Package ‘similaRpeak’

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Type Package

Title Metrics to estimate a level of similarity between two ChIP-Seq profiles

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Description This package calculates metrics which assign a level of similarity between ChIP-Seq profiles.

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Depends R6 (>= 2.0)

Imports rtracklayer, GenomicAlignments, Rsamtools, stats

Suggests RUnit, BiocGenerics, knitr, BiocStyle

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BugReports https://github.com/adeschen/similaRpeak/issues

VignetteBuilder knitr

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**chr7Profiles**

ChIP-Seq profiles of region chr7:61968807-61969730 related to enhancers H3K27ac and H3K4me1 (for demonstration purpose)

**Description**

ChIP-Seq profiles of region chr7:61968807-61969730 of two histone post-transcriptional modifications linked to highly active enhancers H3K27ac (DCC accession: ENCFF000ASG) and H3K4me1 (DCC accession: ENCFF000ARY) from the Encyclopedia of DNA Elements (ENCODE) data (Dunham I et al. 2012).

**Usage**

```r
data(chr7Profiles)
```

**Format**

A list with 1 entry. The entry is a list of 2 ChIP-Seq profiles, one per active enhancer (H3K27ac and H3K4me1). The 2 ChIP-Seq profiles are of identical length and specific to a genomic region. Each ChIP-Seq profile is a numerical vector containing the profiles values at each position, as reported in reads per million (RPM).

```r
chr7Profiles a list containing 1 entry
demoProfiles$chr7.61968807.61969730$H3K27ac a numeric vector containing the profiles values related to the enhancer H3K27ac, as reported in reads per million (RPM). The first entry of the vector is for position chr7:61968807 while the last entry is for position chr7:61969730
demoProfiles$chr7.61968807.61969730$H3K4me1 a numeric vector containing the profiles values related to the enhancer H3K4me1, as reported in reads per million (RPM). The first entry of the vector is for position chr7:61968807 while the last entry is for position chr7:61969730
```

**Source**

The Encyclopedia of DNA Elements (ENCODE) data

**References**


**See Also**

- [MetricFactory](#) for using a interface to calculate all available metrics separately.
- [similarity](#) for calculating all available metrics between two ChIP-Seq profiles.
Examples

```r
data(chr7Profiles)

## Calculating all metrics for the "chr7.61968807.61969730" region
metrics <- similarity(chr7Profiles$chr7.61968807.61969730$H3K4me1,
                      chr7Profiles$chr7.61968807.61969730$H3K27ac,
                      ratioAreaThreshold=10,
                      ratioMaxMaxThreshold=4,
                      ratioIntersectThreshold=5,
                      ratioNormalizedIntersectThreshold=2,
                      diffPosMaxThresholdMinValue=10,
                      diffPosMaxThresholdMaxDiff=100,
                      diffPosMaxTolerance=0.10)
metrics

## You can refer to the vignette to see more examples using ChIP-Seq profiles
## extracted from the Encyclopedia of DNA Elements (ENCODE) data.
```

Description

ChIP-Seq profiles of two histone post-transcriptional modifications linked to highly active enhancers H3K27ac (DCC accession: ENCFF000ASG) and H3K4me1 (DCC accession: ENCFF000ARY) from the Encyclopedia of DNA Elements (ENCODE) data (Dunham I et al. 2012).

Usage

```r
data(demoProfiles)
```

Format

A list with 4 entries. Each entry is a list of 2 ChIP-Seq profiles, one per active enhancer (H3K27ac and H3K4me1). The 2 ChIP-Seq profiles are of identical length and specific to a genomic region. Each ChIP-Seq profile is a numerical vector containing the profiles values at each position, as reported in reads per million (RPM),

demoProfiles a list containing all demo ChIP-Seq profiles
demoProfiles$chr2.70360770.70361098 a list containing 2 ChIP-Seq profiles for the genomic region chr2:70360770-70361098
demoProfiles$chr2.70360770.70361098$H3K27ac a numeric vector containing the profiles values related to the enhancer H3K27ac, as reported in reads per million (RPM). The first entry of the vector is for position chr1:70360770 while the last entry is for position chr2:70361098
demoProfiles$chr2.70360770.70361098$H3K4me1 a numeric vector containing the profiles values related to the enhancer H3K4me1, as reported in reads per million (RPM). The first entry of the vector is for position chr1:70360770 while the last entry is for position chr2:70361098
demoProfiles$chr3.73159773.73160145$H3K4me1 a list containing 2 ChIP-Seq profiles for the genomic region chr3:73159773-73160145
demoProfiles$chr3.73159773.73160145$H3K27ac a numeric vector containing the profiles values related to the enhancer H3K27ac, as reported in reads per million (RPM). The first entry of the vector is for position chr2:73159773 while the last entry is for position chr3:73160145

demoProfiles$chr3.73159773.73160145$H3K4me1 a numeric vector containing the profiles values related to the enhancer H3K4me1, as reported in reads per million (RPM). The first entry of the vector is for position chr3:73159773 while the last entry is for position chr3:73160145

Source

The Encyclopedia of DNA Elements (ENCODE) data

References


See Also

• MetricFactory for using a interface to calculate all available metrics separately.
• similarity for calculating all available metrics between two ChIP-Seq profiles.

Examples

data(demoProfiles)

# Calculate metrics for the "chr3:73159773-73160145" region
metrics <- similarity(demoProfiles$chr3.73159773.73160145$H3K27ac,
                       demoProfiles$chr3.73159773.73160145$H3K4me1)

## You can refer to the vignette to see more examples using ChIP-Seq profiles
## extracted from the Encyclopedia of DNA Elements (ENCODE) data.

MetricFactory-class  MetricFactory object

Description

An object which is a interface to calculate all available metrics separately.

Details

The MetricFactory object is inspired from the factory design pattern. Only one instance of MetricFactory object is necessary to calculate all available metrics for different profiles, as long as the thresholds set in the MetricFactory instance are appropriate for the calculation. The thresholds are set during the MetricFactory object creation and cannot be changed afterwards. If different thresholds are needed, a new MetricFactory object, with the new thresholds, must be instantiated.

Value

MetricFactory$new returns a MetricFactory object which contains the information about the thresholds used to calculate each metric. It can be used, as many times needed, to calculate the specified metrics.
MetricFactory-class

Constructor

MetricFactory$new(ratioAreaThreshold=1, ratioMaxMaxThreshold=1, ratioIntersectThreshold=1, ratioNormalizedIntersectThreshold=1, diffPosMaxThresholdMinValue=1, diffPosMaxThresholdMaxDiff=100, diffPosMaxTolerance=0.01, spearmanCorrSDThreshold=1e-8)

Create a MetricFactory object.

ratioAreaThreshold The minimum denominator accepted to calculate the ratio of the area between both profiles. Default = 1.

diffPosMaxThreshold The minimum denominator accepted to calculate the ratio of the maximum values between both profiles. Default = 1.

diffPosMaxThresholdMaxDiff The maximum distance accepted between 2 peaks positions in one profile to calculate the metric. Default=100.

diffPosMaxTolerance The maximum variation accepted on the maximum value to consider a position as a peak position. Default=0.01.

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See Also

• similarity for calculating all available metrics between two ChIP-Seq profiles.
• demoProfiles for more informations about ChIP-Seq profiles present in the demoProfiles data.

Examples

## Initialized the factory object
factory = MetricFactory$new(ratioAreaThreshold=100, ratioIntersectThreshold=20, diffPosMaxTolerance=0.04)

## Define 2 ChIP-Seq profiles
profile1=c(1,59,6,24,65,34,15,4,53,22)
profile2=c(15,9,46,44,9,39,27,34,34,4)

## Use the factory object to calculate each metric separately
ratio_max_max <- factory$createMetric(metricType="RATIO_MAX_MAX", profile1, profile2)
ratio_max_max
diff_pos_max <- factory$createMetric(metric="DIFF_POS_MAX", profile1, profile2)
diff_pos_max

## Example using ChIP-Seq profiles of H3K27ac (DCC accession: ENCFF000ASG)
## and H3K4me1 (DCC accession: ENCFF000ARY) from the Encyclopedia of DNA
## Elements (ENCODE) for the region
data(demoProfiles)
similarity

Calculate metrics which estimate the level of similarity between two ChIP-Seq profiles

Description

Return a list containing information about both ChIP-Seq profiles and a list of all similarity metrics: the ratio of the maximum values, the ratio of the areas, the ratio between the intersection area and the total area (for normalized and non-normalized profiles), the difference between two profiles maximal peaks positions and the Spearman’s rho statistic.

Usage

similarity(
  profile1,
  profile2,
  ratioAreaThreshold=1,
  ratioMaxMaxThreshold=1,
  ratioIntersectThreshold=1,
  ratioNormalizedIntersectThreshold=1,
  diffPosMaxThresholdMinValue=1,
  diffPosMaxThresholdMaxDiff=100,
  diffPosMaxTolerance=0.01,
  spearmanCorrSDThreshold=1e-8)

# Visualize ChIP-Seq profiles
plot(demoProfiles$chr3.73159773.73160145$H3K27ac,
     type="l", col="blue", xlab="", ylab="", ylim=c(0, 125),
     main="chr3:73159773-73160145")
par(new=TRUE)
plot(demoProfiles$chr3.73159773.73160145$H3K4me1,
     type="l", col="darkgreen", xlab="Position",
     ylab="Coverage in reads per million (RPM)", ylim=c(0, 125))
legend("topright", c("H3K27ac","H3K4me1"), cex=1.2,
       col=c("blue","darkgreen"), lty=1)

# Calculate metrics using factory object
ratio_norm_intersect <- factory$createMetric(metricType =
  "RATIO_NORMALIZED_INTERSECT",
  profile1=demoProfiles$chr3.73159773.73160145$H3K4me1,
  profile2=demoProfiles$chr3.73159773.73160145$H3K27ac)
ratio_norm_intersect
ratio_area <- factory$createMetric(metricType="RATIO_AREA",
  profile1=demoProfiles$chr3.73159773.73160145$H3K4me1,
  profile2=demoProfiles$chr3.73159773.73160145$H3K27ac)
ratio_area

# You can refer to the vignette to see more examples using ChIP-Seq profiles
# extracted from the Encyclopedia of DNA Elements (ENCODE) data.
Arguments

profile1 Vector containing the RPM values of the first ChIP-Seq profile for each position of the selected region.

profile2 Vector containing the RPM values of the second ChIP-Seq profile for each position of the selected region.

ratioAreaThreshold The minimum denominator accepted to calculate the ratio of the area between both profiles. The value has to be positive. Default = 1.

ratioMaxMaxThreshold The minimum denominator accepted to calculate the ratio of the maximal peaks values between both profiles. The value has to be positive. Default = 1.

ratioIntersectThreshold The minimum denominator accepted to calculate the ratio of the intersection area of both profiles over the total area. The value has to be positive. Default = 1.

tauNormalizedIntersectThreshold The minimum denominator accepted to calculate the ratio of the intersection area of both normalized profiles over the total area. The value has to be positive. Default = 1.

diffPosMaxThresholdMinValue The minimum peak accepted to calculate the metric. The value has to be positive. Default = 1.

diffPosMaxThresholdMaxDiff The maximum distance accepted between 2 peaks positions in one profile to calculate the metric. The value has to be positive. Default = 100.

diffPosMaxTolerance The maximum of variation accepted on the maximum value to consider a position as a peak position. The value can be between 0 and 1. Default = 0.01.

tauSpearmanCorrSTDThreshold The minimum standard deviation accepted on both profiles to calculate the metric. Default = 1e-8.

Details

similarity uses the two vectors passed as arguments to calculate the metrics. When the metric is a ratio, it always verify that the threshold for the denominator is respected. If the threshold is not respected, the metric is assigned the NA value.

Value

similarity returns a list which contains the information about both ChIP-Seq profiles and a list of all metrics.

The data structure is a list of list.

The first level contain the following items:

• nbrPosition: The number of positions included in each profile.
• areaProfile1: The area of the first profile.
• areaProfile2: The area of the second profile.
• maxProfile1: The maximum value in the first profile.
• maxProfile2: The maximum value in the second profile.
• maxPositionProfile1: The list of positions of the maximum value in the first profile.
• maxPositionProfile2: The list of positions of the maximum value in the second profile.
• metrics: A list with the following items:
  – RATIO_AREA: The ratio between the areas. The larger value is always divided by the smaller value. NA if minimal threshold is not respected.
  – DIFF_POS_MAX: The difference between the maximal peaks positions. The difference is always the first profile value minus the second profile value. NA is returned if minimal peak value is not respected. A profile can have more than one position with the maximum value. In that case, the median position is used. A threshold argument can be set to consider all positions within a certain range of the maximum value. A threshold argument can also be set to ensure that the distance between two maximum values is not too wide. When this distance is not respected, it is assumed that more than one peak is present in the profile and NA is returned.
  – RATIO_MAX_MAX: The ratio between the maximal peaks values. The first profile is always divided by the second profile. NA if minimal threshold is not respected.
  – RATIO_INTERSECT: The ratio between the intersection area and the total area. NA if minimal threshold is not respected.
  – RATIO_NORMALIZED_INTERSECT: The ratio between the intersection area and the total area of normalized profiles. NA if minimal threshold is not respected.
  – SPEARMAN_CORRELATION: The Spearman’s rho statistic between profiles. NA if minimal threshold is not respected or when no complete element pair is present between both profiles.

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See Also

• MetricFactory for using a interface to calculate all available metrics separately.
• demoProfiles for more informations about ChIP-Seq profiles present in the demoProfiles data.

Examples

```r
## Defining two CHiP-Seq profiles
profile1<-c(3,59,6,24,65,34,15,4,53,22,21,12,11)
profile2<-c(15,9,46,44,9,39,27,34,34,4,3,4,2)

## Example using default thresholds
similarity(profile1, profile2)

## Example using customised thresholds
similarity(profile1, profile2, 
  ratioAreaThreshold=5,
  ratioMaxMaxThreshold=5,
  ratioIntersectThreshold=12,
  ratioNormalizedIntersectThreshold=2.2,
  diffPosMaxThresholdMinValue=2,
  diffPosMaxThresholdMaxDiff=130,
```

## Example using ChIP-Seq profiles of H3K27ac (DCC accession: ENCFF000ASG) and H3K4me1 (DCC accession: ENCFF000ARY) from the Encyclopedia of DNA Elements (ENCODE) for the region

data(demoProfiles)

## Visualize ChIP-Seq profiles

plot(demoProfiles$chr2.70360770.70361098$H3K27ac, type="l", col="blue", xlab="", ylab="", ylim=c(0, 25), main="chr2:70360770-70361098")

par(new=TRUE)
plot(demoProfiles$chr2.70360770.70361098$H3K4me1, type="l", col="darkgreen", xlab="Position", ylab="Coverage in reads per million (RPM)", ylim=c(0, 25))
legend("topright", c("H3K27ac","H3K4me1"), cex=1.2, col=c("blue","darkgreen"), lty=1)

# Calculate metrics

similarity(demoProfiles$chr2.70360770.70361098$H3K4me1, demoProfiles$chr2.70360770.70361098$H3K27ac, ratioAreaThreshold=15, ratioMaxMaxThreshold=5, ratioIntersectThreshold=12, ratioNormalizedIntersectThreshold=2.2, diffPosMaxThresholdMinValue=2, diffPosMaxThresholdMaxDiff=130, diffPosMaxTolerance=0.03, spearmanCorrSDThreshold=0.1)

## You can refer to the vignette to see more examples using ChIP-Seq profiles extracted from the Encyclopedia of DNA Elements (ENCODE) data.

### similaRpeak

**similaRpeak: Metrics to estimate a level of similarity between two ChIP-Seq profiles**

**Description**

**similaRpeak** is calculating six different metrics to estimate a level of similarity between two ChIP-Seq profiles.

**Details**

The R function **similarity** calculates six different metrics:

- **RATIO_AREA**: The ratio between the areas. The larger value is always divided by the smaller value.
- **DIFF_POS_MAX**: The difference between the maximal peaks positions. The difference is always a positive value.
- **RATIO_MAX_MAX**: The ratio between the maximal peaks values. The larger value is always divided by the smaller value.
• RATIO_INTERSECT: The ratio between the intersection area and the total area.

• RATIO_NORMALIZED_INTERSECT: The ratio between the intersection area and the total area of two normalized profiles. The profiles are normalized by dividing them by their average value.

• SPEARMAN_CORRELATION: The Spearman’s rho statistic between profiles.

The function `similarity` also reports basic information about each ChIP profile such as the number of positions, the area, the maximum value and the position of the maximum value.

To learn more about `similaRpeak` package see:

https://github.com/adeschen/similaRpeak/wiki

**Author(s)**


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**See Also**

• `MetricFactory` for using a interface to calculate all available metrics separately.

• `similarity` for calculating all available metrics between two ChIP-Seq profiles.
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