

# Package ‘GenomicInteractionNodes’

June 29, 2025

**Type** Package

**Version** 1.12.0

**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** 7.3.2

**Encoding** UTF-8

**git\_url** <https://git.bioconductor.org/packages/GenomicInteractionNodes>

**git\_branch** RELEASE\_3\_21

**git\_last\_commit** a109a3c

**git\_last\_commit\_date** 2025-04-15

**Repository** Bioconductor 3.21

**Date/Publication** 2025-06-29

**Author** Jianhong Ou [aut, cre] (ORCID: <<https://orcid.org/0000-0002-8652-2488>>),  
Yarui Diao [fnd]

**Maintainer** Jianhong Ou <jou@morgridge.org>

Contents

|                              |          |
|------------------------------|----------|
| annotateNodes . . . . .      | 2        |
| createRandomNodes . . . . .  | 3        |
| detectNodes . . . . .        | 4        |
| enrichmentAnalysis . . . . . | 4        |
| <b>Index</b>                 | <b>6</b> |

---

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

---

Description

Assign 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 <a href="#">Pairs</a> 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 with maximal interactions 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 <a href="#">annotateNodes</a> with comp_id and gene_id in the metadata.               |
| orgDb        | An object of <a href="#">OrgDb</a> 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

annotateNodes, [2](#), [5](#)  
createRandomNodes, [3](#)  
detectNodes, [4](#)  
enrichmentAnalysis, [4](#)  
genes, [2](#)  
OrgDb, [2](#), [5](#)  
Pairs, [4](#)  
promoters, [2](#)  
TxDb, [2](#)