

# 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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checkChrom	<i>checkChrom</i>
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## Description

Check for a valid data.frame with chrom names.

**Usage**

```
checkChrom(df)
```

**Arguments**

```
df          df
```

**Author(s)**

Toby Dylan Hocking

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```
checkPositions      checkPositions
```

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**Description**

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

**Usage**

```
checkPositions(df)
```

**Arguments**

```
df          df
```

**Author(s)**

Toby Dylan Hocking

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```
PeakError          PeakError
```

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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.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")
}

```

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PeakErrorChrom

*PeakErrorChrom*


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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

*Peaks*

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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

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