default for mauve backbone is side_blocks. See <a href="#">gene_types</a> page for more details, or use function gene_types.
sort_by	In BLAST-like tabs, gives the name of the column that will be used to sort the comparisons. Accepted values are per_id (percent identity, default), mism (mismatches), gaps (gaps), e_value (E-value), bit_score (bit score).
filt_high_evalue	A numerical, or NULL (default). Filters out all comparisons that have a e-value higher than this one.

<code>filt_low_per_id</code>	A numerical, or NULL (default). Filters out all comparisons that have a percent identity lower than this one.
<code>filt_length</code>	A numerical, or NULL (default). Filters out all comparisons that have alignments shorter than this value.
<code>color_scheme</code>	A color scheme to apply. See <code>apply_color_scheme</code> for more details. Possible values include <code>grey</code> and <code>red_blue</code> . NULL by default. Color schemes can be applied while running <code>plot_gene_map</code> .
<code>ref</code>	In mauve backbone, which of the dna segments will be the reference, i.e. which one will have its blocks in order.
<code>...</code>	Further arguments passed to generic reading functions and class conversion functions. See <a href="#">as.dna_seg</a> and <a href="#">as.comparison</a> . For <code>read_comparison*</code> functions, see details.
<code>filter_low</code>	A numeric. If larger than 0, all blocks smaller than this number will be filtered out. Defaults to 0.

## Details

Tab files representing DNA segments should have at least the following columns: name, start, end, strand (in that order). Additionally, if the tab file has headers, more columns will be used to define, for example, the color, line width and type, pch and/or cex. See [dna\\_seg](#) for more information. An example:

```
name start end strand col feat1A 2 1345 1 blue feat1B 1399 2034 1
red feat1C 2101 2932 -1 grey feat1D 2800 3120 1 green
```

Embl and Genbank files are two commonly used file types. These file types often contain a great variety of information. To properly extract data from these files, the user has to choose which features to extract. Commonly 'CDS' features are of interest, but other feature tags such as 'gene' or 'misc\_feature' may be of interest. Should a feature contain an inner "pseudo" tag indicating this CDS or gene is a pseudo gene, this will be presented as a 'CDS\_pseudo' or a 'gene\_pseudo' feature type respectively in the resulting table. Certain constraints apply to these file types, of which some are: embl files must contain one and only one ID tag; genbank files may only contain one and only one locus tag.

Ptt (or protein table) files are a tabular format giving a bunch of information on each protein of a genome (or plasmid, or virus, etc). They are available for each published genome on the NCBI ftp site (<ftp://ftp.ncbi.nlm.nih.gov/genomes/>). As an example, look at [ftp://ftp.ncbi.nlm.nih.gov/genomes/Bacteria/Bartonella\\_1/NC\\_005956.ptt](ftp://ftp.ncbi.nlm.nih.gov/genomes/Bacteria/Bartonella_1/NC_005956.ptt).

Tabular comparison files should have at least the following columns: start1, end1, start2, end2. If no header is specified, the fifth column is parsed as the color.

start1	end1	start2	end2	col
2	1345	10	1210	red
1399	2034	2700	1100	blue
500	800	3000	2500	blue

BLAST tabular result files are produced either with `blastall` using `-m8` or `-m9` parameter, or with any of the newer `blastn/blastp/blastx/tblastx` using `-outfmt 6` or `-outfmt 7`.

For both comparison functions, several further arguments can be passed to the generic reading functions:



- `color_scheme` Passed to `apply_color_scheme`. See this function for supported values. Default to `NULL`.
- `filt_low` Filter low comparison values. Only similarities whose values in the `color_from` (for BLAST files) or `col` columns are greater than `filt_low` will be considered.
- `filt_len` Filter comparisons by length. Comparisons whose average length is below `filt_len` are not considered.
- `reverse` If numeric and `> 0`, the comparison is passed to `reverse.comparison`.

Mauve backbone is another tabular data file that summarizes the blocks that are similar between all compared genomes. Each genome gets two columns, one start and one end of the block. There is one row per block and eventually a header row. If named, columns have sequence numbers, not actual names, so be careful to input the same order in both Mauve and genoPlotR. See <http://asap.ahabs.wisc.edu/mauve-aligner/mauve-user-guide/mauve-output-file-formats.html> for more info on the file format. Normally, the function should be able to read both `progressiveMauve` and `mauveAligner` outputs. The function returns both the blocks as `dna_segs` and the links between the blocks as `comparisons`.

## Value

`read_dna_seg_from_tab`, `read_dna_seg_from_file`, `read_dna_seg_from_emb1`, `read_dna_seg_from_genbank` and `read_dna_seg_from_ptt` return `dna_seg` objects. `read_comparison_from_tab` and `read_comparison_from_blast` return comparison objects. `read_mauve_backbone` returns a list containing a list of `dna_segs` and comparisons objects.

### Note

Formats are changing and it maybe that some functions are temporarily malfunctioning. Please report any bug to the author. Mauve examples were prepared with Mauve 2.3.1.

**Author(s)**

Lionel Guy, Jens Roat Kultima

## References

For BLAST: <http://www.ncbi.nlm.nih.gov/blast/> For Mauve: <http://asap.ahabs.wisc.edu/mauve/>

## See Also

```
comparison, dna_seg, apply_color_scheme.
```

## Examples

```
##
## From tabs
##
## Read DNA segment from tab
dna_seg3_file <- system.file('extdata/dna_seg3.tab', package = 'genoPlotR')
dna_seg3 <- read_dna_seg_from_tab(dna_seg3_file)

## Read comparison from tab
comparison2_file <- system.file('extdata/comparison2.tab',
                                package = 'genoPlotR')
```

```

comparison2 <- read_comparison_from_tab(comparison2_file)

##
## Mauve backbone
##
## File
bbone_file <- system.file('extdata/barto.backbone', package = 'genoPlotR')
## Read backbone
bbone <- read_mauve_backbone(bbone_file)
names <- c("B_bacilliformis", "B_grahamii", "B_henselae", "B_quintana")
names(bbone$dna_segs) <- names
## Plot
plot_gene_map(dna_segs=bbone$dna_segs, comparisons=bbone$comparisons)

## Using filter_low & changing reference sequence
bbone <- read_mauve_backbone(bbone_file, ref=2, filter_low=2000)
names(bbone$dna_segs) <- names
plot_gene_map(dna_segs=bbone$dna_segs, comparisons=bbone$comparisons)

## Read guide tree
tree_file <- system.file('extdata/barto.guide_tree', package = 'genoPlotR')
tree_str <- readLines(tree_file)
for (i in 1:length(names)){
  tree_str <- gsub(paste("seq", i, sep=""), names[i], tree_str)
}
tree <- newick2phylog(tree_str)
## Plot
plot_gene_map(dna_segs=bbone$dna_segs, comparisons=bbone$comparisons,
              tree=tree)

##
## From embl file
##
bq_embl_file <- system.file('extdata/BG_plasmid.embl', package = 'genoPlotR')
bq <- read_dna_seg_from_embl(bq_embl_file)

##
## From genbank file
##
bq_genbank_file <- system.file('extdata/BG_plasmid.gbk', package = 'genoPlotR')
bq <- read_dna_seg_from_file(bq_genbank_file, fileType="detect")

##
## From ptt files
##
## From a file
bq_ptt_file <- system.file('extdata/BQ.ptt', package = 'genoPlotR')
bq <- read_dna_seg_from_ptt(bq_ptt_file)
## Read directly from NCBI ftp site:
url <- "ftp://ftp.ncbi.nih.gov/genomes/Bacteria/Bartonella_henselae-Houston-1/NC_005956.p
attempt <- 0
## Not run:
while (attempt < 5){
  attempt <- attempt + 1
  bh <- try(read_dna_seg_from_ptt(url))
  if (!inherits(bh, "try-error")) {
    attempt <- 99
  }
}

```

```

    } else {
      print(paste("Tried", attempt, "times, retrying in 5s"))
      Sys.sleep(5)
    }
  }

## End(Not run)
## If attempt to connect to internet fails
if (!exists("bh")){
  data(barto)
  bh <- barto$dna_segs[[3]]
}

##
## Read from blast
##
bh_vs_bq_file <- system.file('extdata/BH_vs_BQ.blastn.tab',
                             package = 'genoPlotR')
bh_vs_bq <- read_comparison_from_blast(bh_vs_bq_file, color_scheme="grey")

## Plot
plot_gene_map(dna_segs=list(BH=bh, BQ=bq), comparisons=list(bh_vs_bq),
              xlims=list(c(1,50000), c(1, 50000)))

```

reverse

*Reverse objects***Description**

Reverse objects, mainly `dna_seg` and `comparison`

**Usage**

```

reverse(x, ...)
## Default S3 method:
reverse(x, ...)
## S3 method for class 'dna\_seg':
reverse(x, ...)
## S3 method for class 'comparison':
reverse(x, side = 0, ...)

```

**Arguments**

<code>x</code>	The object to reverse.
<code>...</code>	Unused.
<code>side</code>	In the case of comparisons, the side of the comparison that should be reversed. If <code>side=1</code> , the first side will be reversed. If <code>side=2</code> , the second side will be reversed. If <code>side&lt;1</code> , no side is reversed. If <code>side&gt;2</code> , both sides are reversed.

**Value**

The same object as input.

**Author(s)**

Lionel Guy

**See Also**[dna\\_seg](#), [comparison](#)**Examples**

```
## load data
data(three_genes)

## on dna_seg
dna_segs[[1]]
reverse(dna_segs[[1]])
## on comparison
reverse(comparisons[[2]], side=1)
reverse(comparisons[[2]], side=3)

## With mauve backbone
data(mauve_bbone)
## Plot
plot_gene_map(dna_segs=bbone$dna_segs, comparisons=bbone$comparisons)

## Reverse B_bacilliformis, and the corresponding comparison (first "side")
bbone$dna_segs[[1]] <- reverse(bbone$dna_segs[[1]])
bbone$comparisons[[1]] <- reverse(bbone$comparisons[[1]], 1)
plot_gene_map(dna_segs=bbone$dna_segs, comparisons=bbone$comparisons)
```

---

three\_genes

*Three genes data set*


---

**Description**

A set of three made-up genes, compared in three chromosomes.

**Usage**

```
data(three_genes)
```

**Format**

Two dataframes, representing the three genes in three DNA segments:

- `dna_segs` which is a list of three `dna_seg` objects, containing each three rows (or genes).
- `comparisons` which is a list of two `comparison` objects.

**Examples**

```
data(three_genes)
plot_gene_map(dna_segs, comparisons)
```

---

trim	<i>Trimming data frames with <math>\geq 2</math> numeric columns</i>
------	--

---

## Description

Trims data frames with 2 or more numeric columns using a xlim. xlim(s) are as used to filter rows whose numeric values are included in this interval.

## Usage

```
trim(x, ...)
## Default S3 method:
trim(x, xlim = NULL, ...)
## S3 method for class 'dna\_seg':
trim(x, xlim = NULL, ...)
## S3 method for class 'comparison':
trim(x, xlim1 = c(-Inf, Inf), xlim2 = c(-Inf, Inf), ...)
## S3 method for class 'annotation':
trim(x, xlim = NULL, ...)
```

## Arguments

x	An object to trim., generally a data frame or a matrix.
xlim	A numeric of length 2. In a general case, the rows whose values are included in this interval are returned.
...	Unused.
xlim1	A numeric of length 2. In the case of comparison, where the comparison can be filtered on two sides, the interval to filter the first side.
xlim2	A numeric of length 2. The interval to filter the second side.

## Value

Returns the same object as input, with the rows corresponding to the interval given.

## Author(s)

Lionel Guy

## See Also

[dna\\_seg](#), [comparison](#)

## Examples

```
## Load
data(barto)
xlim_ref <- c(10000, 45000)
## Seg 2 (ref)
barto$dna_segs[[2]] <- trim(barto$dna_segs[[2]], xlim=xlim_ref)
## Seg 1
barto$comparisons[[1]] <- trim(barto$comparisons[[1]], xlim2=xlim_ref)
```

```
xlim1 <- range(barto$comparisons[[1]], overall=FALSE)$xlim1
barto$dna_segs[[1]] <- trim(barto$dna_segs[[1]], xlim=xlim1)
## Seg 3
barto$comparisons[[2]] <- trim(barto$comparisons[[2]], xlim1=xlim_ref)
xlim3 <- range(barto$comparisons[[2]], overall=FALSE)$xlim2
barto$dna_segs[[3]] <- trim(barto$dna_segs[[3]], xlim=xlim3)
## Seg 4
barto$comparisons[[3]] <- trim(barto$comparisons[[3]], xlim1=xlim3)
xlim4 <- range(barto$comparisons[[3]], overall=FALSE)$xlim2
barto$dna_segs[[4]] <- trim(barto$dna_segs[[4]], xlim=xlim4)
## Plot
plot_gene_map(barto$dna_segs, barto$comparisons)
```

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