

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

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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

<code>restab</code>	A data.frame. The result of a peptide microarray analysis, as returned by pepStat's restab function.
<code>clade</code>	A character. The clade to plot.
<code>name</code>	A character. The name of the track, used in the title panel when plotting. By default, the clade name.
<code>...</code>	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 <code>data.frame</code> . The result of a peptide microarray analysis, as returned by <code>pepStat</code> 's <code>restab</code> function.
clade	A character. The clade to plot.
sequence	An optional character or <code>AAString</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_inter`, [plotTracks](#)

Examples

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

plot_inter

Plot frequency of response for each group

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 Alsorestab, plot_clade, [plotTracks](#)**Examples**

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

 ProbeTrack

ProbeTrack

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

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

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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