Package 'annoLinker'

April 16, 2026

Type Package

Title Annotating genomic regions through chromatin interaction links

Version 0.99.7

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

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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.eg.db, future

URL `https://github.com/jianhong/annoLinker`

BugReports `https://github.com/jianhong/annoLinker/issues`

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`annoLinker-package` *Annotating genomic regions through chromatin interaction links*

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`

`annoLinker` *Annotate Peaks with DNA Interaction Networks Using Graph Clustering*

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 supper 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 cluster_louvain, cluster_walktrap, and cluster_infomap.

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)
```

`annoLinkerResult-class`

Class "annoLinkerResult"

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()
)
```

`plotEvidence` *Plot interaction network for visualization*

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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