

# Package ‘annoLinker’

June 4, 2026

**Type** Package

**Title** Annotating genomic regions through chromatin interaction links

**Version** 1.1.0

**Description** Fast annotation of genomic peaks using DNA interaction data by constructing interaction networks with igraph, where peaks overlapping any node in a connected subgraph are annotated with all genes in that subgraph. The annotation evidence could be visualized as either a network graph or a genomic track integrated with gene annotation information.

**LazyData** false

**License** GPL-3

**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.3

**VignetteBuilder** knitr

**biocViews** Network, Annotation, Visualization

**Depends** R (>= 4.5.0)

**Imports** AnnotationDbi, BiocGenerics, future.apply, GenomicRanges, GenomeInfoDb, igraph, IRanges, InteractionSet, methods, progressr, S4Vectors, Seqinfo, trackViewer, visNetwork

**Suggests** BiocStyle, knitr, rtracklayer, rmarkdown, testthat, TxDb.Drerio.UCSC.danRer10.refGene, org.Dr.e.g.db, future

**URL** <https://github.com/jianhong/annoLinker>

**BugReports** <https://github.com/jianhong/annoLinker/issues>

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annoLinker-package	<i>Annotating genomic regions through chromatin interaction links</i>
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### Description

Fast annotation of genomic peaks using DNA interaction data by building interaction networks with igraph. Peaks overlapping any node in a connected subgraph are annotated with all genes in that subgraph.

### Author(s)

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### See Also

Useful links:

- <https://github.com/jianhong/annoLinker>
- Report bugs at <https://github.com/jianhong/annoLinker/issues>

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annoLinker	<i>Annotate Peaks with DNA Interaction Networks Using Graph Clustering</i>
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### Description

Fast annotation of genomic peaks using DNA interaction data by building interaction networks with igraph. Peaks overlapping any node in a connected subgraph are annotated with all genes in that subgraph.

### Usage

```
annoLinker(
  peaks,
  annoData,
  interactions,
  bindingType = c("startSite", "body", "endSite"),
  bindingRegion = c(-5000, 5000),
  cluster_method = c("components", "louvain", "walktrap", "infomap"),
  maxgap = 0,
```

```

    interactionDistanceRange = c(10000, 1e+07),
    addEvidence = FALSE,
    parallel = FALSE,
    verbose = FALSE,
    ...
)

```

### Arguments

peaks	GRanges object containing peak regions
annoData	annoGR or GRanges object with gene annotations
interactions	GInteractions, or Pairs object with interaction data (e.g., Hi-C, ChIA-PET)
bindingType	Character, one of "startSite", "body", or "endSite"
bindingRegion	Numeric vector of length 2 defining promoter window (e.g., c(-5000, 5000))
cluster_method	Character, clustering method: "components" (connected components), "louvain", "walktrap", or "infomap"
maxgap	Integer, bp to extend interaction anchors for overlap detection (default: 0)
interactionDistanceRange	Numeric vector of length 2 defining the minimal and maximal distance of interactions. This is used to make sure the annotations are not super far away.
addEvidence	Logical, add evidence to the metadata or not.
parallel	Logical, use future_lapply to do parallel computing or not.
verbose	Logical, print the message or not
...	Parameters for cluster. see <a href="#">cluster_louvain</a> , <a href="#">cluster_walktrap</a> , and <a href="#">cluster_infomap</a> .

### Value

An [annoLinkerResult](#) object or NULL if no annotations found

### Examples

```

## read the peaks and interactions
library(rtracklayer)
extPath <- system.file("extdata", package = "annoLinker")
peaks <- rtracklayer::import(file.path(extPath, "peaks.bed"))
interactions <- rtracklayer::import(file.path(extPath, "interaction.bedpe"))
library(TxDb.Drerio.UCSC.danRer10.refGene)
annoData <- genes(TxDb.Drerio.UCSC.danRer10.refGene)
anno <- annoLinker(peaks, annoData, interactions, verbose = TRUE)

```

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annoLinkerResult-class

*Class "annoLinkerResult"*

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### Description

An object of class "annoLinkerResult" represent the annotated peaks, which is a GRanges object with peaks annotated by gene clusters, and interaction graph, which is an igraph graph.

**Usage**

```
## S4 method for signature 'annoLinkerResult'  
as.data.frame(x, row.names = NULL, optional = FALSE, ...)  
  
anno_peaks(x)  
  
## S4 method for signature 'annoLinkerResult'  
anno_peaks(x)  
  
anno_graph(x)  
  
## S4 method for signature 'annoLinkerResult'  
anno_graph(x)  
  
anno_clusters(x)  
  
## S4 method for signature 'annoLinkerResult'  
anno_clusters(x)  
  
anno_evidence(x, i)  
  
## S4 method for signature 'annoLinkerResult'  
anno_evidence(x, i)  
  
anno_event(x, i)  
  
## S4 method for signature 'annoLinkerResult'  
anno_event(x, i)  
  
anno_feature(x, i)  
  
## S4 method for signature 'annoLinkerResult'  
anno_feature(x, i)  
  
anno_peakbin(x, i)  
  
## S4 method for signature 'annoLinkerResult'  
anno_peakbin(x, i)  
  
anno_featurebin(x, i)  
  
## S4 method for signature 'annoLinkerResult'  
anno_featurebin(x, i)  
  
## S4 method for signature 'annoLinkerResult'  
length(x)  
  
## S4 method for signature 'annoLinkerResult'  
show(object)  
  
## S4 method for signature 'annoLinkerResult'  
head(x, ...)
```

**Arguments**

x, object            An annoLinkerResult object.  
 row.names, optional, ...  
                       parameters used by [as.data.frame](#)  
 i                     Numeric, index value.

**Value**

The object of 'annoLinkerResult', 'GRanges', 'igraph' or 'data.frame'

**Objects from the Class**

Objects can be created by calls of the form `new("annoLinkerResult", annotated_peaks, graph, clusters)`.

**Examples**

```
library(igraph)
library(GenomicRanges)
new("annoLinkerResult",
    annotated_peaks = GRanges(),
    graph = make_empty_graph(),
    clusters = data.frame()
)
```

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 plotEvidence

*Plot interaction network for visualization*


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**Description**

Plot interaction network for visualization

**Usage**

```
plotEvidence(
  anno,
  event,
  output = c("graph", "htmlWidget", "trackPlot"),
  colors = c(peak = "darkgreen", feature = "brown", node = "tomato", background =
    "lightgray"),
  txdb,
  org
)
```

**Arguments**

anno                 An object of annoLinkerResult output by [annoLinker](#)  
 event                Number to indicate the event to be plot  
 output               Output of the plot.  
 colors               Colors setting for the plot.  
 txdb, org            The TxDb and OrgDb object used for annotation plot.

**Value**

htmlWidget or plots.

**Examples**

```
anno <- readRDS(system.file("extdata", "sample_res.rds",  
  package = "annoLinker"  
)  
)  
library(org.Dr.eg.db)  
library(TxDb.Drerio.UCSC.danRer10.refGene)  
n <- 1 # length(anno$annotated_peaks$evidences)  
plotEvidence(anno,  
  event = n,  
  output = "htmlWidget"  
)  
plotEvidence(anno,  
  event = n,  
  output = "trackPlot"  
)
```

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