Package ‘Pviz’
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ATrack  

Description

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

Usage

```r
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

```r
# 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)
```
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**

```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.

**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), ...)
```
plot_inter

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.
...  Aditinal 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.
...  Aditinal 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)
}

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.
**ProteinAxisTrack**

**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`

**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
ProteinSequenceTrack

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", ...)

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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