Package 'FindIT2'

July 3, 2025

Title find influential TF and Target based on multi-omics data

Version 1.15.0

Description This package implements functions to find influential TF and target based on different input type. It have five module:
Multi-peak multi-gene annotaion(mmPeakAnno module),
Calculate regulation potential(calcRP module),
Find influential Target based on ChIP-Seq and RNA-Seq data(Find influential Target module),
Find influential TF based on different input(Find influential TF module),
Calculate peak-gene or peak-peak correlation(peakGeneCor module).
And there are also some other useful function like integrate different source information, calculate jaccard similarity for your TF.

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URL https://github.com/shangguandong1996/FindIT2

BugReports https://support.bioconductor.org/t/FindIT2

biocViews Software, Annotation, ChIPSeq, ATACSeq, GeneRegulation, MultipleComparison, GeneTarget

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Contents

`ATAC_normCount` *ATAC normCount of E50h-72h in Chr5*

Description

ATAC normCount of E50h-72h in Chr5

Usage

```
data(ATAC_normCount)
```

Format

A matrix

Source

https://doi.org/10.1016/j.devcel.2020.07.003

`calcRP_coverage` *calcRP_coverage*

Description

calculate regulatory potential using big wig files, which is useful for ATAC or H3K27ac histone modification data.

Usage

```
calcRP_coverage(
  bwFile,
  Txdb,
  gene_included,
  Chrs_included,
  decay_dist = 1000,
  scan_dist = 20000,
  verbose = TRUE
)
```

Arguments

`bwFile`	bw file
`Txdb`	Txdb
`gene_included`	a character vector which represent gene set which you want to calculate RP for
`Chrs_included`	a character vector which represent chromosomes where you want to calculate gene RP in
`decay_dist`	decay distance
`scan_dist`	scan distance
`verbose`	whether you want to report detailed running message

Details

Please note that because of rtracklayer::import has some issue on 32 bit R of windows, so the calcRP_coverage can not work on this system. But if your R is 64 bit, which now be applied on the most windows R, this function still work.

Value

data.frame

Examples

```
if (.Platform$OS.type != "windows" & require(TxDb.Athaliana.BioMart.plantsmart28)) {
    Txdb <- TxDb.Athaliana.BioMart.plantsmart28
    seqlevels(Txdb) <- paste0("Chr", c(1:5, "M", "C"))
    bwFile <- system.file("extdata", "E50h_sampleChr5.bw", package = "FindIT2")

    RP_df <- calcRP_coverage(
        bwFile = bwFile,
        Txdb = Txdb,
        Chrs_included = "Chr5"
    )

}
```

---

calcRP_region *calcRP_region*

Description

calculate regulatory potential based on mm_geneScan result and peakCount matrix, which is useful for ATAC or H3K27ac histone modification data.

Usage

```
calcRP_region(
  mmAnno,
  peakScoreMt,
  Txdb,
  Chrs_included,
  decay_dist = 1000,
  log_transform = FALSE,
  verbose = TRUE
)
```

Arguments

mmAnno	the annotated GRange object from mm_geneScan
peakScoreMt	peak count matrix. The rownames are feature_id in mmAnno, while the colnames are sample names
Txdb	Txdb
Chrs_included	a character vector which represent chromosome where you want to calculate gene RP in. If Chromosome is not be set, it will calculate gene RP in all chromosomes in Txdb.
decay_dist	decay distance
log_transform	whether you want to log and norm your RP
verbose	whether you want to report detailed running message

Value

a MultiAssayExperiment object containg detailed peak-RP-gene relationship and sumRP info

Examples

```
if (require(TxDb.Athaliana.BioMart.plantsmart28)) {
    data("ATAC_normCount")
    library(SummarizedExperiment)
    Txdb <- TxDb.Athaliana.BioMart.plantsmart28
    seqlevels(Txdb) <- paste0("Chr", c(1:5, "M", "C"))

    peak_path <- system.file("extdata", "ATAC.bed.gz", package = "FindIT2")
    peak_GR <- loadPeakFile(peak_path)
    mmAnno <- mm_geneScan(peak_GR, Txdb)

    regionRP <- calcRP_region(
        mmAnno = mmAnno,
        peakScoreMt = ATAC_normCount,
        Txdb = Txdb,
        Chrs_included = "Chr5"
    )

    sumRP <- assays(regionRP)$sumRP
    fullRP <- assays(regionRP)$fullRP
}
```

`calcRP_TFHit` *calcRP_TFHit*

Description

calculate regulatory potential based on ChIP-Seq peak data, which is useful for TF ChIP-seq data.

Usage

```
calcRP_TFHit(
  mmAnno,
  Txdb,
  decay_dist = 1000,
  report_fullInfo = FALSE,
  verbose = TRUE
)
```

Arguments

`mmAnno`	the annotated GRange object from mm_geneScan
`Txdb`	Txdb
`decay_dist`	decay distance
`report_fullInfo`	whether you want to report full peak-RP-gene info
`verbose`	whether you want to report detailed running message

Details

If your origin peak_GR of mmAnno have column named feature_score, calcRP_TFHit will consider this column when calculating sumRP. Otherwise, it will consider all peak Hit feature_score is 1.

Value

if report_fullInfo is TRUE, it will output GRanges with detailed info. While FALSE, it will output data frame

Examples

```
if (require(TxDb.Athaliana.BioMart.plantsmart28)){
    Txdb <- TxDb.Athaliana.BioMart.plantsmart28
    seqlevels(Txdb) <- paste0("Chr", c(1:5, "M", "C"))
    peak_path <- system.file("extdata", "ChIP.bed.gz", package = "FindIT2")
    peak_GR <- loadPeakFile(peak_path)
    mmAnno <- mm_geneScan(peak_GR, Txdb)

    # if you just want to get RP_df, you can set report_fullInfo FALSE
    fullRP_hit <- calcRP_TFHit(
        mmAnno = mmAnno,
        Txdb = Txdb,
        report_fullInfo = TRUE
    )

    RP_df <- metadata(fullRP_hit)$peakRP_gene

}
```

`enhancerPromoterCor` *enhancerPromoterCor*

Description

enhancerPromoterCor

Usage

```
enhancerPromoterCor(
  peak_GR,
  Txdb,
  up_scanPromoter = 500,
  down_scanPromoter = 500,
  up_scanEnhancer = 20000,
  down_scanEnhacner = 20000,
  peakScoreMt,
  parallel = FALSE,
  verbose = TRUE
)
```

Arguments

`peak_GR`	peak GRange with a column named feature_id representing you peak name
`Txdb`	Txdb
`up_scanPromoter`	the scan distance which is used to scan nearest promoter

down_scanPromoter
: the scan distance which is used to scan nearest promoter

up_scanEnhancer
: the scan distance which is used to scan feature

down_scanEnhacner
: the scan distance which is used to scan feature

peakScoreMt
: peak count matrix. The rownames are feature_id in peak_GR

parallel
: whether you want to parallel to speed up

verbose
: whether you want to report detailed running message

Value

mmAnno with Cor, pvalue,padj,qvalue column

Examples

```
if (require(TxDb.Athaliana.BioMart.plantsmart28)){
    data("ATAC_normCount")
    Txdb <- TxDb.Athaliana.BioMart.plantsmart28
    seqlevels(Txdb) <- paste0("Chr", c(1:5, "M", "C"))
    peak_path <- system.file("extdata", "ATAC.bed.gz", package = "FindIT2")
    peak_GR <- loadPeakFile(peak_path)[1:100]
    mm_ePLink <- enhancerPromoterCor(
    peak_GR = peak_GR,
    Txdb = Txdb,
    peakScoreMt = ATAC_normCount,
    parallel = FALSE)
}
```

---

findIT_enrichFisher *findI(nfluential)T(F)_enrichFisher*

Description

find influential TF of your input peak set compared with your whole peak sets based on TF ChIP-Seq or motif data.

Usage

```
findIT_enrichFisher(input_feature_id, peak_GR, TF_GR_database)
```

Arguments

input_feature_id
: a character vector which represent peaks set which you want to find influential TF for

peak_GR
: a GRange object represent your whole feature location with a column named feature_id, which your input_feature_id should a part of it.

TF_GR_database
: TF peak GRange with a column named TF_id representing you TF name

Value

data.frame

Examples

```
data("test_featureSet")
peak_path <- system.file("extdata", "ATAC.bed.gz", package = "FindIT2")
peak_GR <- loadPeakFile(peak_path)
ChIP_peak_path <- system.file("extdata", "ChIP.bed.gz", package = "FindIT2")
ChIP_peak_GR <- loadPeakFile(ChIP_peak_path)
ChIP_peak_GR$TF_id <- "AT1G28300"

 result_findIT_enrichFisher <- findIT_enrichFisher(
    input_feature_id = test_featureSet,
    peak_GR = peak_GR,
    TF_GR_database = ChIP_peak_GR
)
```

`findIT_enrichWilcox` *findIT_enrichWilcox*

Description

findIT_enrichWilcox

Usage

```
findIT_enrichWilcox(
  input_feature_id,
  peak_GR,
  TF_GR_database,
  background_peaks = NULL,
  background_number = 3000
)
```

Arguments

`input_feature_id`	a character vector which represent peaks set which you want to find influential TF for
`peak_GR`	a GRange object represent your whole feature location with a column named feature_id, which your input_feature_id should a part of it.
`TF_GR_database`	TF peak GRange with a column named TF_id representing you TF name
`background_peaks`	a character vector which represent background peak set. If you do not assign background peaks, program will sample background_number peaks as background peaks from all feature_id in your peak_GR
`background_number`	background peaks number

Value

data.frame

Examples

```
data("test_featureSet")
peak_path <- system.file("extdata", "ATAC.bed.gz", package = "FindIT2")
peak_GR <- loadPeakFile(peak_path)
ChIP_peak_path <- system.file("extdata", "ChIP.bed.gz", package = "FindIT2")
ChIP_peak_GR <- loadPeakFile(ChIP_peak_path)
ChIP_peak_GR$TF_id <- "AT1G28300"

result_findIT_enrichWilcox <- findIT_enrichWilcox(
    input_feature_id = test_featureSet,
    peak_GR = peak_GR,
    TF_GR_database = ChIP_peak_GR
)
```

`findIT_MARA` *findIT_MARA*

Description

findIT_MARA

Usage

```
findIT_MARA(
  input_feature_id,
  peak_GR,
  peakScoreMt,
  TF_GR_database,
  log = TRUE,
  meanScale = TRUE,
  output = c("coef", "cor"),
  verbose = TRUE
)
```

Arguments

`input_feature_id`	a character vector which represent peaks set which you want to find influential TF for
`peak_GR`	a GRange object represent your whole feature location with a column named feature_id, which your input_feature_id should a part of it.
`peakScoreMt`	peak count matrix.
`TF_GR_database`	TF peak GRange with a column named TF_id representing you TF name. If you have TF_score column, MARA will consider it. otherwise, MARA will consider each hit is 1.
`log`	whether you want to log your peakScoreMt

meanScale	whether you want to mean-centered per row
output	one of 'coef' and 'cor'. Default is coef
verbose	whether you want to report detailed running message

Value

a data.frame

Examples

```
data("ATAC_normCount")
data("test_featureSet")

peak_path <- system.file("extdata", "ATAC.bed.gz", package = "FindIT2")
peak_GR <- loadPeakFile(peak_path)

ChIP_peak_path <- system.file("extdata", "ChIP.bed.gz", package = "FindIT2")
ChIP_peak_GR <- loadPeakFile(ChIP_peak_path)
ChIP_peak_GR$TF_id <- "AT1G28300"

set.seed(20160806)

result_findIT_MARA <- findIT_MARA(
    input_feature_id = test_featureSet,
    peak_GR = peak_GR,
    peakScoreMt = ATAC_normCount,
    TF_GR_database = ChIP_peak_GR
)
```

---

findIT_regionRP *findI(nfluential)T(F)_regionRP*

Description

find Influential TF of your input gene set based on regulatory potential data and TF ChIP-Seq or motif data

Usage

```
findIT_regionRP(
  regionRP,
  Txdb,
  TF_GR_database,
  input_genes,
  background_genes = NULL,
  background_number = 3000,
  verbose = TRUE
)
```

Arguments

regionRP	the MultiAssayExperiment object from calcRP_region
Txdb	Txdb
TF_GR_database	TF peak GRange with a column named TF_id representing you TF name
input_genes	a character vector which represent genes set which you want to find influential TF for
background_genes	a character vector which represent background genes set. If you do not assign background gene , program will sample background_number genes as background genes from all gene sets.
background_number	background genes number
verbose	whether you want to report detailed running message

Value

a MultiAssayExperiment object containg detailed TF-percent and TF-pvalue

Examples

```
if (require(TxDb.Athaliana.BioMart.plantsmart28)) {
    data("ATAC_normCount")
    data("test_geneSet")
    Txdb <- TxDb.Athaliana.BioMart.plantsmart28
    seqlevels(Txdb) <- paste0("Chr", c(1:5, "M", "C"))

    peak_path <- system.file("extdata", "ATAC.bed.gz", package = "FindIT2")
    peak_GR <- loadPeakFile(peak_path)

    ChIP_peak_path <- system.file("extdata", "ChIP.bed.gz", package = "FindIT2")
    ChIP_peak_GR <- loadPeakFile(ChIP_peak_path)
    ChIP_peak_GR$TF_id <- "AT1G28300"

    mmAnno <- mm_geneScan(peak_GR, Txdb)

    regionRP <- calcRP_region(
        mmAnno = mmAnno,
        peakScoreMt = ATAC_normCount,
        Txdb = Txdb,
        Chrs_included = "Chr5"
    )

    set.seed(20160806)
    result_findIT_regionRP <- findIT_regionRP(
        regionRP = regionRP,
        Txdb = Txdb,
        TF_GR_database = ChIP_peak_GR,
        input_genes = test_geneSet,
        background_number = 3000
    )

}
```

findIT_TFHit *findI(nfluential)T(F)_TFHit*

Description

find influential TF of your input gene set based on TF ChIP-Seq or motif data

Usage

```
findIT_TFHit(
  input_genes,
  Txdb,
  TF_GR_database,
  scan_dist = 20000,
  decay_dist = 1000,
  Chrs_included,
  background_genes = NULL,
  background_number = 3000,
  verbose = TRUE
)
```

Arguments

input_genes	a character vector which represent genes set which you want to find influential TF for
Txdb	Txdb
TF_GR_database	TF peak GRange with a column named TF_id representing you TF name
scan_dist	scan distance
decay_dist	decay distance
Chrs_included	a character vector represent chromosomes which you want to sample background genes from
background_genes	a character vector which represent background genes set. If you do not assign background gene , program will sample background_number genes as background genes from all gene sets.
background_number	background genes number
verbose	whether you want to report detailed running message

Value

data.frame

Examples

```
if (require(TxDb.Athaliana.BioMart.plantsmart28)) {
    data("test_geneSet")
    Txdb <- TxDb.Athaliana.BioMart.plantsmart28
    seqlevels(Txdb) <- paste0("Chr", c(1:5, "M", "C"))
```

```
    ChIP_peak_path <- system.file("extdata", "ChIP.bed.gz", package = "FindIT2")
    ChIP_peak_GR <- loadPeakFile(ChIP_peak_path)
    ChIP_peak_GR$TF_id <- "AT1G28300"

    set.seed(20160806)
    result_findIT_TFHit <- findIT_TFHit(
        input_genes = test_geneSet,
        Txdb = Txdb,
        TF_GR_database = ChIP_peak_GR
    )

}
```

`findIT_TTPair` *findI(nfluential)T(F)_T(F)T(arget)Pair*

Description

find influential TF of your input gene set based on public TF-Target data

Usage

```
findIT_TTPair(
  input_genes,
  TF_target_database,
  gene_background = NULL,
  TFHit_min = 5,
  TFHit_max = 10000
)
```

Arguments

`input_genes`	a character vector which represent genes set which you want to find influential TF for
`TF_target_database`	TF_target pair data with two column named TF_id and target_gene
`gene_background`	a character vector represent your bakcaground gene. If you do not assign background gene, program will consider all target gene as background
`TFHit_min`	minimal size of target gene regulated by TF
`TFHit_max`	maximal size of target gene regulated by TF

Value

data.frame

Examples

```
data("TF_target_database")
data("test_geneSet")

result_findIT_TTPair <- findIT_TTPair(
    input_genes = test_geneSet,
    TF_target_database = TF_target_database
)
```

---

getAssocPairNumber *getAssocPairNumber*

Description

get associated peak number of gene and vice verse.

Usage

```
getAssocPairNumber(
  mmAnno,
  output_type = c("gene_id", "feature_id"),
  output_summary = FALSE
)
```

Arguments

mmAnno	the annotated GRange object from mm_geneScan or mm_nearestGene
output_type	one of 'gene_id' or 'feature_id'
output_summary	whether you want to detailed info

Value

data.frame

Examples

```
if (require(TxDb.Athaliana.BioMart.plantsmart28)) {
    Txdb <- TxDb.Athaliana.BioMart.plantsmart28
    seqlevels(Txdb) <- paste0("Chr", c(1:5, "M", "C"))

    peak_path <- system.file("extdata", "ChIP.bed.gz", package = "FindIT2")
    peak_GR <- loadPeakFile(peak_path)
    peakAnno <- mm_nearestGene(peak_GR, Txdb)

    getAssocPairNumber(peakAnno)

}
```

integrate_ChIP_RNA *integrate_ChIP_RNA*

Description

integrate ChIP-Seq and RNA-Seq data to find TF target genes

Usage

```
integrate_ChIP_RNA(
  result_geneRP,
  result_geneDiff,
  lfc_threshold = 1,
  padj_threshold = 0.05
)
```

Arguments

result_geneRP	the simplify result from calcRP_TFHit(report_fullInfo = FALSE) or RP_df <- metadata(fullRP_hit)$peakRP_gene.
result_geneDiff	the result from RNA diff result with three column gene_id, log2FoldChange, padj
lfc_threshold	the threshold which decide significant genes
padj_threshold	the threshold which decide significant genes

Value

a ggplot object if having significant genes in your result. If not, it will report a data.frame with integrated info.

Examples

```
if (require(TxDb.Athaliana.BioMart.plantsmart28)) {
    data("RNADiff_LEC2_GR")
    Txdb <- TxDb.Athaliana.BioMart.plantsmart28
    seqlevels(Txdb) <- paste0("Chr", c(1:5, "M", "C"))
    peak_path <- system.file("extdata", "ChIP.bed.gz", package = "FindIT2")
    peak_GR <- loadPeakFile(peak_path)
    mmAnno <- mm_geneScan(peak_GR, Txdb)

    result_geneRP <- calcRP_TFHit(
        mmAnno = mmAnno,
        Txdb = Txdb
    )
    # output a plot
    merge_data <- integrate_ChIP_RNA(
        result_geneRP = result_geneRP,
        result_geneDiff = RNADiff_LEC2_GR
    )
    # if you want to extract merge target data
    target_data <- merge_data$data
```

```
}
```

`integrate_replicates` *integrate_replicates*

Description

integrate value from replicates

Usage

```
integrate_replicates(
  mt,
  colData,
  fun = NULL,
  type = c("value", "rank", "rank_zscore", "pvalue")
)
```

Arguments

`mt`	value matrix
`colData`	a data.frame with a single column named with "type". Rows of colData correspond to columns of mt.
`fun`	the function you want to use. If set NULL, program will decide integrate method according to your 'type' parameter.
`type`	one of 'value', 'rank', 'rank_zscore', pvalue'. value will use mean to integrate replicates, rank will use product, rank_zscore will use Stouffer's method and pvalue will use CCT(Cauchy distribution)

Value

matrix

Examples

```
mt <- matrix(runif(100, 0, 1), nrow = 10)
colnames(mt) <- paste0(paste0("type", 1:5), "_", rep(1:2, 5))
rownames(mt) <- paste0("TF", 1:10)

colData <- data.frame(
    type = gsub("_[0-9]", "", colnames(mt)),
    row.names = colnames(mt)
)


integrate_replicates(mt, colData, type = "value")
```

jaccard_findIT_enrichFisher *jaccard_findIT_enrichFisher*

Description

jaccard_findIT_enrichFisher

Usage

```
jaccard_findIT_enrichFisher(
  input_feature_id,
  peak_GR,
  TF_GR_database,
  input_TF_id
)
```

Arguments

input_feature_id	a character vector which represent peaks set which you want to find influential TF for (same as your find_IT_enrichFisher parameter)
peak_GR	a GRange object represent your whole feature location with a column named feature_id, which your input_feature_id should a part of it.
TF_GR_database	TF peak GRange with a column named TF_id representing you TF name
input_TF_id	TF_id which you want to calculate jaccard index for

Value

jaccard similarity matrix

Examples

```
data("test_featureSet")
peak_path <- system.file("extdata", "ATAC.bed.gz", package = "FindIT2")
peak_GR <- loadPeakFile(peak_path)

ChIP_peak_path <- system.file("extdata", "ChIP.bed.gz", package = "FindIT2")
ChIP_peak_GR <- loadPeakFile(ChIP_peak_path)
ChIP_peak_GR$TF_id <- "AT1G28300"
result_findIT_enrichFisher <- findIT_enrichFisher(
    input_feature_id = test_featureSet,
    peak_GR = peak_GR,
    TF_GR_database = ChIP_peak_GR
)

jaccard_findIT_enrichFisher(
    input_feature_id = test_featureSet,
    peak_GR = peak_GR,
    TF_GR_database = ChIP_peak_GR,
    input_TF_id = result_findIT_enrichFisher$TF_id[1]
)
```

jaccard_findIT_TTpair *jaccard_findIT_TTpair*

Description

jaccard_findIT_TTpair

Usage

```
jaccard_findIT_TTpair(input_genes, TF_target_database, input_TF_id)
```

Arguments

input_genes	a character vector which represent gene set which you want to find influential TF for (same as your find_IT_TTpair parameter)
TF_target_database	TF_target pair data
input_TF_id	TF_id which you want to calculate jaccard index for

Value

jaccard similarity matrix

Examples

```
data("TF_target_database")
data("test_geneSet")
result_findIT_TTPair <- findIT_TTPair(
    input_genes = test_geneSet,
    TF_target_database = TF_target_database
)

jaccard_findIT_TTpair(
    input_genes = test_geneSet,
    TF_target_database = TF_target_database,
    input_TF_id = result_findIT_TTPair$TF_id[1:3]
)
```

loadPeakFile *loadPeakFile*

Description

read peak file and transform it into GRanges object

Usage

```
loadPeakFile(filePath, TFBS_database = FALSE)
```

Arguments

filePath	peak Path
TFBS_database	whether your peak file is a TFBS database file. If you want the final GRanges have a column named "TF_id", you should set TFBS_database TRUE. The GRanges with TF_id can be applied in "TF_GR_database" parameter of findIT_TFHit, findIT_enrichFisher, findIT_enrichWilcox, findIT_regionRP. If FALSE, the GRanges will have a column named "feature_id", which always be the input of "peak_GR" parameter.

Details

The GRanges with TF_id always be the input of "TF_GR_database" parameter. It represents the TFBS database like motif scan result, public database ChIP-seq site and so on.

The GRanges with feature_id always be the input of "peak_GR" parameter.

Value

GRanges object with a column named feature_id or TF_id

Examples

```
peakfile <- system.file("extdata", "ChIP.bed.gz", package = "FindIT2")
loadPeakFile(peakfile)
```

---

mm_geneBound *mm_geneBound*

Description

find related peaks of your input genes, which is useful when you want to plot volcano plot or heatmap of peaks.

Usage

```
mm_geneBound(peak_GR, Txdb, input_genes, verbose = TRUE, ...)
```

Arguments

peak_GR	peak GRange with a column named feature_id representing you peak name
Txdb	Txdb
input_genes	a character vector which represent genes set which you want to find related peak for
verbose	whether you want to report detailed running message
...	additional arguments in distanceToNearest

Value

data.frame with three column: related peak id, your input gene id, and distance

Examples

```
if (require(TxDb.Athaliana.BioMart.plantsmart28)) {
    Txdb <- TxDb.Athaliana.BioMart.plantsmart28
    seqlevels(Txdb) <- paste0("Chr", c(1:5, "M", "C"))
    peak_path <- system.file("extdata", "ChIP.bed.gz", package = "FindIT2")
    peak_GR <- loadPeakFile(peak_path)
    peak_pair <- mm_geneBound(peak_GR, Txdb, c("AT5G01015", "AT5G67570"))
    peak_pair
}
```

---

mm_geneScan *mm_geneScan*

Description

Annotate peaks using geneScan mode, which means every peak have more than one related genes.

Usage

```
mm_geneScan(
  peak_GR,
  Txdb,
  upstream = 3000,
  downstream = 3000,
  reportGeneInfo = FALSE,
  verbose = TRUE,
  ...
)
```

Arguments

peak_GR	peak GRange with a column named feature_id representing you peak name
Txdb	Txdb
upstream	distance to start site(upstream)
downstream	distance to start site(downstream)
reportGeneInfo	whether you want to add gene info
verbose	whether you want to report detailed running message
...	additional arguments in findOverlaps

Value

Granges object with annotated info

Examples

```
if (require(TxDb.Athaliana.BioMart.plantsmart28)) {
    Txdb <- TxDb.Athaliana.BioMart.plantsmart28
    seqlevels(Txdb) <- paste0("Chr", c(1:5, "M", "C"))
    peak_path <- system.file("extdata", "ChIP.bed.gz", package = "FindIT2")
    peak_GR <- loadPeakFile(peak_path)
    peakAnno <- mm_geneScan(peak_GR, Txdb)
    peakAnno
}
```

`mm_nearestGene` *mm_nearestGene*

Description

Annotate peaks using nearest gene mode, which means every peak only have one related gene.

Usage

```
mm_nearestGene(peak_GR, Txdb, reportGeneInfo = FALSE, verbose = TRUE, ...)
```

Arguments

`peak_GR`	peak GRange with a column named feature_id representing you peak name
`Txdb`	Txdb
`reportGeneInfo`	whether you want to report full gene info
`verbose`	whether you want to report detailed running message
`...`	additional arguments in distanceToNearest

Value

Granges object with annotated info

Examples

```
if (require(TxDb.Athaliana.BioMart.plantsmart28)) {
    Txdb <- TxDb.Athaliana.BioMart.plantsmart28
    seqlevels(Txdb) <- paste0("Chr", c(1:5, "M", "C"))

    peak_path <- system.file("extdata", "ChIP.bed.gz", package = "FindIT2")
    peak_GR <- loadPeakFile(peak_path)
    peakAnno <- mm_nearestGene(peak_GR, Txdb)
    peakAnno
}
```

peakGeneCor *peakGeneCor*

Description

peakGeneCor

Usage

```
peakGeneCor(mmAnno, peakScoreMt, geneScoreMt, parallel = FALSE, verbose = TRUE)
```

Arguments

mmAnno	the annotated GRange object from mm_geneScan or mm_nearestGene
peakScoreMt	peak count matrix. The rownames are feature_id in mmAnno, while the colnames are sample names.
geneScoreMt	gene count matirx. The rownames are gene_id in mmAnno, while the colnames are sample names.
parallel	whehter you want to using bplapply to speed up calculation
verbose	whether you want to report detailed running message

Value

mmAnno with Cor, pvalue,padj,qvalue column

Examples

```
if (require(TxDb.Athaliana.BioMart.plantsmart28)){
    Txdb <- TxDb.Athaliana.BioMart.plantsmart28
    seqlevels(Txdb) <- paste0("Chr", c(1:5, "M", "C"))
    data("RNA_normCount")
    data("ATAC_normCount")
    peak_path <- system.file("extdata", "ATAC.bed.gz", package = "FindIT2")
    peak_GR <- loadPeakFile(peak_path)[1:100]
    mmAnno <- mm_geneScan(peak_GR, Txdb)

    ATAC_colData <- data.frame(
        row.names = colnames(ATAC_normCount),
        type = gsub("_R[0-9]", "", colnames(ATAC_normCount))
    )

    ATAC_normCount_merge <- integrate_replicates(ATAC_normCount, ATAC_colData)
    RNA_colData <- data.frame(
        row.names = colnames(RNA_normCount),
        type = gsub("_R[0-9]", "", colnames(RNA_normCount))
    )
    RNA_normCount_merge <- integrate_replicates(RNA_normCount, RNA_colData)
    mmAnnoCor <- peakGeneCor(
        mmAnno = mmAnno,
        peakScoreMt = ATAC_normCount_merge,
        geneScoreMt = RNA_normCount_merge,
        parallel = FALSE
```

```
    )

    mmAnnoCor

}
```

---

plot_annoDistance *plot_annoDistance*

Description

plot the distance distribution of mmAnno from mm_nearestGene, which helps you decide whehter your TF is promoter or enhancer dominant

Usage

```
plot_annoDistance(mmAnno, quantile = c(0.01, 0.99))
```

Arguments

mmAnno	the annotated GRange object from mm_nearestGene
quantile	the quantile of distanceToTSS you want to show

Value

a ggplot2 object

Examples

```
if (require(TxDb.Athaliana.BioMart.plantsmart28)) {
    Txdb <- TxDb.Athaliana.BioMart.plantsmart28
    seqlevels(Txdb) <- paste0("Chr", c(1:5, "M", "C"))

    peak_path <- system.file("extdata", "ChIP.bed.gz", package = "FindIT2")
    peak_GR <- loadPeakFile(peak_path)
    peakAnno <- mm_nearestGene(peak_GR, Txdb)
    plot_annoDistance(peakAnno)

}
```

---

plot_peakGeneAlias_summary
plot_peakGeneAlias_summary

Description

plot_peakGeneAlias_summary

Usage

```
plot_peakGeneAlias_summary(
  mmAnno,
  mmAnno_corFilter = NULL,
  output_type = c("gene_id", "feature_id"),
  fillColor = "#ca6b67"
)
```

Arguments

mmAnno	the annotated GRange object from mm_geneScan or mm_nearestGene
mmAnno_corFilter	the filter mmAnno object according to p-value or cor, defalut is NULL
output_type	one of 'gene_id' or 'feature_id'
fillColor	the bar plot color

Value

a ggplot object

Examples

```
if (require(TxDb.Athaliana.BioMart.plantsmart28)) {
    Txdb <- TxDb.Athaliana.BioMart.plantsmart28
    seqlevels(Txdb) <- paste0("Chr", c(1:5, "M", "C"))

    peak_path <- system.file("extdata", "ChIP.bed.gz", package = "FindIT2")
    peak_GR <- loadPeakFile(peak_path)
    peakAnno <- mm_nearestGene(peak_GR, Txdb)

    plot_peakGeneAlias_summary(peakAnno)

}
```

---

plot_peakGeneCor *plot_peakGeneCor*

Description

plot_peakGeneCor

Usage

```
plot_peakGeneCor(
  mmAnnoCor,
  select_gene,
  addLine = TRUE,
  addFullInfo = TRUE,
  sigShow = c("pvalue", "padj", "qvalue")
)
```

Arguments

mmAnnoCor	the annotated GRange object from peakGeneCor or enhancerPromoterCor
select_gene	a gene_id which you want to show
addLine	whether add cor line
addFullInfo	whether add full feature info on plot
sigShow	one of 'pvalue' 'padj' 'qvalue'

Value

ggplot2 object

Examples

```
if (require(TxDb.Athaliana.BioMart.plantsmart28)) {
    data("RNA_normCount")
    data("ATAC_normCount")
    Txdb <- TxDb.Athaliana.BioMart.plantsmart28
    seqlevels(Txdb) <- paste0("Chr", c(1:5, "M", "C"))
    peak_path <- system.file("extdata", "ATAC.bed.gz", package = "FindIT2")
    peak_GR <- loadPeakFile(peak_path)[1:100]
    mmAnno <- mm_geneScan(peak_GR, Txdb)

    ATAC_colData <- data.frame(
        row.names = colnames(ATAC_normCount),
        type = gsub("_R[0-9]", "", colnames(ATAC_normCount))
    )

    integrate_replicates(ATAC_normCount, ATAC_colData) -> ATAC_normCount_merge
    RNA_colData <- data.frame(
        row.names = colnames(RNA_normCount),
        type = gsub("_R[0-9]", "", colnames(RNA_normCount))
    )
    integrate_replicates(RNA_normCount, RNA_colData) -> RNA_normCount_merge
    mmAnnoCor <- peakGeneCor(
        mmAnno = mmAnno,
        peakScoreMt = ATAC_normCount_merge,
        geneScoreMt = RNA_normCount_merge,
        parallel = FALSE
    )

    plot_peakGeneCor(mmAnnoCor, select_gene = "AT5G01010")

}
```

RNADiff_LEC2_GR *RNA diff result from LEC2_GR VS LEC2_DMSO*

Description

RNA diff result from LEC2_GR VS LEC2_DMSO

Usage

```
data(RNADiff_LEC2_GR)
```

Format

a data frame

Source

https://doi.org/10.1016/j.devcel.2020.07.003

RNA_normCount *RNA normCount of E50h-72h in Chr5*

Description

RNA normCount of E50h-72h in Chr5

Usage

```
data(RNA_normCount)
```

Format

A matrix

Source

https://doi.org/10.1016/j.devcel.2020.07.003

---

test_featureSet *test_featureSet*

Description

test_featureSet

Usage

```
data(test_featureSet)
```

Format

character vector represent your interesting feature_id set

Details

For the detailed progress producing input_feature_id, you can see ?test_geneSet

test_geneSet *test_geneSet*

Description

test_geneSet

Usage

```
data(test_geneSet)
```

Format

character vector represent your interesting gene set

Examples

```
## Not run:
# source
if (require(TxDb.Athaliana.BioMart.plantsmart28)) {
    library(FindIT2)
    Txdb <- TxDb.Athaliana.BioMart.plantsmart28
    seqlevels(Txdb) <- paste0("Chr", c(1:5, "M", "C"))
    ChIP_peak_path <- system.file("extdata", "ChIP.bed.gz", package = "FindIT2")
    ChIP_peak_GR <- loadPeakFile(ChIP_peak_path)
    ATAC_peak_path <- system.file("extdata", "ATAC.bed.gz", package = "FindIT2")
    ATAC_peak_GR <- loadPeakFile(ATAC_peak_path)

    mmAnno_geneScan <- mm_geneScan(
        peak_GR = ChIP_peak_GR,
        Txdb = Txdb,
        upstream = 2e4,
        downstream = 2e4
    )

    peakRP_gene <- calcRP_TFHit(
        mmAnno = mmAnno_geneScan,
        Txdb = Txdb,
        report_fullInfo = FALSE
    )

    data("RNADiff_LEC2_GR")
     merge_result <- integrate_ChIP_RNA(
        result_geneRP = peakRP_gene,
        result_geneDiff = RNADiff_LEC2_GR
    )

    target_result <- merge_result$data
    test_geneSet <- target_result$gene_id[1:50]

    related_peaks <- mm_geneBound(
        peak_GR = ATAC_peak_GR,
        Txdb = Txdb,
        input_genes = test_geneSet
```

```
    )
    test_featureSet <- unique(related_peaks$feature_id)
    # save(test_geneSet, file = "data/test_geneSet.rda", version = 2)
    # save(test_featureSet, file = "data/test_featureSet.rda", version = 2)
}

## End(Not run)
```

TF_target_database *TF-target database*

Description

TF-target database

Usage

```
data(TF_target_database)
```

Format

a data frame

Source

http://bioinformatics.psb.ugent.be/webtools/iGRN/pages/download

Examples

```
## Not run:
# source
library(dplyr)
data <- read.table("~/reference/annoation/Athaliana/TF_target/iGRN_network_full.txt",
                   sep = "\t",
                   stringsAsFactors = FALSE)

data %>%
rename(TF_id = V1, target_gene = V2) %>%
select(TF_id, target_gene) %>%
TF_target_database <- filter(TF_id %in% c("AT1G28300",
"AT5G63790", "AT5G24110", "AT3G23250")) %>%
as.data.frame()

save(TF_target_database, file = "inst/extdata/TF_target_database.rda", version = 2,
     compress = "bzip2")


## End(Not run)
```

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