Package 'GenomicInteractionNodes'

October 15, 2023

Type Package

Version 1.4.0

Title A R/Bioconductor package to detect the interaction nodes from HiC/HiChIP/HiCAR data

Description The GenomicInteractionNodes package can import interactions from bedpe file and define the interaction nodes, the genomic interaction sites with multiple interaction loops.
The interaction nodes is a binding platform regulates one or multiple genes. The detected interaction nodes will be annotated for downstream validation.

License file LICENSE

Depends R (>= 4.2.0), stats

Imports AnnotationDbi, graph, GO.db, GenomicRanges, GenomicFeatures, GenomeInfoDb, methods, IRanges, RBGL, S4Vectors

Suggests RUnit, BiocStyle, knitr, rmarkdown, rtracklayer, testthat, TxDb.Hsapiens.UCSC.hg19.knownGene, org.Hs.eg.db

URL https://github.com/jianhong/GenomicInteractionNodes

BugReports https://github.com/jianhong/GenomicInteractionNodes/issues

biocViews HiC, Sequencing, Software

VignetteBuilder knitr

RoxygenNote 7.1.2

Encoding UTF-8

git_url https://git.bioconductor.org/packages/GenomicInteractionNodes

git_branch RELEASE_3_17

git_last_commit ba14b80

git_last_commit_date 2023-04-25

Date/Publication 2023-10-15

Author Jianhong Ou [aut, cre],
Yarui Diao [fnd]

Maintainer Jianhong Ou <jianhong.ou@duke.edu>

R topics documented:

`annotateNodes` *Annotate node regions*

Description

Assigne gene id and gene symbols to node regions by interacted.

Usage

```
annotateNodes(
  node_regions,
  txdb,
  orgDb,
  upstream = 2000,
  downstream = 500,
  ...
)
```

Arguments

`node_regions`	GRanges object represent regions interacted with nodes.
`txdb`	An object of TxDb to extract gene information
`orgDb`	An object of OrgDb to extract gene symbols
`upstream, downstream`	An integer(1) value indicating the number of bases upstream or downstream from the transcription start site. For additional details see promoters.
`...`	parameter can be passed to genes

Value

GRanges object with gene_id and symbols metadata.

Examples

```
library(TxDb.Hsapiens.UCSC.hg19.knownGene) ## for human hg19
library(org.Hs.eg.db) ## used to convert gene_id to gene_symbol
set.seed(123)
node_regions <- createRandomNodes(TxDb.Hsapiens.UCSC.hg19.knownGene)
annotateNodes(node_regions, TxDb.Hsapiens.UCSC.hg19.knownGene, org.Hs.eg.db)
```

createRandomNodes *Create a list of random nodes*

Description

Generate a list of random nodes used for example or test.

Usage

```
createRandomNodes(
  txdb,
  seq = "chr22",
  size = 500,
  upstream = 500,
  downstream = 500,
  maxDist = 1e+06,
  wid = 5000
)
```

Arguments

txdb	An TxDb object.
seq	seqlevels to be kept.
size	the length of regions involved in nodes
upstream, downstream	upstream or downstream for promoters
maxDist	maximal distance from promoters
wid	regions width.

Value

An GRanges object with comp_id metadata.

Examples

```
library(TxDb.Hsapiens.UCSC.hg19.knownGene)
set.seed(123)
node_regions <- createRandomNodes(TxDb.Hsapiens.UCSC.hg19.knownGene)
```

detectNodes *Detect the interaction node*

Description

Define the interaction node from input Pairs.

Usage

```
detectNodes(interaction, pval_cutoff = 0.05, ...)
```

Arguments

interaction	An object of Pairs to represent interactions.
pval_cutoff	Cutoff P value for interaction node by poisson distribution
...	Not used.

Value

A list of interaction nodes with elements: node_connection, Pairs object represent interactions interacted with nodes; nodes, GRanges object represent regions involved in nodes; node_regions, GRanges object represent regions interacted with nodes.

Examples

```
library(rtracklayer)
p <- system.file("extdata", "WT.2.bedpe",
                 package = "GenomicInteractionNodes")
interactions <- import(con=p, format="bedpe")
nodes <- detectNodes(interactions)
```

enrichmentAnalysis *Gene ontology enrichment analysis*

Description

GO enrichment analysis for nodes

Usage

```
enrichmentAnalysis(
  node_regions,
  orgDb,
  onto = c("BP", "CC", "MF"),
  minGeneNum = 3,
 evidence = list(Experimental_evidence_codes = c("EXP", "IDA", "IPI", "IMP", "IGI",
  "IEP", "HTP", "HDA", "HMP", "HGI", "HEP"), `Phylogenetically-inferred_annotations` =
  c("IBA", "IBD", "IKR", "IRD"), Computational_analysis_evidence_codes = c("ISS",
  "ISO", "ISA", "ISM", "IGC", "RCA"), Author_statement_evidence_codes = c("TAS",
   "NAS"), Curator_statement_evidence_codes = c("IC", "ND"),
   Electronic_annotation_evidence_code = c("IEA")),
  ...
)
```

Arguments

node_regions	GRanges object represent regions interacted with nodes. The object must be annotated by annotateNodes with comp_id and gene_id in the metadata.
orgDb	An object of OrgDb to extract gene symbols.
onto	Ontology category.
minGeneNum	An integer(1) value indicating the minimal number of gene to start the enrichment analysis. If total gene counts is smaller than the 'minGeneNum', the NULL will be returned.
evidence	The acceptable evidence code.
...	Not used.

Value

A list with element enriched and enriched_in_compound. Or NULL if total counts of gene is smaller than 'minGeneNum'.

Examples

```
library(TxDb.Hsapiens.UCSC.hg19.knownGene) ## for human hg19
library(org.Hs.eg.db) ## used to convert gene_id to gene_symbol
library(GO.db)
set.seed(123)
node_regions <- createRandomNodes(TxDb.Hsapiens.UCSC.hg19.knownGene)
node_regions <-
    annotateNodes(node_regions,
                  TxDb.Hsapiens.UCSC.hg19.knownGene,
                  org.Hs.eg.db)
enr <- enrichmentAnalysis(node_regions, org.Hs.eg.db, onto="BP")
```

Index