

# Package ‘GenomicInteractionNodes’

August 10, 2025

**Type** Package

**Version** 1.13.1

**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, Seqinfo, 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

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

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## 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 <a href="#">TxDb</a> to extract gene information                                                                                                       |
| orgDb                | An object of <a href="#">OrgDb</a> 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 <a href="#">promoters</a> . |
| ...                  | parameter can be passed to <a href="#">genes</a>                                                                                                                    |

## 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)
```

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

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**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)
```

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

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**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)
```

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enrichmentAnalysis      *Gene ontology enrichment analysis*

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**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")
```

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