

GenomeGraphs

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AnnotationTrack-class

Class "AnnotationTrack"

Description

A generic object to store annotation

Objects from the Class

Objects can be created by calls of the form `new("AnnotationTrack", ...)`.

Slots

chr: Object of class "numeric"
strand: Object of class "numeric"
regions: Object of class "dfOrNULL"
dp: Object of class "DisplayPars"

Extends

Class "[gdObject](#)", directly.

Methods

drawGD signature(`gdObject = "AnnotationTrack"`):...
getPlotId signature(`obj = "AnnotationTrack"`):...
initialize signature(`.Object = "AnnotationTrack"`):...

Author(s)

James Bullard

Examples

```
showClass("AnnotationTrack")
```

BaseTrack-class *Class "BaseTrack" represents base specific data*

Description

Represents specific data, e.g. how many times was every base sequenced

Objects from the Class

Objects can be created by calls of the form `new("BaseTrack", ...)`.

Slots

base: Object of class "numeric". Is a vector of base positions

value: Object of class "numeric". Is a vector of corresponding values for every base

strand: Object of class "character" represents that DNA strand

dp: Object of class DisplayPars to control various features of how the track is displayed.

Extends

Class "[gdObject](#)", directly.

Methods

show signature(object = "BaseTrack"): ...

Author(s)

Steffen Durinck

References

<http://www.stat.berkeley.edu/~steffen/>

See Also

objects to See Also as [gdPlot](#)

Examples

```
if (interactive()) {
  data("exampleData", package="GenomeGraphs")
  ga <- new("GenomeAxis")
  bt <- new("BaseTrack", base = yeastCons1[,1], value = yeastCons1[,2],
           dp = DisplayPars(color = "darkblue"))
  gdPlot(list(ga, bt))
}
```

 cn

Contains dummy copy number data

Description

Contains dummy copy number data

Examples

```
#
```

 DisplayPars-class *Class "DisplayPars" is used to specify graphical parameters to gObjects.*

Description

The DisplayPars functions analogously to par and gp. Generally the class is instantiated using the DisplayPars function rather than directly.

Objects from the Class

Objects can be created by calls of the form `DisplayPars(...)` rather than calls to: `new("DisplayPars", ...)` by calling the `DisplayPars` function directly in the constructor the `gObjects` are guaranteed to have the appropriate defaults.

Slots

pars: Object of class "environment" Generally this slot is not accessed directly.

Methods

getPar signature(`obj = "DisplayPars"`): gets a graphical parameter by name

initialize signature(`.Object = "DisplayPars"`): This constructor should not be called directly.

setPar signature(`obj = "DisplayPars"`): sets a graphical parameter - see the example below. Often it is easier to set the graphical parameter from within the `gObject`.

show signature(`object = "DisplayPars"`): prints current graphical parameters

Warning

The `DisplayPars` class should not be manipulated directly. The preferred method for interacting with the class can be seen in the example below.

Author(s)

James Bullard

Examples

```
showClass("DisplayPars")

if (interactive()) {
  minbase = 10000
  maxbase = 15000
  mart <- useMart("ensembl", dataset = "scerevisiae_gene_ensembl")
  genesplus <- new("GeneRegion", start = minbase, end = maxbase, biomart = mart,
                 strand = "+", chromosome = "I", dp = DisplayPars(size = 2))
  ## plot it.
  gdPlot(list(genesplus, new("Title", title = "genes")), minbase, maxbase)

  ## to obtain a list of the current graphical parameters:
  print(genesplus@dp)

  ## to set a parameter:
  setPar(genesplus, "protein_coding", "pink")
  gdPlot(list(genesplus, new("Title", title = "genes")), minbase, maxbase)
}
```

DisplayPars

DisplayPars constructs objects of type DisplayPars which are used to effect the display of gObjects

Description

DisplayPars takes any number of named arguments which will be used by the drawGD method of the gObject. These arguments are analogous to both par and gp of the traditional and grid graphics systems respectively. Different functions support different graphical parameters - thus it is necessary to consult the documentation of the particular gObject to determine which DisplayPars will be used.

Usage

```
DisplayPars(...)
```

Arguments

... name value pairs

Details

It is not recommended to call `new("DisplayPars", ...)` directly; rather this function `DisplayPars()` should be called instead. If a gObject has already been instantiated then the appropriate method for changing graphical parameters is: `setPar`.

Value

Returns an object of type DisplayPars, generally this will be called during a call to the `new` function for a particular gObject.

Author(s)

James Bullard

Examples

```
minbase = 10000
maxbase = 15000
mart <- useMart("ensembl", dataset = "scerevisiae_gene_ensembl")
genesplus <- new("GeneRegion", start = minbase, end = maxbase, biomart = mart,
  strand = "+", chromosome = "I", dp = DisplayPars(color =
  "red"))
gaxis <- new("GenomeAxis", add53 = TRUE, add35 = TRUE)
genesminus <- new("GeneRegion", start = minbase, end = maxbase, biomart = mart,
  strand = "-", chromosome = "I", dp = DisplayPars(color =
  "purple", size = 2))
title <- new("Title", title = "genes in a region")
gdPlot(list(genesplus, gaxis, genesminus, title), minbase, maxbase)
```

drawGD

Generic called on each gdObject to do the plotting.

Description

This generic gets called on each of the gdObjects (obviously the generic is implemented by a method for each object) and thus if a user wishes to implement new gdObjects they need to have access to this generic.

Usage

```
drawGD(gdObject, minBase, maxBase, vpPosition, ...)
```

Arguments

gdObject

minBase

maxBase

vpPosition

... Ignored

ExonArray-class *Class "ExonArray" representing probe level exon array data from Affymetrix*

Description

Represents probe level exon array data from Affymetrix. Makes it possible to visualize alternative splicing as measured by the Affymetrix exon array platform and relate it to known transcript isoforms annotated by Ensembl

Objects from the Class

Objects can be created by calls of the form `new("ExonArray", ...)`.

Slots

intensity: Object of class "matrix", array data matrix containing probes as the rows and samples as the columns

probeStart: Object of class "numeric" vector with the start positions of the probes

probeEnd: Object of class "numeric" vector with the end positions of the probes

probeId: Object of class "character" vector containing the probeset identifiers

nProbes: Object of class "numeric" vector defining how many probes there are for each exon/probeset

size: Object of class "numeric" specifying the size of the ExonArray plot in the final plot

displayProbesets: Object of class "logical" used to indicate if probe set names should be plotted or not

probesetSize: Object of class "numeric" font size of the probeset identifiers to be plotted

color: Object of class "character" vector of colors or one color that will be used to draw the intensity values

mapColor: Object of class "character" specifying the color of the lines that map the probeset positions to the Ensembl gene annotation

lwd: Object of class "numeric" vector of line widths to be used to plot the intensity data.

lty: Object of class "character" vector of line types to be used to plot the intensity data.

Extends

Class "[gdObject](#)", directly.

Methods

show signature(object = "ExonArray"): ...

Author(s)

Steffen Durinck

References

<http://www.stat.berkeley.edu/~steffen/>

See Also

objects to See Also as [gdPlot](#)

Examples

```
if(interactive()){
  data("unrData", package="GenomeGraphs")
  library(biomaRt)
  mart = useMart("ensembl", dataset="hsapiens_gene_ensembl")

  title = new("Title", title = "ENSG00000009307", dp = DisplayPars(color = "darkslategray"))
  exmapcol = rep("khaki", length(unrNProbes))
  exmapcol[28]="darkred"
  probeSetCol = rep("grey", length(unrNProbes))
  probeSetCol[27:28]="darkslategray"
  probeSetLwd = rep(1, length(unrNProbes))
  probeSetLwd[27:28]=3

  exon = new("ExonArray", intensity = unrData, probeStart = unrPositions[,3], probeEnd=unrP
  exon2 = new("ExonArray", intensity = unrData, probeStart = unrPositions[,3], probeEnd=unrP

  affyModel = new("GeneModel", exonStart = unrPositions[,3], exonEnd = unrPositions[,4])
  gene = new("Gene", id = "ENSG00000009307", biomaRt = mart)
  transcript = new("Transcript", id = "ENSG00000009307" , biomaRt = mart)
  legend = new("Legend", legend = c("affyModel", "gene"), dp = DisplayPars(color= c("darkgre

  gdPlot(list(title,exonarray1 = exon2,exonarray2= exon, AffymetrixModel= affyModel, gene,
  }
```

exonProbePos	<i>Contains dummy exon probe positions</i>
--------------	--

Description

Contains dummy exon probe positions

Examples

```
#
```

gdObject-class	<i>Class "gdObject" is the parent class of all of the objects in the system.</i>
----------------	--

Description

The gdObject is the superclass of all the classes in the system and provides some basic functionality for displaying and managing graphical parameters.

Objects from the Class

Objects can be created by calls of the form `new("gdObject", ...)`. Generally, this class is meant to be subclassed and not created directly.

Slots

dp: Object of class "DisplayPars" ~~

Methods

getCex signature(obj = "gdObject"): ...
getColor signature(obj = "gdObject"): ...
getLty signature(obj = "gdObject"): ...
getLwd signature(obj = "gdObject"): ...
getPar signature(obj = "gdObject"): ...
getPch signature(obj = "gdObject"): ...
getPointSize signature(obj = "gdObject"): ...
getSize signature(obj = "gdObject"): ...
initialize signature(.Object = "gdObject"): ...
setPar signature(obj = "gdObject"): ...
showDisplayOptions signature(obj = "gdObject"): ...
showDisplayOptions signature(obj = "character"): ...

Author(s)

James Bullard

Examples

```
showClass("gdObject")
```

 gdPlot

gdPlot is the main plotting function of the GenomeGraphs package

Description

gdPlot is the main plotting function of the GenomeGraphs package. A collection of objects are given as a list and these will then be plotten in the order given.

Usage

```
gdPlot(gdObjects, minBase = NA, maxBase = NA, overlays = NULL,
       labelColor = "black", labelCex = 1, labelRot = 90)
```

Arguments

gdObjects	This is either a list of gdObjects which will be plotted from top to bottom or a single gdObjects to be plotted.
minBase	minBase defines the minimum base that will be plotted, if ommitted a minimum is determined from the objects in gdObjects if possible.
maxBase	maxBase defines the maximum base that will be plotted,if ommitted a minimum is determined from the objects in gdObjects if possible.

overlays	overlays defines a set of regions to overlay on the plot. This argument is either a list or a single Overlay object.
labelColor	Draw the labels with the given colors.
labelCex	Character expansion factor.
labelRot	Rotate the track labels labelRot degrees.

Author(s)

Steffen Durinck and James Bullard

References

<http://www.stat.berkeley.edu/~steffen/>

Examples

```
data("exampleData", package="GenomeGraphs")

minbase = min(probestart)
maxbase = max(probestart)

mart = useMart("ensembl", dataset="hsapiens_gene_ensembl")

genesplus = new("GeneRegion", start = minbase, end = maxbase, strand = "+", chromosome = "3")
genesmin = new("GeneRegion", start = minbase, end = maxbase, strand = "-", chromosome = "3")

seg <- new("Segmentation", segments = segments,
           segmentStart = segStart, segmentEnd = segEnd, dp = DisplayPars(color = "dodgerblue"))

cop <- new("GenericArray", intensity = cn, probeStart = probestart,
           segmentation = seg, dp = DisplayPars(size=3, color = "seagreen", type="dot"))

ideog = new("Ideogram", chromosome = "3")
expres = new("GenericArray", intensity = intensity, probeStart = exonProbePos, dp = DisplayPars(size=3, color = "seagreen", type="dot"))
genomeAxis = new("GenomeAxis", add53 = TRUE, add35=TRUE)
gdPlot(list(ideog,expres,cop,genesplus,genomeAxis,genesmin), minBase = minbase, maxBase = maxbase)
```

geneBiomart

AnnotationTrack objects from biomaRt

Description

Convenience function to construct an AnnotationTrack object from biomaRt.

Usage

```
geneBiomart(id, biomaRt, type = "ensembl_gene_id", dp = NULL)
```

Arguments

id ~~Describe id here~~
biomart ~~Describe biomart here~~
type ~~Describe type here~~
dp ~~Describe dp here~~

Value

An AnnotationTrack object

Author(s)

James Bullard

Gene-class

Class "Gene" represents the Ensembl Gene level annotation

Description

Class "Gene" represents the Ensembl Gene level annotation. Upon creation of an object of this class, intron and exon boundaries are retrieved from Ensembl

Objects from the Class

Objects can be created by calls of the form `new("Gene", ...)`.

Slots

id: Object of class "character", representing a unique identifier for the gene or a vector of identifiers for genes that are located near each other (or at least on the same chromosome)

type: Object of class "character", representing the type of identifier used, e.g. hgnc_symbol, entrezgene and ensembl_gene_id, check the listFilters function of the biomaRt package for more identifier options

size: Object of class "numeric", specifies the size of the plot

color: Object of class "character", specifies the color of the exons

biomart: Object of class "Mart", contains the link to the Ensembl database and should be created using the useMart function from the biomaRt package

ens: Object of class "data.frame", contains the output from the Ensembl query, users don't need to give a value to this

Methods

initialize signature(.Object = "Gene"): ...

drawGD signature(.Object = "Gene"): ...

show signature(object = "Gene"): ...

Author(s)

Jim Bullard and Steffen Durinck

References

<http://www.stat.berkeley.edu/~steffen/>

See Also

objects to See Also as [gdPlot](#)

Examples

```
if(interactive()){
  mart = useMart("ensembl", dataset="hsapiens_gene_ensembl")
  gene = new("Gene", id = "ENSG00000095203", type="ensembl_gene_id", biomart = mart)
  gdPlot(list(gene), minBase= 110974000, maxBase = 111122900)
}
```

GeneModel-class *Class "GeneModel", represents a custom gene model*

Description

This class represents a custom gene model defined by exon boundaries. An example of this class could be an Affymetrix gene model used to create the Affy Exon array

Objects from the Class

Objects can be created by calls of the form `new("GeneModel", ...)`.

Slots

exonStart: Object of class "numeric", vector containing the start positions of the exons that are to be drawn

exonEnd: Object of class "numeric", vector containing the end positions of the exons that are to be drawn

chromosome: Object of class "numeric", chromosome name

dp: Object of class "DisplayPars", color of the exons and size of the exon model in the final plot

Methods

No methods defined with class "GeneModel" in the signature.

Author(s)

Steffen Durinck

References

<http://www.stat.berkeley.edu/~steffen/>

See Also

objects to See Also as [gdPlot](#)

Examples

```
data("unrData", package="GenomeGraphs")
affyModel = new("GeneModel", exonStart = unrPositions[,3], exonEnd = unrPositions[,4])
gdPlot(list(affyModel), minBase = min(unrPositions[,3]), maxBase=max(unrPositions[,4]))
```

geneRegionBiomart *Construct an AnnotationTrack object from biomart.*

Description

This function constructs an AnnotationTrack object from Biomart. It is a convenience function.

Usage

```
geneRegionBiomart(chr, start, end, strand, biomart, dp = NULL, chrFunction = fun
```

Arguments

chr	chr An integer
start	start The start location
end	end The end location
strand	strand An integer -1, 0, 1
biomart	biomart A mart
dp	dp DisplayPars object
chrFunction	chrFunction A function which takes chr and converts it into the correct representation for biomart. For instance yeast likes to have chromosomes as roman numerals so you can use as.roman here.
strandFunction	strandFunction Analogous to chrFunction, but for strand. The internal representation of strand is -1,0,1 whereas biomart has different species dependent representations.

Value

An AnnotationTrack object.

Author(s)

James Bullard

GeneRegion-class *Class "GeneRegion", representing gene structures in a defined genomic region*

Description

Given a start and end position and a chromosome name, all gene structures in this region will be retrieved from Ensembl upon creation of the object.

Objects from the Class

Objects can be created by calls of the form `new("GeneRegion", ...)`.

Slots

start: Object of class "numeric", start position

end: Object of class "numeric", end position

chromosome: Object of class "character", chromosome name

strand: Object of class "character", represents the strand from which the gene structures should be retrieved. Value is either + or -

size: Object of class "numeric", represents the size of the GeneRegion in the final plot

color: Object of class "character", represents the color to be used to plot the exons

biomart: Object of class "Mart", containing the link to the Ensembl database. This should be created by the `useMart` function from the `biomaRt` package

ens: Object of class "data.frame", output of the `biomaRt` query, should not be used by users

Methods

drawGD signature(.Object = "GeneRegion"): ...

initialize signature(.Object = "GeneRegion"): ...

show signature(object = "GeneRegion"): ...

Author(s)

Steffen Durinck

References

<http://www.stat.berkeley.edu/~steffen/>

See Also

objects to See Also as [gdPlot](#)

Examples

```

if(interactive()){
  mart = useMart("ensembl", dataset="hsapiens_gene_ensembl")
  plusStrand = new("GeneRegion", chromosome = "17", start = 30450000, end = 30550000, strand = "+")
  genomeAxis = new("GenomeAxis", add53=TRUE)
  gdPlot(list(genomeAxis, plusStrand), minBase = 30450000, maxBase = 30550000)
}

```

GenericArray-class *Class "GenericArray", representing array data*

Description

The Generic Array class is a class that can be used to create plots from array data such as microarrays and arrayCGH platforms. It can represent the data as line plots or dot plots and segments can be included as well

Objects from the Class

Objects can be created by calls of the form `new("GenericArray", ...)`.

Slots

intensity: Object of class "matrix", matrix containing the intensities of expression or cgh data. Rows should be probes, columns samples

probeStart: Object of class "numeric", start position of the probes

probeEnd: Object of class "numeric", end position of the probes if available

type: Object of class "character", has two values: line and point. If line is selected then a line will be plotted for each sample. If point is selected, points will be plotted.

segments: Object of class "list", if segments are available they have to be represented as a list, each position in the list should correspond to each sample as defined by the columns of the intensity matrix

segmentStart: Object of class "list", containing the start positions of the segments

segmentEnd: Object of class "list", containing the end positions of the segments

color: Object of class "character", represents the color to be used to plot the intensity matrix, can be a vector of colors for multiple samples

lty: Object of class "character", if line is selected as type, lty specifies which line type should be used. Can be a vector of line types for multiple samples

pch: Object of class "numeric", if point is selected as type then pch represents which symbol should be used to plot the points

pointSize: Object of class "numeric", specifies the point size if point is selected as type

lwd: Object of class "numeric", specifies the line width if line is selected as type. Can be a vector of line widths if multiple samples are present

size: Object of class "numeric" representing the size of the Array plot in the final plot

segmentColor: Object of class "character". If segments are to be plotted, this will define the color of the segment lines

Methods

show signature(object = "GenericArray"): ...

Author(s)

Steffen Durinck

References

<http://www.stat.berkeley.edu/~steffen/>

See Also

objects to See Also as [gdPlot](#)

Examples

```
if(interactive()){
  data("exampleData", package="GenomeGraphs")

  minbase <- 180292097
  maxbase <- 180492096
  ideog <- new("Ideogram", chromosome = "3")
  expres <- new("GenericArray", intensity = intensity, probeStart = exonProbePos,
               dp = DisplayPars(color="darkred", type="point"))
  gdPlot(list(ideog, expres), minBase = minbase, maxBase =maxbase)
}
```

GenomeAxis-class *Class "GenomeAxis", representing a genomic coordinate axis*

Description

Represents a genomic coordinate axis

Objects from the Class

Objects can be created by calls of the form `new("GenomeAxis", ...)`.

Slots

add53: Object of class "logical", indicating if 5 to 3 prime direction needs to be plotted

add35: Object of class "logical", indicating if 3 to 5 prime direction needs to be plotted

dp: Object of class "DisplayPars", containing the display parameters such as size of the plot and color

littleTicks: Object of class "logical", indicating if the genome axis should be dense for improved locating of regions of interest.

Methods

No methods defined with class "GenomeAxis" in the signature.

Author(s)

Steffen Durinck

References

<http://www.stat.berkeley.edu/~steffen/>

See Also

objects to See Also as [gdPlot](#)

Examples

```
if(interactive()){
  mart = useMart("ensembl", dataset="hsapiens_gene_ensembl")
  genomeAxis = new("GenomeAxis", add53=TRUE)
  plusStrand = new("GeneRegion", chromosome = "17", start = 30450000, end = 30550000, strand = "+")
  gdPlot(list(genomeAxis, plusStrand), minBase = 30450000, maxBase = 30550000)
}
```

getPar

Retrieves a display parameter from an object.

Description

Retrieves a display parameter from an object.

Usage

```
getPar(obj, name, ...)
```

Arguments

obj	A gdObject or DisplayPars object.
name	Name of parameter to return.
...	Ignored

Examples

```
a <- new("GenomeAxis")
getPar(a, "size")
```

 HighlightRegion-class

Class "HighlightRegion" is used to highlight vertical blocks of genomic regions.

Description

HighlightRegion is used to highlight a genomic region of interest. The class offers the ability to highlight or block out regions of interest.

Objects from the Class

Objects can be created by calls of the form `new("HighlightRegion", ...)`.

Slots

start: Object of class "numeric" genomic start position.

end: Object of class "numeric" genomic end position.

region: Object of class "numericOrNull" start and end number of the tracks to be covered by the region. These start from the first track (top = 1) to the last track: `length(gdObjects)` in the call to `gdObject`

coords: Object of class "character" can be either "genomic" or "absolute", if the coordinates are "absolute" then one can plot things using the coordinate space defined by: lower-left (0,0) upper-right (1,1). In this case, `start = x0`, `end = x1` and then `region = (y0, y1)`. See the examples for more details.

dp: Object of class "DisplayPars" specifies the various display parameters.

Extends

Class "[gdObject](#)", directly.

Methods

No methods defined with class "HighlightRegion" in the signature.

Author(s)

James Bullard

Examples

```
if (interactive()) {
  data("exampleData", package="GenomeGraphs")

  ga <- new("GenomeAxis")
  grF <- new("GeneRegion", start = 10000, end = 20000, chromosome = "I", strand = "+", biom
  grR <- new("GeneRegion", start = 10000, end = 20000, chromosome = "I", strand = "-", biom
  bt <- new("BaseTrack", base = yeastCons1[,1], value = yeastCons1[,2])
  hr1 <- new("HighlightRegion", start = 11000, end = 13000,
            dp = DisplayPars(alpha = 1, color = "red", lty = "dashed", lwd = 3))
  hr2 <- new("HighlightRegion", start = 15900, end = 16500)
```

```
gdPlot(list(grF, ga, grR, bt), highlightRegions = list(hr1, hr2))
}
```

Ideogram-class *Class "Ideogram", represent an Ideogram*

Description

An ideogram is a representation of a chromosome containing the banding pattern. Note that currently ideograms are only available for hsapiens.

Objects from the Class

Objects can be created by calls of the form `new("Ideogram", ...)`.

Slots

chromosome: Object of class "character", representing the chromosome that needs to be drawn. E.g. 3 if chromosome 3 needs to be drawn or Y for Y chromosome.

dp: Object of class "DisplayPars", can be used to specify the size (default 1) of the ideogram in the final plot and to specify the highlighting color

Methods

No methods defined with class "Ideogram" in the signature.

Author(s)

Steffen Durinck

References

<http://www.stat.berkeley.edu/~steffen/>

See Also

objects to See Also as [gdPlot](#)

Examples

```
if(interactive()){
  data("exampleData", package="GenomeGraphs")

  minbase <- 180292097
  maxbase <- 180492096
  ideog <- new("Ideogram", chromosome = "3")
  expres <- new("GenericArray", intensity = intensity, probeStart = exonProbePos,
               dp = DisplayPars(color="darkred", type="point"))
  gdPlot(list(ideog, expres), minBase = minbase, maxBase =maxbase)
}
```

ideogramTab	<i>Contains info to plot ideograms</i>
-------------	--

Description

Contains info to plot ideograms

Format

The format is: chr "ideogramTab"

Source

NCBI

Examples

```
data(ideogramTab)
## maybe str(ideogramTab) ; plot(ideogramTab) ...
```

intensity	<i>Contains dummy intensity data</i>
-----------	--------------------------------------

Description

Contains dummy intensity data

Examples

```
#
```

Legend-class	<i>Class "Legend", represents a legend to add to a plot</i>
--------------	---

Description

This class represents a legend

Objects from the Class

Objects can be created by calls of the form `new("Legend", ...)`.

Slots

legend: Object of class "character", vector with names of the items in the legend

dp: Object of class "DisplayPars" size of the legend (size), the size of the font (cex) and the colors (color) of the legend

Methods

No methods defined with class "Legend" in the signature.

Author(s)

Steffen Durinck

References

<http://www.stat.berkeley.edu/~steffen/>

See Also

objects to See Also as [gdPlot](#)

Examples

```
showClass("Legend")
```

```
makeAnnotationTrack
```

Create objects of class AnnotationTrack

Description

Convenience function for constructing objects of class AnnotationTrack.

Usage

```
makeAnnotationTrack(regions = NULL, chr = NULL, strand = NULL, start = NULL, end = NULL, feature = NULL, group = NULL, ID = NULL, dp = NULL)
```

Arguments

regions	A dataframe with columns start, end, feature, group, ID. start and end delineate the boundaries of the boxes feature can be used to color the boxes. Group denotes linking so generally exons from a gene form a group. Finally, ID can be used to plot names on boxes.
chr	The chromosome of the regions (can be ignored)
strand	The strand of the regions (can be ignored)
start	If regions is missing then we construct a dataframe from the remaining parameters.
end	Construct regions with this vector
feature	Construct regions with this feature vector or scalar
group	Defines a grouping
ID	Defines an ID for each annotation bit
dp	DisplayPars, in this case we can create a mapping between feature and color. So lets say in the feature column you have: gene, transcript, gene, then in the dp you can say gene = 'blue' and transcript = 'green'

Value

Returns an object of class AnnotationTrack

Examples

```
a <- makeAnnotationTrack(start = c(10, 15, 25), end = c(12, 19, 31),
                        group = c(1,1,2), feature = c("gene", "gene", "tf"),
                        ID = paste("id", 1:3, sep = ""), dp = DisplayPars(gene = 'blue'))
gdPlot(a, minBase = 0, maxBase = 40)
```

makeBaseTrack	<i>Creates an object of class BaseTrack</i>
---------------	---

Description

Creates an object of class BaseTrack, which can represent many datasets containing a base given by a vector of positions and a corresponding vector with values for these base positions

Usage

```
makeBaseTrack(base, value, strand, segmentation, dp = NULL)
```

Arguments

base	Numeric vector of base positions
value	Numeric vector with values for these base positions
strand	Character either + or - representing the strand
segmentation	Object of class Segmentation, used when segments are needed to be drawn
dp	Object of class DisplayPars representing the display parameters of the plot

Value

Object of class BaseTrack

Author(s)

Jim Bullard and Steffen Durinck

References

~put references to the literature/web site here ~

See Also

[DisplayPars](#), [gdPlot](#)

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--    or do help(data=index) for the standard data sets.

## The function is currently defined as
function (base, value, strand, segmentation, dp = NULL)
{
  pt <- getClass("BaseTrack")@prototype
  if (is.null(dp))
    dp <- pt@dp
  if (missing(strand))
    strand <- pt@strand
  if (missing(segmentation))
    segmentation <- pt@segmentation
  if (missing(base))
    stop("Need base argument to know the base positions to plot the data on the genome")
  if (missing(value))
    stop("Need value argument")
  new("BaseTrack", base = base, value = value, strand = strand,
      dp = dp, segmentation = segmentation)
}
```

makeExonArray

Creates and object of class ExonArray

Description

Creates an object of class ExonArray, representing exon array microarray data

Usage

```
makeExonArray(intensity, probeStart, probeEnd, probeId, nProbes, displayProbesets)
```

Arguments

intensity	Matrix of intensities, probes in the rows, samples in the columns
probeStart	Vector of probe start positions
probeEnd	Vector of probe end positions (optional)
probeId	Character vector containing the probe identifiers
nProbes	Vector indicating how many probes are in each probeset
displayProbesets	Logical indicating if the probeset identifier should be displayed or not
dp	Object of class DisplayPars to set the display parameters

Value

Object of ExonArray class

Author(s)

Steffen Durinck and Jim Bullard

References

~put references to the literature/web site here ~

See Also

[gdPlot](#)

Examples

```
##----- Should be DIRECTLY executable !! -----
##-- ==> Define data, use random,
##--      or do help(data=index) for the standard data sets.

## The function is currently defined as
function (intensity, probeStart, probeEnd, probeId, nProbes,
         displayProbesets = FALSE, dp = NULL)
{
  pt <- getClass("ExonArray")@prototype
  if (is.null(dp))
    dp <- pt@dp
  if (missing(probeEnd))
    probeEnd <- pt@probeEnd
  if (missing(probeId))
    probeId <- pt@probeId
  if (missing(nProbes))
    nProbes <- pt@nProbes
  if (is.null(dp))
    dp <- getClass("ExonArray")@prototype@dp
  new("ExonArray", intensity = intensity, probeStart = probeStart,
      probeEnd = probeEnd, probeId = probeId, nProbes = nProbes,
      displayProbesets = displayProbesets, dp = dp)
}
```

makeGeneModel

Creates an object of class GeneModel

Description

Creates an object of class GeneModel representing a custom annotation or gene model

Usage

```
makeGeneModel(start, end, chromosome, dp = NULL)
```

Arguments

start	Vector of start positions for exons
end	Vector of end positions for exons
chromosome	chromosome name
dp	Display parametes represented as an object of class DisplayPars

Value

Object of class GeneModel

Author(s)

Steffen Durinck and Jim Bullard

References

~put references to the literature/web site here ~

See Also

[DisplayPars](#)

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--    or do help(data=index) for the standard data sets.

## The function is currently defined as
function (start, end, chromosome, dp = NULL)
{
  if (is.null(dp))
    dp <- getClass("GeneModel")@prototype@dp
  new("GeneModel", exonStart = start, exonEnd = end, dp = dp)
}
```

makeGene

Creates an object of class Gene

Description

Creates an object of class Gene. This represents a gene structure as annotated in Ensembl.

Usage

```
makeGene(id, type, biomart, dp = NULL)
```

Arguments

id	An identifier used to specify of which gene the intron-exon structure should be retrieved
type	The type of identifiers used, examples are ensembl_gene_id, hgnc_symbol, entrezgene. See listAttributes function of the biomaRt package for more info
biomart	Mart object, created by the useMart function of biomaRt
dp	object of class DisplayPars, determines the display of features on the plot

Value

An object of class Gene

Author(s)

Steffen Durinck and Jim Bullard

References

~put references to the literature/web site here ~

See Also[gdPlot](#)**Examples**

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--    or do help(data=index) for the standard data sets.

## The function is currently defined as
function (id, type, biomaRt, dp = NULL)
{
  if (missing(id))
    stop("Need to specify a gene identifier for creating a Gene")
  pt <- getClass("Gene")@prototype
  if (is.null(dp))
    dp <- pt@dp
  if (missing(type))
    type = pt@type
  new("Gene", id = id, type = type, biomaRt = biomaRt, dp = dp)
}
```

makeGeneRegion	<i>Creates an object of class Gene containing the intron-exon structures of genes</i>
----------------	---

Description

Creates an object of class Gene containing the intron-exon structures of genes. Given a start and end position, strand and chromosome, all the intron-exon structures of all genes laying in this region will be retrieved.

Usage

```
makeGeneRegion(start, end, chromosome, strand, biomaRt, dp = NULL)
```

Arguments

start	Start position on chromosome
end	End position on chromosome
chromosome	Chromosome name
strand	Strand either + or -
biomaRt	Mart object, created by the useMart function of biomaRt
dp	Object of class DisplayPars, determines the display of features on the plot

Value

An object of class Gene

Author(s)

Steffen Durinck and Jim Bullard

References

~put references to the literature/web site here ~

See Also

[gdPlot](#)

Examples

```
##----- Should be DIRECTLY executable !! -----
##-- ==> Define data, use random,
##--    or do help(data=index) for the standard data sets.

## The function is currently defined as
function (start, end, chromosome, strand, biomart, dp = NULL)
{
  if (missing(start))
    stop("Need to specify a start for creating a GeneRegion")
  pt <- getClass("GeneRegion")@prototype
  if (is.null(dp))
    dp <- pt@dp
  if (is.numeric(chromosome))
    chromosome = as.character(chromosome)
  new("GeneRegion", start = start, end = end, chromosome = chromosome,
      strand = strand, biomart = biomart, dp = dp)
}
```

makeGenericArray *Creates an object of class GenericArray*

Description

Creates an object of class Generic Array representing microarray data. This could be gene expression, array CGH, etc.

Usage

```
makeGenericArray(intensity, probeStart, probeEnd, segmentation, dp = NULL)
```

Arguments

intensity	Matrix of intensities, probes in the rows, samples in the columns
probeStart	Vector of start positions for the probes
probeEnd	Vector of end positions for probes (optional)
segmentation	Object of class Segmentation, needs to be added if segments should be plotted as well
dp	Object of class DisplayPars which handles the display parameters for plotting

Value

Object of class GenericArray

Author(s)

Jim Bullard and Steffen Durinck

References

BMC bioinformatics 2009

See Also

gdPlot

Examples

```
function (intensity, probeStart, probeEnd, segmentation, dp = NULL)
{
  pt <- getClass("GenericArray")@prototype
  if (is.null(dp))
    dp <- pt@dp
  if (missing(probeEnd))
    probeEnd <- pt@probeEnd
  if (missing(segmentation))
    segmentation <- pt@segmentation
  if (missing(probeStart))
    stop("Need probeStart argument to know where to plot the data on the genome")
  new("GenericArray", intensity = intensity, probeStart = probeStart,
      probeEnd = probeEnd, dp = dp, segmentation = segmentation)
}
```

makeGenomeAxis *Creates an object of class GenomeAxis*

Description

Creates an object of class GenomeAxis, representing a genome coordinate axis.

Usage

```
makeGenomeAxis(add53 = FALSE, add35 = FALSE, littleTicks = FALSE, dp = NULL)
```

Arguments

add53	Add a 5 to 3 prime label
add35	Add a 3 to 5 prime label
littleTicks	Add smaller ticks between larger ticks
dp	Set the display parameters see DisplayPars

Value

Object of class GenomeAxis

Author(s)

Jim Bullard and Steffen Durinck

References

~put references to the literature/web site here ~

See Also

[DisplayPars](#), [gdPlot](#)

Examples

```
##----- Should be DIRECTLY executable !! -----
##-- ==> Define data, use random,
##--    or do help(data=index) for the standard data sets.

## The function is currently defined as
function (add53 = FALSE, add35 = FALSE, littleTicks = FALSE,
         dp = NULL)
{
  if (is.null(dp))
    dp <- getClass("GenomeAxis")@prototype@dp
  new("GenomeAxis", add53 = add53, add35 = add35, dp = dp)
}
```

makeIdeogram

Creates object of class Ideogram

Description

Creates object of class Ideogram

Usage

```
makeIdeogram(chromosome, dp = NULL)
```

Arguments

chromosome	Chromosome to represent (currently human only)
dp	Display parameters such as color and size

Value

Object of class Ideogram

Author(s)

Jim Bullard and Steffen Durinck

References

~put references to the literature/web site here ~

See Also

[gdPlot](#)

Examples

```
##----- Should be DIRECTLY executable !! -----
##-- ==> Define data, use random,
##--      or do help(data=index) for the standard data sets.

## The function is currently defined as
function (chromosome, dp = NULL)
{
  if (missing(chromosome))
    stop("Need to specify chromosome for creating an Ideogram")
  if (is.numeric(chromosome)) {
    chromosome = as.character(chromosome)
  }
  if (is.null(dp))
    dp <- getClass("Ideogram")@prototype@dp
  new("Ideogram", chromosome = chromosome, dp = dp)
}
```

makeLegend

Creates an object of class Legend

Description

Creates an object of class Legend which can be used to plot a legend

Usage

```
makeLegend(text, fill, cex)
```

Arguments

text	Vector of characters representing the legend
fill	Vector of colors to fill the legend boxes
cex	Font size of the legend

Value

Object of class Legend

Author(s)

Jim Bullard and Steffen Durinck

References

~put references to the literature/web site here ~

See Also

See Also as [gdPlot](#)

Examples

```
##----- Should be DIRECTLY executable !! -----
##-- ==> Define data, use random,
##--      or do help(data=index) for the standard data sets.

## The function is currently defined as
function (text, fill, cex)
{
  dp <- getClass("Legend")@prototype@dp
  if (!missing(cex))
    setPar(dp, "cex", cex)
  if (!missing(fill))
    setPar(dp, "color", fill)
  new("Legend", legend = text, dp = dp)
}
```

makeRectangleOverlay

Create a rectangular overlay

Description

Construct ractangular overlays.

Usage

```
makeRectangleOverlay(start, end, region = NULL, coords = c("genomic", "absolute"))
```

Arguments

start	Start position in coords coordinates
end	End position in coords coordinates
region	Which tracks to span, or the y (vertical range)
coords	Which coordinate system to use, if absolute then the range is from 0,1 and region become the y coordinates
dp	The display parameters

Details

The rectangular overlay can be used to plot overlays in either genomic or absolute coordinates. If coordinates are absolute then the region argument becomes the y arguments.

Value

An object of class RectangleOverlay

Examples

```
data("exampleData", package = "GenomeGraphs")
cop <- makeGenericArray(intensity = cn, probeStart = probestart,
                        dp = DisplayPars(size=3, color = "seagreen", type="dot"))
gdPlot(list(makeGenomeAxis(), cop), overlays =
        makeRectangleOverlay(start = 180350000, end = 180350000 + 1e5, dp = DisplayPars(al
```

makeSegmentation *Create objects of class segmentation*

Description

Construct objects of class segmentation

Usage

```
makeSegmentation(start, end, value, dp = NULL)
```

Arguments

start	Either a list or a vector. If it is a list then it is a list of vectors of start position (this is the way it is represented in the segmentation class) If it is a vector it is a vector of start positions.
end	Same as start, but the corresponding end positions.
value	The y value of the segmentation, ie. segments(start[i], value[i], end[i], value[i])
dp	The Display parameters.

Value

An object of class Segmentation

Examples

```
data("exampleData", package="GenomeGraphs")
seg <- makeSegmentation(segStart, segEnd, segments,
                        dp = DisplayPars(color = "black", lwd=2, lty = "solid"))
cop <- makeGenericArray(intensity = cn, probeStart = probestart,
                        segmentation = seg, dp = DisplayPars(size=3, color = "seagreen",
gdPlot(cop)
```

makeTextOverlay *Create objects of class TextOverlay*

Description

Create objects of class TextOverlay

Usage

```
makeTextOverlay(text, xpos, ypos, region = NULL, coords = c("genomic", "absolute"))
```

Arguments

text	The text to plot
xpos	The xposition of the text
ypos	The yposition of the text
region	
coords	
dp	The display parameters

Value

Returns class of TextOverlay

Examples

```
data("exampleData", package="GenomeGraphs")
seg <- makeSegmentation(segStart, segEnd, segments,
                        dp = DisplayPars(color = "black", lwd=2, lty = "solid"))
cop <- makeGenericArray(intensity = cn, probeStart = probestart,
                        segmentation = seg, dp = DisplayPars(size=3, color = "seagreen",
                                                                lwd=2, lty = "solid"))
gdPlot(cop, overlay = makeTextOverlay("Overlay Text", xpos = .5, ypos = .5, coords = "absolute"))
```

makeTitle *Creates an object of class Title*

Description

Creates an object of class Title which can be used to add a title to the plot

Usage

```
makeTitle(text, cex, color, size)
```

Arguments

text	The text that will make up the title
cex	Font size of the title
color	Font color of the title
size	Size of the viewport in which the title resides

Value

Object of class Title

Author(s)

Steffen Durinck and Jim Bullard

References

~put references to the literature/web site here ~

See Also

[gdPlot](#)

Examples

```
##----- Should be DIRECTLY executable !! -----
##-- ==> Define data, use random,
##--      or do help(data=index) for the standard data sets.

## The function is currently defined as
function (text, cex, color, size)
{
  dp <- getClass("Title")@prototype@dp
  if (!missing(cex))
    setPar(dp, "cex", cex)
  if (!missing(color))
    setPar(dp, "color", color)
  if (!missing(size))
    setPar(dp, "size", size)
  new("Title", title = text, dp = dp)
}
```

makeTranscript

Creates an object of class Transcript

Description

Creates an object of class Transcript. This represents all known transcript structures in Ensembl.

Usage

```
makeTranscript(id, type, biomaRt, dp = NULL)
```

Arguments

id	An identifier used to specify of which gene/transcript the transcript structures should be retrieved
type	The type of identifiers used, examples are <code>ensembl_gene_id</code> , <code>hgnc_symbol</code> , <code>entrezgene</code> . See <code>listAttributes</code> function of the <code>biomaRt</code> package for more info
biomaRt	Mart object, created by the <code>useMart</code> function of <code>biomaRt</code>
dp	object of class <code>DisplayPars</code> , determines the display of features on the plot

Value

An object of class Transcript

Author(s)

Steffen Durinck and Jim Bullard

References

~put references to the literature/web site here ~

See Also

[gdPlot](#)

Examples

```
##----- Should be DIRECTLY executable !! -----
##-- ==> Define data, use random,
##--      or do help(data=index) for the standard data sets.

## The function is currently defined as
function (id, type, biomaRt, dp = NULL)
{
  if (missing(id))
    stop("Need to specify a gene identifier for creating a Transcript")
  pt <- getClass("Transcript")@prototype
  if (is.null(dp))
    dp <- pt@dp
  if (missing(type))
    type = pt@type
  new("Transcript", id = id, type = type, biomaRt = biomaRt,
      dp = dp)
}
```

MappedRead-class *Represents mapped reads*

Description

Represents mapped reads

Slots

start: Object of class "numeric", containing start position of the reads

end: Object of class "numeric", containing end position of the reads

strand: Object of class "numeric", containing strand to which the reads map

chromosome: Object of class "numeric", containing chromosome to which the reads map

Methods

show signature(object = "MappedRead"): ...

Author(s)

Steffen Durinck

References

<http://www.stat.berkeley.edu/~steffen/>

Examples

```
## maybe str(MappedRead) ; plot(MappedRead) ...
```

Overlay-class	<i>Class "Overlay"</i>
---------------	------------------------

Description

Superclass of overlay objects.

Objects from the Class

Objects from this class are generally not created.

Slots

dp: Object of class "DisplayPars"

Extends

Class "[gdObject](#)", directly.

Methods

No methods defined with class "Overlay" in the signature.

Examples

```
showClass("Overlay")
```

probestart	<i>Contains dummy expression array probe start positions</i>
------------	--

Description

Contains dummy expression array probe start positions

Examples

```
#
```

```
RectangleOverlay-class
      Class "RectangleOverlay"
```

Description

Rectangular Overlay

Objects from the Class

Objects can be created by calls of the form `makeRectangleOverlay` ([makeRectangleOverlay](#)).

Slots

start: Object of class "numeric" ~~
end: Object of class "numeric" ~~
region: Object of class "numericOrNull" ~~
coords: Object of class "character" ~~
dp: Object of class "DisplayPars" ~~

Extends

Class "[Overlay](#)", directly. Class "[gdObject](#)", by class "[Overlay](#)", distance 2.

Methods

drawOverlay signature(obj = "RectangleOverlay"):...

Examples

```
showClass("RectangleOverlay")
```

```
segEnd          Contains dummy copy number segmentation end positions
```

Description

Contains dummy copy number segmentation end positions

Examples

```
#
```

Segmentable-class *Class "Segmentable"*

Description

The Segmentable class is used as an interface to determine whether or not a segmentation should be plotted.

Objects from the Class

This object is mostly intended to be extended.

Slots

segmentation: Object of class "SegmentationOrNULL"

Methods

getSegmentation signature(obj = "Segmentable"): returns the segmentation, this is essentially the method which is implemented by subclasses.

See Also

[Segmentation](#)

Examples

```
showClass("Segmentable")
```

Segmentation-class *Class "Segmentation" is used to specify segmentations to any class that extends Segmentable (GenericArray, BaseTrack)*

Description

A Segmentation object provides line segments to various gObjects

Objects from the Class

Objects can be created by calls of the form `new("Segmentation", segments = list(1), segmentStart = list(1000), segmentEnd = list(1010))`.

Slots

segments: Object of class "list" ~~

segmentStart: Object of class "list" ~~

segmentEnd: Object of class "list" ~~

dp: Object of class "DisplayPars" ~~

Extends

Class "gdObject", directly.

Methods

getSegmentEnd signature(obj = "Segmentation"):...

getSegmentStart signature(obj = "Segmentation"):...

getSegments signature(obj = "Segmentation"):...

Author(s)

James Bullard

Examples

```
showClass("Segmentation")
```

segments

Contains dummy copy number segment data

Description

Contains dummy copy number segment data

Examples

```
#
```

segStart

Contains dummy copy number segmentation start positions data

Description

Contains dummy copy number segmentation start positions

Examples

```
#
```

seqDataEx	<i>This is an example data set from chromosome 4 of yeast from various publicly available datasets.</i>
-----------	---

Description

This was a small dataset constructed from publicly available datasets. Please see references for details.

Usage

```
data(seqDataEx)
```

Format

```
data("seqDataEx", package = "GenomeGraphs") names(seqDataEx)
```

References

Ugrappa Nagalakshmi et. al. The transcriptional landscape of the yeast genome defined by RNA sequencing. *Science*, 2008

Lior David et. al. A high-resolution map of transcription in the yeast genome. *Proc Natl Acad Sci U S A*, (2006)

William Lee A high-resolution atlas of nucleosome occupancy in yeast. *Nat Genet*, 2007

Adam Siepel, et. al. Evolutionarily conserved elements in vertebrate, insect, worm, and yeast genomes. *Genome Res*, 2005

Examples

```
data(seqDataEx)
```

setPar	<i>Sets a display parameter</i>
--------	---------------------------------

Description

Sets a display parameter

Usage

```
setPar(obj, name, val, ...)
```

Arguments

obj	An object, usually a gDObject.
name	Name of display parameter to set.
val	Value of display parameter.
...	Ignored

Examples

```
a <- new("GenomeAxis")
setPar(a, "size", 100)
gdPlot(a, minBase = 10, maxBase = 10000)
```

showDisplayOptions *Print standard display options, DisplayPars for an object or a class*

Description

Prints the available display options for a class or name of a class.

Usage

```
showDisplayOptions(obj, ...)
```

Arguments

obj	Either an object of subclass <code>gdObject</code> or a character naming a class
...	~~Describe ... here~~

Value

Returns a `DisplayPars` object which is generally printed to the screen.

Examples

```
showDisplayOptions("GenericArray")
```

TextOverlay-class *Class "TextOverlay"*

Description

Textual overlay classes

Objects from the Class

Objects can be created by calls of the form `makeTextOverlay`

Slots

text: Object of class "character"
xpos: Object of class "numeric"
ypos: Object of class "numeric"
region: Object of class "numericOrNull"
coords: Object of class "character"
dp: Object of class "DisplayPars"

Extends

Class `"Overlay"`, directly. Class `"gdObject"`, by class `"Overlay"`, distance 2.

Methods

drawOverlay signature(obj = "TextOverlay"):...

Examples

```
showClass("TextOverlay")
```

Title-class

Class "Title" representing the title of a plot

Description

Represent the title of a plot

Objects from the Class

Objects can be created by calls of the form `new("Title", ...)`.

Slots

title: Object of class `"character"` which will be used as title

dp: Object of class `"DisplayPars"` specifying the size and color of the title in the final plot

Methods

No methods defined with class `"Title"` in the signature.

Author(s)

Steffen Durinck

References

<http://www.stat.berkeley.edu/~steffen/>

See Also

objects to See Also as `gdPlot`

Examples

```
showClass("Title")
```

Transcript-class *Represent known transcript isoforms as annotated by Ensembl*

Description

Represent known transcript isoforms as annotated by Ensembl

Objects from the Class

Objects can be created by calls of the form `new("Transcript", ...)`.

Slots

id: Object of class "character", represents the gene identifier that should be used to retrieve the transcript level annotation

type: Object of class "character", represents the type of identifiers used to specify the gene e.g. hgnc_symbol, entrezgene and ensembl_gene_id

size: Object of class "numeric", represents the size of the plot of this object

transcriptSize: Object of class "numeric", represents the size of the transcripts in the plot

numOfTranscripts: Object of class "numeric", should not be used by users

color: Object of class "character", color of the exons

biomart: Object of class "Mart", containing the links to the Ensembl database. This object should be created with the useMart function of the biomaRt package

ens: Object of class "data.frame", should not be used by the users. Contains the output from the biomaRt query

Methods

drawGD signature(.Object = "Transcript"): ...

initialize signature(.Object = "Transcript"): ...

show signature(object = "Transcript"): ...

Author(s)

Steffen Durinck

References

<http://www.stat.berkeley.edu/~steffen/>

See Also

objects to See Also as [gdPlot](#)

Examples

```

if(interactive()){
data("unrData", package="GenomeGraphs")
mart = useMart("ensembl", dataset="hsapiens_gene_ensembl")
transcript = new("Transcript", id="ENSG00000009307", biomart = mart)
gdPlot(list(transcript), minBase = min(exon@probeStart), maxBase=max(exon@probeEnd))
}

```

TranscriptRegion-class

Class "TranscriptRegion", representing a genomic region with transcripts

Description

Upon creation of this object, transcripts present in a specified region will be retrieved from Ensembl

Objects from the Class

Objects can be created by calls of the form `new("TranscriptRegion", ...)`

Slots

start: Object of class "numeric", the start base of the genomic region

end: Object of class "numeric", the end base of the genomic region

chromosome: Object of class "character", the chromosome

size: Object of class "numeric", the size of the plot for this object

biomart: Object of class "Mart", contains link to Ensembl and should be created using the useMart function of the biomaRt package

ens: Object of class "data.frame", users should not specify this, it contains the output of the query to Ensembl

Methods

show signature(object = "TranscriptRegion"):...

Author(s)

Steffen Durinck

References

<http://www.stat.berkeley.edu/~steffen/>

See Also

objects to See Also as [gdPlot](#)

Examples

```
showClass("TranscriptRegion")
```

unrData	<i>Contains exon array data</i>
---------	---------------------------------

Description

Contains exon array data from the publically available dataset on human tissue panels, given by Affymetrix. The data was contributed to the package by Elizabeth Purdom.

Examples

#

unrNProbes	<i>Contains exon array data</i>
------------	---------------------------------

Description

Contains the number of probes per exon array probeset id from the publically available dataset on human tissue panels, given by Affymetrix. The data was contributed to the package by Elizabeth Purdom.

Examples

#

unrPositions	<i>Contains probe start and end positions of exon array probes</i>
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Description

Contains probe start and end positions from the publically available dataset on human tissue panels, given by Affymetrix. The data was contributed to the package by Elizabeth Purdom.

Examples

#

yeastCons1	<i>Contains dummy yeast conservation data</i>
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Description

Contains dummy yeast base conservation data.

Examples

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