

# Package ‘FindIT2’

February 20, 2025

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

**Version** 1.13.0

**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/shangguandong1996/FindIT2>

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

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## Contents

ATAC_normCount . . . . .	3
calcRP_coverage . . . . .	3
calcRP_region . . . . .	4
calcRP_TFHit . . . . .	6
enhancerPromoterCor . . . . .	7
findIT_enrichFisher . . . . .	8
findIT_enrichWilcox . . . . .	9
findIT_MARA . . . . .	10
findIT_regionRP . . . . .	11
findIT_TFHit . . . . .	13
findIT_TTPair . . . . .	14
getAssocPairNumber . . . . .	15
integrate_ChIP_RNA . . . . .	16
integrate_replicates . . . . .	17
jaccard_findIT_enrichFisher . . . . .	18
jaccard_findIT_TTpair . . . . .	19
loadPeakFile . . . . .	20
mm_geneBound . . . . .	21
mm_geneScan . . . . .	22
mm_nearestGene . . . . .	23
peakGeneCor . . . . .	23
plot_annoDistance . . . . .	25
plot_peakGeneAlias_summary . . . . .	25
plot_peakGeneCor . . . . .	26
RNADiff_LEC2_GR . . . . .	28
RNA_normCount . . . . .	28
test_featureSet . . . . .	29
test_geneSet . . . . .	29
TF_target_database . . . . .	30

<b>Index</b>	<b>32</b>
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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**

<code>bwFile</code>	bw file
<code>Txdb</code>	Txdb
<code>gene_included</code>	a character vector which represent gene set which you want to calculate RP for
<code>Chrs_included</code>	a character vector which represent chromosomes where you want to calculate gene RP in
<code>decay_dist</code>	decay distance
<code>scan_dist</code>	scan distance
<code>verbose</code>	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\_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(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 GRRange 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 GRRange 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 containing 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(nfluentia)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 GRRange 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(nfluentia)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 GRRange 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 GRRange 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 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	<i>mm_geneScan</i>
-------------	--------------------

---

### 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

*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	<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)
```

# Index

## \* datasets

- ATAC\_normCount, [3](#)
  - RNA\_normCount, [28](#)
  - RNADiff\_LEC2\_GR, [28](#)
  - test\_featureSet, [29](#)
  - test\_geneSet, [29](#)
  - TF\_target\_database, [30](#)
  - RNA\_normCount, [28](#)
  - RNADiff\_LEC2\_GR, [28](#)
  - test\_featureSet, [29](#)
  - test\_geneSet, [29](#)
  - TF\_target\_database, [30](#)
- ATAC\_normCount, [3](#)
- calcRP\_coverage, [3](#)
- calcRP\_region, [4](#)
- calcRP\_TFHit, [6](#)
- enhancerPromoterCor, [7](#)
- findIT\_enrichFisher, [8](#)
- findIT\_enrichWilcox, [9](#)
- findIT\_MARA, [10](#)
- findIT\_regionRP, [11](#)
- findIT\_TFHit, [13](#)
- findIT\_TTPair, [14](#)
- getAssocPairNumber, [15](#)
- integrate\_ChIP\_RNA, [16](#)
- integrate\_replicates, [17](#)
- jaccard\_findIT\_enrichFisher, [18](#)
- jaccard\_findIT\_TTpair, [19](#)
- loadPeakFile, [20](#)
- mm\_geneBound, [21](#)
- mm\_geneScan, [22](#)
- mm\_nearestGene, [23](#)
- peakGeneCor, [23](#)
- plot\_annoDistance, [25](#)
- plot\_peakGeneAlias\_summary, [25](#)
- plot\_peakGeneCor, [26](#)