Package ‘PeakError’

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Title Compute the Label Error of Peak Calls

Description Chromatin immunoprecipitation DNA sequencing results in genomic tracks that show enriched regions or peaks where proteins are bound. This package implements fast C code that computes the true and false positives with respect to a database of annotated region labels.

Suggests testthat, ggplot2

NeedsCompilation yes

Repository CRAN

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Contents

`checkChrom` *checkChrom*

Description

Check for a valid data.frame with chrom names.

Usage

```
checkChrom(df)
```

Arguments

`df`	df

Author(s)

Toby Dylan Hocking

`checkPositions` *checkPositions*

Description

Check for a valid data.frame with chromStart, chromEnd.

Usage

```
checkPositions(df)
```

Arguments

`df`	df

Author(s)

Toby Dylan Hocking

`PeakError` *PeakError*

Description

Compute true and false positive peak calls, with respect to a database of annotated `regions`.

Usage

```
PeakError(peaks, regions)
```

Arguments

`peaks`	data.frame with columns chrom, chromStart, chromEnd. NOTE: chromStart should be 0-based and chromEnd should be 1-based. EXAMPLE: the first 100 base of of a chromosome are chromStart=0, chromEnd=100. The second 100 bases are chromStart=100, chromEnd=200.
`regions`	data.frame with columns chrom, chromStart, chromEnd, annotation.

Value

data.frame for each region with additional counts of true positives (tp, possible.tp), false positives (fp, possible.fp, fp.status), and false negatives (fn, fn.status).

Author(s)

Toby Dylan Hocking

Examples

```
x <- seq(5, 85, by=5)
peaks <- rbind(
  Peaks("chr2", x, x+3),
  Peaks("chr3", c(25, 38, 57), c(33, 54, 75)),
  Peaks("chr4", c(5, 32, 38, 65), c(15, 35, 55, 85)),
  Peaks("chr5", c(12, 26, 56, 75), c(16, 54, 59, 85)))
regions.list <- list()
for(chr in 1:5){
  regions.list[[chr]] <- data.frame(
    chrom=paste0("chr", chr),
    chromStart=c(10, 30, 50, 70),
    chromEnd=c(20, 40, 60, 80),
    annotation=c("noPeaks", "peakStart", "peakEnd", "peaks"))
}
regions <- do.call(rbind, regions.list)
err <- PeakError(peaks, regions)
ann.colors <- c(
  noPeaks="#f6f4bf",
  peakStart="#ffafaf",
  peakEnd="#ff4c4c",
  peaks="#a445ee")
if(require(ggplot2)){
  ggplot()+
    geom_rect(aes(
      xmin=chromStart+1/2, xmax=chromEnd+1/2,
      ymin=-1, ymax=1,
      fill=annotation,
      linetype=fn.status,
      size=fp.status),
      data=err, color="black")+
    scale_y_continuous("", breaks=NULL)+
    scale_linetype_manual(
      values=c("false negative"="dotted", correct="solid"))+
    scale_size_manual(
      values=c("false positive"=3, correct=1))+
    scale_fill_manual(
      values=ann.colors,
      breaks=names(ann.colors))+
    facet_grid(chrom ~ .)+
    theme_bw()+
    guides(
      fill=guide_legend(order=1),
```

```
      linetype=guide_legend(order=2, override.aes=list(fill="white")),
      size=guide_legend(order=3, override.aes=list(fill="white")))+
    theme(panel.margin=grid::unit(0, "cm"))+
    geom_segment(aes(
      chromStart+1/2, 1/2, xend=chromEnd+1/2, yend=1/2),
      data=peaks, color="deepskyblue", size=2)+
    scale_x_continuous(
      "position on chromosome",
      breaks=seq(10, 90, by=10))+
    geom_text(aes(
      base, -1/2, label="N"),
      data.frame(base=10:90),
      color="deepskyblue")
}
```

`PeakErrorChrom` *PeakErrorChrom*

Description

Compute the `PeakError` assuming that `peaks` and `regions` are on the same chrom.

Usage

```
PeakErrorChrom(peaks,
    regions)
```

Arguments

`peaks`	data.frame with columns chromStart, chromEnd. NOTE: chromStart should be 0-based and chromEnd should be 1-based. EXAMPLE: the first 100 base of of a chromosome are chromStart=0, chromEnd=100. The second 100 bases are chromStart=100, chromEnd=200.
`regions`	data.frame with columns chromStart, chromEnd.

Value

data.frame with 1 row for each region and error columns.

Author(s)

Toby Dylan Hocking

`Peaks` *Peaks*

Description

Make a data.frame that represents a list of peaks.

Usage

```
Peaks(chrom = factor(),
    base.before = integer(),
    last.base = integer())
```

Arguments

`chrom`	character or factor with `chrom` name for example "chr22"
`base.before`	integer, base before peak.
`last.base`	integer, last base of peak.

Value

data.frame with columns `chrom`, chromStart, chromEnd.

Author(s)

Toby Dylan Hocking

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