

Package ‘Pviz’

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Type Package

Title Peptide Annotation and Data Visualization using Gviz

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Description Pviz adapts the Gviz package for protein sequences and data.

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Depends R(>= 3.0.0), Gviz(>= 1.7.10)

Imports biovizBase, Biostrings, GenomicRanges, IRanges, data.table,
methods

Suggests knitr, pepDat

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VignetteBuilder knitr

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 ATrack

ATrack class

Description

This class contains Gviz's AnnotationTrack and adds default values to the genome and chromosome slot

Usage

```
ATrack(range = NULL, start = NULL, end = NULL, width = NULL, group, id,
        stacking = "squish", name = "ATrack", fun, selectFun, ...)
```

Arguments

range, start, end, width, group, id, stacking, name, fun, selectFun, ...
Arguments to be passed to AnnotationTrack.

Author(s)

Renan Sauteraud

See Also

[AnnotationTrack](#), [GdObject](#)

Examples

```
# Object construction
aTrack <- ATrack(start = c(20, 60), end = c(40, 100), name = "random.anno",
  id=c("small","big"))
#Stacking example
a2Track <- ATrack(start = c(20, 30), end = c(40, 100), name = "stacking=dense",
  id = c("small", "big"), stacking = "dense", fill=c("black", "orange"))
a3Track <- ATrack(start = c(20, 30), end = c(40, 100), name = "no stacking",
  id = c("small", "big"), fill = c("black", "orange"))
#Plotting
plotTracks(trackList = c(aTrack, a2Track, a3Track), showFeatureId = TRUE)
```

 CladeTrack

CladeTrack

Description

This track can be used to display the result of pepStat analysis for a single clade. It contains DTrack.

Usage

```
CladeTrack(restab, clade, name = clade, ...)
```

Arguments

restab	A data.frame. The result of a peptide microarray analysis, as returned by pepStat's restab function.
clade	A character. The clade to plot.
name	A character. The name of the track, used in the title panel when plotting. By default, the clade name.
...	Additional argument to be passed to DataTrack. They will be treated as display parameters.

Slots

clade A character. The clade to display.

Author(s)

Renan Sauteraud

See Also

DTrack

Examples

```
if(require(pepDat)){
  data(restab)
  ct <- CladeTrack(restab, clade = "M", type = "1", legend = TRUE)
  plotTracks(ct)
}
```

DTrack

DTrack class

Description

This class contains Gviz's DataTrack and adds default values to the genome and chromosome slot

Usage

```
DTrack(range = NULL, start = NULL, end = NULL, width = NULL, data,
       name = "DTrack", ...)
```

Arguments

range, start, end, width, data, name, ...
Arguments to be passed to DataTrack.

Details

Refer to DataTrack for details regarding the constructor.

Author(s)

Renan Sauteraud

See Also[DataTrack](#), [GdObject](#)**Examples**

```
dTrack <- DTrack(start=seq(1,1000, len=100), width=10, data=matrix(runif(400),
  nrow=4), name="random data")
```

 plot_clade

Plot frequency of response for a single clade.

Description

Plot an axis and the frequency of response of a single selected clade.

Usage

```
plot_clade(restab, clade, sequence = NULL, from = 0,
  to = max(restab$position), ...)
```

Arguments

restab	A data.frame. The result of a peptide microarray analysis, as returned by pepStat's restab function.
clade	A character. The clade to plot.
sequence	An optional character or AAString. The sequence of the ProteinSequenceTrack to plot. It should be the sequence of the reference genome used in the peptideSet that generated the restab.
from	A numeric, the start coordinate of the plot.
to	A numeric, the end coordinate of the plot.
...	Additional arguments to be passed to plotTracks.

Author(s)

Renan Sauteraud

See Also[restab](#), [plot_inter](#), [plotTracks](#)**Examples**

```
if(require(pepDat)){
  data(restab)
  plot_clade(restab, clade = c("A", "M"))
}
```

plot_inter	<i>Plot frequency of response for each group</i>
------------	--

Description

Plot an axis and the frequency of response of each group, averaged by peptides at each position.

Usage

```
plot_inter(restab, sequence = NULL, from = 0, to = max(restab$position),
  ...)
```

Arguments

restab	A <code>data.frame</code> . The result of a peptide microarray analysis, as returned by <code>pepStat</code> 's <code>restab</code> function.
sequence	A character or an <code>AAString</code> . If not <code>NULL</code> , the sequence of the <code>ProteinSequenceTrack</code> to plot. It should be the sequence of the reference genome used in the <code>peptideSet</code> that generated the <code>restab</code> .
from	A numeric, the start coordinate of the plot.
to	A numeric, the end coordinate of the plot.
...	Additional arguments to be passed to <code>plotTracks</code> .

Author(s)

Renan Sauteraud

See Also

`restab`, `plot_clade`, [plotTracks](#)

Examples

```
if(require(pepDat)){
  data(restab_aggregate)
  plot_inter(restab_aggregate)
}
```

ProbeTrack	<i>ProbeTrack</i>
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Description

This track can be used to display the frequency of antibody binding for each probe on an array as predicted by `pepStat`'s function `makeCalls`.

Usage

```
ProbeTrack(sequence, intensity, probeStart, restab = NULL, group = NULL,
  name = "ProbeTrack", ...)
```

Arguments

sequence	A character vector. The sequence of peptides to display.
intensity	A numeric vector. The frequency of binding or the baseline corrected intensity for the peptides.
probeStart	A numeric vector. The start position of the peptides.
name	A character. The name of the track used in the title panel when plotting
restab	A data.frame containing all the above parameters, as outputted by pepStat's restab function.
group	A character. The group to display on the ProbeTrak. This is only required when restab is not NULL. See details section for more information.
...	Arguments to be passed to DataTrack.

Details

The vectors for the arguments `sequence`, `freq` and `probeStart` should be of the same length. If `restab` is provided, the three previous arguments will be ignored and `group` must be specified. `group` must be a valid column name in `restab`, data.frame.

Slots

sequence	A character vector. The probes sequence.
probeStart	A numeric vector. The start position of the probes.
intensity	A numeric vector. The frequency of response of each probe. Or the baseline corrected intensity of the signal.

Author(s)

Renan Sauteraud

See Also

[GdObject](#)

`restab`

Examples

```
if(require(pepDat)){
  data(restab)
  pt <- ProbeTrack(sequence = restab$peptide,
                   intensity = restab$group2,
                   probeStart = restab$start)
  plotTracks(pt)
  plotTracks(pt, from = 460, to = 560, legend=TRUE)
}
```

ProteinAxisTrack *ProteinAxisTrack*

Description

A track to display an axis for protein or peptide sequences

Usage

```
ProteinAxisTrack(range = NULL, name = "Axis", addNC = FALSE, id = NULL,
...)
```

Arguments

range, name, id, ...	Arguments to be passed to GenomeAxisTrack.
addNC	A logical. If TRUE, display the Amino-terminal and Carboxyl-terminal ends on the axis.

Author(s)

Renan Sauteraud

See Also

[GenomeAxisTrack](#)

Examples

```
# Object construction
paxTrack <- ProteinAxisTrack()
pax2 <- ProteinAxisTrack(addNC=TRUE)
pax3 <- ProteinAxisTrack(littleTicks=TRUE)
# Plotting
plotTracks(c(paxTrack,pax2,pax3), from=1, to=100)
```

ProteinSequenceTrack *ProteinSequenceTrack*

Description

A track to display peptides and protein sequences.

Usage

```
ProteinSequenceTrack(sequence = NULL, name = "Sequence", ...)
```

Arguments

sequence	A character or AAString of length one. The sequence to display.
name	A character. The name of the track used in the title panel when plotting
...	Additional items which will all be interpreted as display parameters.

Author(s)

Renan Sauteraud

See Also

[SequenceTrack](#), [DisplayPars](#)

Examples

```
if(require(pepDat)){
  data(pep_hxb2)
  hxb2_seq <- metadata(pep_hxb2)$sequence
  st<-ProteinSequenceTrack(sequence=hxb2_seq, name="env")

  # Plotting amino acids
  plotTracks(st, to = 20)

  # When the range becomes wider, only coloured squares are displayed
  plotTracks(st, to = 100)

  # When overplotting, a single line will mark the ProteinSequenceTrack
  plotTracks(st)
}
```


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