

# Package ‘FindIT2’

November 20, 2024

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

**Version** 1.12.0

**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.

**License** Artistic-2.0

**URL** <https://github.com/shanguandong1996/FindIT2>

**BugReports** <https://support.bioconductor.org/t/FindIT2>

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---

ATAC_normCount	<i>ATAC normCount of E50h-72h in Chr5</i>
----------------	---

---

## 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	<i>calcRP_coverage</i>
-----------------	------------------------

---

**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_scanEnhancer = 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\_scanEnhancer      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(nfluentia)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(nfluentia)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	<i>findI(nfluentia)T(F)_TFHit</i>
--------------	-----------------------------------

---

### 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 back-ground 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	<i>mm_geneBound</i>
--------------	---------------------

---

**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 GRRange 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	<i>mm_nearestGene</i>
----------------	-----------------------

---

**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	<i>peakGeneCor</i>
-------------	--------------------

---

## 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 matrix. The rownames are gene_id in mmAnno, while the colnames are sample names.
parallel	whether you want to use 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 whether 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, default 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	<i>RNA normCount of E50h-72h in Chr5</i>
---------------	--

---

**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	<i>test_featureSet</i>
-----------------	------------------------

---

**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	<i>test_geneSet</i>
--------------	---------------------

---

## 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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