

# Package ‘PeakError’

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**License** GPL-3

**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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## R topics documented:

checkChrom . . . . .	1
checkPositions . . . . .	2
PeakError . . . . .	2
PeakErrorChrom . . . . .	4
Peaks . . . . .	4

<b>Index</b>	<b>6</b>
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checkChrom	<i>checkChrom</i>
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## Description

Check for a valid data.frame with chrom names.

**Usage**

```
checkChrom(df)
```

**Arguments**

```
df
```

**Author(s)**

Toby Dylan Hocking

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checkPositions	<i>checkPositions</i>
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**Description**

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

**Usage**

```
checkPositions(df)
```

**Arguments**

```
df
```

**Author(s)**

Toby Dylan Hocking

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PeakError	<i>PeakError</i>
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**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 <- NULL
for(chr in 1:5){
  regions <- rbind(regions, {
    data.frame(chrom=paste0("chr", chr),
              chromStart=c(10, 30, 50, 70),
              chromEnd=c(20, 40, 60, 80),
              annotation=c("noPeaks", "peakStart", "peakEnd", "peaks"))
  })
}
err <- PeakError(peaks, regions)
ann.colors <-
  c(noPeaks="#f6f4bf",
    peakStart="#ffafaf",
    peakEnd="#ff4c4c",
    peaks="#a445ee")
library(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")
```

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PeakErrorChrom	<i>PeakErrorChrom</i>
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### 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

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Peaks	<i>Peaks</i>
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### 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

# Index

checkChrom, 1  
checkPositions, 2

PeakError, 2  
PeakErrorChrom, 4  
Peaks, 4