Package: annoLinker (via r-universe)

November 1, 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.

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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

Config/pak/sysreqs cmake libglpk-dev make libbz2-dev libicu-dev liblzma-dev libpng-dev libuv1-dev libxml2-dev libssl-dev xz-utils zlib1g-dev

Repository https://bioc.r-universe.dev

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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)

Jianhong Ou

Maintainer: Jianhong Ou jianhong.ou@morgridge.org

See Also

Useful links:

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

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`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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