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

VignetteBuilder knitr

NeedsCompilation no

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ATrack

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

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, ...)
**DTrack**

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

```r
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

```r
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.
plot_clade

Author(s)
Renan Sauteraud

See Also
DataTrack, GdObject

Examples

```r
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

```r
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

```r
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**

```r
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.
- `...` Additional arguments to be passed to `plotTracks`.

**Author(s)**

Renan Sauteraud

**See Also**

`restab`, `plot_clade`, `plotTracks`

**Examples**

```r
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**

```r
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 ProbeTrack. 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

```r
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

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

Description
A track to display peptides and protein sequences.

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