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

biocViews Visualization, Proteomics, Microarray

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Contents

ATrack 2
CladeTrack 3
DTrack 4
plot_clade 4
plot_inter 5
ProbeTrack 6
ProteinAxisTrack 7
ProteinSequenceTrack 8

Index **10**

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 = "l", 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.
...	Aditional 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 *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 data.frame. The result of a peptide microarray analysis, as returned by pepStat's restab function.
sequence	A character or an AAString. If not NULL, 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.
...	Aditional arguments to be passed to plotTracks.

Author(s)

Renan Sauteraud

See Also

restab, 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 arrayas 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)
}
```

Index

AnnotationTrack, *2*
ATrack, 2
ATrack-class *(*ATrack*)*, 2

CladeTrack, 3
CladeTrack-class *(*CladeTrack*)*, 3

DataTrack, *4*
DisplayPars, *8*
DTrack, 4
DTrack-class *(*DTrack*)*, 4

GdObject, *2*, *4*, *7*
GenomeAxisTrack, *8*

plot_clade, 4
plot_inter, 5
plotTracks, *5*, *6*
ProbeTrack, 6
ProbeTrack-class *(*ProbeTrack*)*, 6
ProteinAxisTrack, 7
ProteinAxisTrack-class
        *(*ProteinAxisTrack*)*, 7
ProteinSequenceTrack, 8
ProteinSequenceTrack-class
        *(*ProteinSequenceTrack*)*, 8

SequenceTrack, *8*