

Package ‘GenomicInteractionNodes’

November 22, 2024

Type Package

Version 1.11.0

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.

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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 devel

git_last_commit 60276ee

git_last_commit_date 2024-10-29

Repository Bioconductor 3.21

Date/Publication 2024-11-21

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| | |
|---------------|------------------------------|
| annotateNodes | <i>Annotate node regions</i> |
|---------------|------------------------------|

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 | <i>Create a list of random nodes</i> |
|-------------------|--------------------------------------|

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 | <i>Detect the interaction node</i> |
|-------------|------------------------------------|

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 | <i>Gene ontology enrichment analysis</i> |
|--------------------|--|

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")
```

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