

# Package ‘FindIT2’

December 4, 2025

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

**Version** 1.17.0

**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> |
|--------------|-----------|

---

|                |                                           |
|----------------|-------------------------------------------|
| 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 | <i>calcRP_region</i> |
|---------------|----------------------|

---

**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.plantmart28)) {
  data("ATAC_normCount")
  library(SummarizedExperiment)
  Txdb <- TxDb.Athaliana.BioMart.plantmart28
  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 | <i>calcRP_TFHit</i> |
|--------------|---------------------|

---

**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 | <i>findIT_enrichWilcox</i> |
|---------------------|----------------------------|

---

**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 | <i>findIT_MARA</i> |
|-------------|--------------------|

---

**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 | <i>findI(nfluentia)T(F)_regionRP</i> |
|-----------------|--------------------------------------|

---

**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(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 | <i>getAssocPairNumber</i> |
|--------------------|---------------------------|

---

**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.plantmart28)) {
  Txdb <- TxDb.Athaliana.BioMart.plantmart28
  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 | <i>integrate_ChIP_RNA</i> |
|--------------------|---------------------------|

---

**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.plantmart28)) {
  data("RNADiff_LEC2_GR")
  Txdb <- TxDb.Athaliana.BioMart.plantmart28
  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 | <i>loadPeakFile</i> |
|--------------|---------------------|

---

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

*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.plantmart28)) {
  Txdb <- TxDb.Athaliana.BioMart.plantmart28
  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.plantmart28)) {  
  Txdb <- Txdb.Athaliana.BioMart.plantmart28  
  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.plantmart28)){
  Txdb <- TxDb.Athaliana.BioMart.plantmart28
  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 | <i>plot_annoDistance</i> |
|-------------------|--------------------------|

---

**Description**

plot the distance distribution of mmAnno from mm\_nearestGene, which helps you decide whehther 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 | <i>plot_peakGeneAlias_summary</i> |
|----------------------------|-----------------------------------|

---

**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.plantmart28)) {
  Txdb <- TxDb.Athaliana.BioMart.plantmart28
  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 | <i>plot_peakGeneCor</i> |
|------------------|-------------------------|

---

**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 | <i>RNA diff result from LEC2_GR VS LEC2_DMSO</i> |
|-----------------|--------------------------------------------------|

---

**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 | <i>TF-target database</i> |
|--------------------|---------------------------|

---

### 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](#)