

# Package ‘linkSet’

November 1, 2025

**Title** Base Classes for Storing Genomic Link Data

**Version** 1.0.0

**Description** Provides a comprehensive framework for representing, analyzing, and visualizing genomic interactions, particularly focusing on gene-enhancer relationships. The package extends the GenomicRanges infrastructure to handle paired genomic regions with specialized methods for chromatin interaction data from Hi-C, Promoter Capture Hi-C (PCHi-C), and single-cell ATAC-seq experiments. Key features include conversion from common interaction formats, annotation of promoters and enhancers, distance-based analyses, interaction strength metrics, statistical modeling using CHiCANE methodology, and tailored visualization tools. The package aims to standardize the representation of genomic interaction data while providing domain-specific functions not available in general genomic interaction packages.

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<https://gilberthan1011.github.io/linkSet>

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## Contents

|                                                                 |    |
|-----------------------------------------------------------------|----|
| linkSet-package . . . . .                                       | 3  |
| annotateInter,linkSet-method . . . . .                          | 4  |
| annotatePromoter,linkSet-method . . . . .                       | 4  |
| as.data.frame,linkSet-method . . . . .                          | 5  |
| as.GInteractions . . . . .                                      | 6  |
| bait<- . . . . .                                                | 6  |
| baitGInteractions . . . . .                                     | 9  |
| character_Or_missing-class . . . . .                            | 10 |
| checkPackages . . . . .                                         | 11 |
| checkSplitDataNumericalFit . . . . .                            | 11 |
| cleanUnusedRegions . . . . .                                    | 12 |
| Convert,GInteractions-method . . . . .                          | 12 |
| convertToGrange . . . . .                                       | 14 |
| countInteractability . . . . .                                  | 14 |
| countInteractions . . . . .                                     | 15 |
| createSampleLinkSet . . . . .                                   | 15 |
| crossGeneEnhancer,linkSet-method . . . . .                      | 16 |
| diagnoseLinkSet,linkSet-method . . . . .                        | 16 |
| Embryo_body . . . . .                                           | 17 |
| enforceOrder . . . . .                                          | 18 |
| exportInterBed . . . . .                                        | 18 |
| exportToLinkSet . . . . .                                       | 19 |
| exportWashU . . . . .                                           | 19 |
| filterLinks,linkSet-method . . . . .                            | 20 |
| geom_linkset . . . . .                                          | 21 |
| getDistOutput . . . . .                                         | 22 |
| linkExample . . . . .                                           | 23 |
| linkSet . . . . .                                               | 24 |
| linkSet,character,GRanges,character_Or_missing-method . . . . . | 25 |
| linkSet,GRanges,GRanges,character_Or_missing-method . . . . .   | 26 |
| linkSet-class . . . . .                                         | 26 |
| oe<- . . . . .                                                  | 27 |
| orderLinks,linkSet-method . . . . .                             | 28 |
| pairedist,linkSet-method . . . . .                              | 29 |
| pasteAnchor . . . . .                                           | 29 |
| plotBaits . . . . .                                             | 30 |
| plotGenomicRanges . . . . .                                     | 31 |

|                                            |           |
|--------------------------------------------|-----------|
| <i>linkSet-package</i>                     | 3         |
| plotGenomicRanges,linkSet-method . . . . . | 34        |
| reduceRegions . . . . .                    | 36        |
| regionsBait<- . . . . .                    | 36        |
| run_chicane . . . . .                      | 37        |
| show,linkSet-method . . . . .              | 39        |
| showLinkSet . . . . .                      | 40        |
| subsetBait,linkSet-method . . . . .        | 41        |
| themeLinkset . . . . .                     | 42        |
| themeRange . . . . .                       | 42        |
| trim,linkSet-method . . . . .              | 43        |
| unchecked_anchor1<- . . . . .              | 45        |
| unchecked_anchor2<- . . . . .              | 45        |
| verifyLinkSet . . . . .                    | 46        |
| withTxDb . . . . .                         | 48        |
| <b>Index</b>                               | <b>50</b> |

---

|                 |                                                            |
|-----------------|------------------------------------------------------------|
| linkSet-package | <i>linkSet: Base Classes for Storing Genomic Link Data</i> |
|-----------------|------------------------------------------------------------|

---

## Description

Provides a comprehensive framework for representing, analyzing, and visualizing genomic interactions, particularly focusing on gene-enhancer relationships. The package extends the GenomicRanges infrastructure to handle paired genomic regions with specialized methods for chromatin interaction data from Hi-C, Promoter Capture Hi-C (PCHi-C), and single-cell ATAC-seq experiments. Key features include conversion from common interaction formats, annotation of promoters and enhancers, distance-based analyses, interaction strength metrics, statistical modeling using CHiCANE methodology, and tailored visualization tools. The package aims to standardize the representation of genomic interaction data while providing domain-specific functions not available in general genomic interaction packages.

## Author(s)

**Maintainer:** Gilbert Han <GilbertHan1011@gmail.com> ([ORCID](#))

## See Also

Useful links:

- <https://github.com/GilbertHan1011/linkSet>
- <https://gilberthan1011.github.io/linkSet>
- Report bugs at <https://github.com/GilbertHan1011/linkSet/issues/new>

---

```
annotateInter,linkSet-method
```

*Annotate linkSet with inter/intra chromosome interactions*

---

### Description

Annotate linkSet with inter/intra chromosome interactions

### Usage

```
## S4 method for signature 'linkSet'
annotateInter(x)
```

### Arguments

x                      A linkSet object

### Value

A linkSet object with an additional metadata column 'inter\_type'

### Examples

```
data(linkExample)
linkExample <- annotateInter(linkExample)
```

---

```
annotatePromoter,linkSet-method
```

*Annotate the link set with txDb. Give a gene list, and return a*

---

### Description

Annotate the link set with txDb. Give a gene list, and return a

### Usage

```
## S4 method for signature 'linkSet'
annotatePromoter(
  x,
  genome = "hg38",
  keyType = "symbol",
  upstream = 5000,
  overwrite = FALSE
)
```

### Arguments

|           |                                                           |
|-----------|-----------------------------------------------------------|
| x         | linkSet                                                   |
| genome    | the genome you want to annotate                           |
| keyType   | the key type. You can check with AnnotationDbi::keytypes  |
| upstream  | The upstream base from the gene                           |
| overwrite | Whether to overwrite the regionsBait if it already exists |

**Value**

linkSet object

**Examples**

```

gr1 <- GRanges(seqnames = c("chr1", "chr2", "chr3"),
               ranges = IRanges(start = c(1000, 2000, 3000), width = 100),
               strand = "+", symbol = c("BRCA1", "TP53", "NONEXISTENT"))
gr2 <- GRanges(seqnames = c("chr1", "chr2", "chr3"),
               ranges = IRanges(start = c(5000, 6000, 7000), width = 100),
               strand = "+")
linkset_obj <- linkSet(gr1, gr2, specificCol = "symbol")

# Test annotatePromoter
annotated_linkset <- suppressWarnings(annotatePromoter(linkset_obj,
                                                       genome = "hg38",
                                                       upstream = 500,
                                                       overwrite = TRUE))

```

---

as.data.frame,linkSet-method

*coerce linkSet to DataFrame*


---

**Description**

coerce linkSet to DataFrame

**Usage**

```

## S4 method for signature 'linkSet'
as.data.frame(x)

```

**Arguments**

x                      A linkSet object

**Value**

A DataFrame object

**Examples**

```

# Create a linkSet object
data(linkExample)
# Convert linkSet to DataFrame
df <- as.data.frame(linkExample)
print(df)

```

---

|                  |                                 |
|------------------|---------------------------------|
| as.GInteractions | <i>Convert to GInteractions</i> |
|------------------|---------------------------------|

---

### Description

Convert linkSet object to GInteractions

### Usage

```
as.GInteractions(x)

## S4 method for signature 'linkSet'
as.GInteractions(x)
```

### Arguments

x                      A linkset object

### Value

A GInteractions object

### Examples

```
data(linkExample)
gi <- as.GInteractions(linkExample)
gi
```

---

|        |                          |
|--------|--------------------------|
| bait<- | <i>linkSet-accessors</i> |
|--------|--------------------------|

---

### Description

Methods to get and set fields in an linkSet object.

This method returns the anchor IDs of a linkSet object.

This method returns the anchors of a linkSet object.

This method returns the bait anchors of a linkSet object.

This method returns the other end (oe) anchors of a linkSet object.

This method is an alias for 'first' and returns the bait anchors of a linkSet object.

This method is an alias for 'second' and returns the other end (oe) anchors of a linkSet object.

This method returns the regions of a linkSet object.

This method returns the regions corresponding to the bait anchors of a linkSet object.

This method replaces the bait anchors of a linkSet object with new values.

This method replaces the regions of a linkSet object with new values.

This method replaces the anchor1 of a linkSet object with new values.

This method replaces the anchor2 of a linkSet object with new values.

This method replaces the regions of a linkSet object with new values.

This method returns the metadata column of a linkSet object.

This method replaces the metadata column of a linkSet object with new values.

This method returns the names of a linkSet object.

This method replaces the names of a linkSet object.

## Usage

```
bait(x) <- value

regions(x) <- value

anchor1(x) <- value

anchor2(x) <- value

unchecked_regions(x) <- value

## S4 method for signature 'linkSet'
anchor1(x)

## S4 method for signature 'linkSet'
anchor2(x)

## S4 method for signature 'linkSet'
regions(x)

## S4 method for signature 'linkSet'
seqinfo(x)

## S4 method for signature 'linkSet'
anchorIds(x, type = "both")

## S4 method for signature 'linkSet'
anchors(x, type = "both", id = FALSE)

## S4 method for signature 'linkSet'
first(x)

## S4 method for signature 'linkSet'
second(x)

## S4 method for signature 'linkSet'
bait(x)

## S4 method for signature 'linkSet'
oe(x)

## S4 method for signature 'linkSet'
regions(x)
```

```
## S4 method for signature 'linkSet'
regionsBait(x)

## S4 replacement method for signature 'linkSet'
bait(x) <- value

## S4 replacement method for signature 'linkSet'
unchecked_regions(x) <- value

## S4 replacement method for signature 'linkSet'
unchecked_anchor1(x) <- value

## S4 replacement method for signature 'linkSet'
unchecked_anchor2(x) <- value

## S4 replacement method for signature 'linkSet'
regions(x) <- value

## S4 replacement method for signature 'linkSet'
regionsBait(x) <- value

## S4 replacement method for signature 'linkSet'
oe(x) <- value

## S4 method for signature 'linkSet'
x$name

## S4 replacement method for signature 'linkSet'
x$name <- value

## S4 method for signature 'linkSet'
names(x)

## S4 replacement method for signature 'linkSet'
names(x) <- value
```

### Arguments

|                    |                                                                           |
|--------------------|---------------------------------------------------------------------------|
| <code>x</code>     | A linkSet object                                                          |
| <code>value</code> | A character vector of new names                                           |
| <code>type</code>  | The type of anchor to return. Can be "both", "bait", or "oe".             |
| <code>id</code>    | If TRUE, returns the anchor IDs instead of the anchors.                   |
| <code>name</code>  | A character string specifying the name of the metadata column to replace. |

### Value

For the getters, values in various slots of `x` are returned, while for the setters, the slots of `x` are modified accordingly – see Details.

A vector of the regions

A list of anchor IDs.

A list of anchors or anchor IDs.

A GRanges object containing the bait anchors.  
 A GRanges object containing the oe anchors.  
 A GRanges object containing the bait anchors.  
 A GRanges object containing the oe anchors.  
 A GRanges object containing the regions.  
 A GRanges object containing the regions corresponding to the bait anchors.  
 The modified linkSet object with the new bait anchors.  
 The modified linkSet object with the new regions.  
 The modified linkSet object with the new anchor1 values.  
 The modified linkSet object with the new anchor2 values.  
 The modified linkSet object with the new regions.  
 The value of the specified metadata column.  
 The modified linkSet object with the new metadata column value.  
 A character vector of names  
 The modified linkSet object with updated names

### Author(s)

Gilbert Han

### Examples

```

data(linkExample)
anchor1(linkExample)
data(linkExample)
anchor2(linkExample)
data(linkExample)
regions(linkExample)
data(linkExample)
anchorIds(linkExample, type="both")
data(linkExample)
anchors(linkExample, type="both", id=FALSE)

```

---

|                   |                                                               |
|-------------------|---------------------------------------------------------------|
| baitGInteractions | <i>Convert GInteractions to linkSet with bait annotations</i> |
|-------------------|---------------------------------------------------------------|

---

### Description

Convert GInteractions with bait range and oe ranges to linkSet

### Usage

```

baitGInteractions(x, geneGr, peakGr, ...)

## S4 method for signature 'GInteractions,GRanges,GRanges'
baitGInteractions(x, geneGr, peakGr, geneSymbol = NULL)

```

**Arguments**

|                         |                                                                                                                          |
|-------------------------|--------------------------------------------------------------------------------------------------------------------------|
| <code>x</code>          | A <code>GInteractions</code> object                                                                                      |
| <code>geneGr</code>     | A <code>GRanges</code> object representing genes                                                                         |
| <code>peakGr</code>     | A <code>GRanges</code> object representing peaks                                                                         |
| <code>...</code>        | Additional arguments                                                                                                     |
| <code>geneSymbol</code> | A character vector with same length as <code>geneGr</code> or column name in <code>mcols(geneGr)</code> for gene symbols |

**Value**

A `linkSet` object

**Examples**

```
# Example usage:
library(GenomicRanges)
library(InteractionSet)

# Create example GRanges objects for genes and peaks
geneGr <- GRanges(seqnames = "chr1",
                  ranges = IRanges(start = c(100, 200), end = c(150, 250)),
                  geneSymbol = c("Gene1", "Gene2"))
peakGr <- GRanges(seqnames = "chr1",
                  ranges = IRanges(start = c(300, 400), end = c(350, 450)))

# Create example GInteractions object
gi <- GInteractions(anchor1 = geneGr, anchor2 = peakGr)

# Convert to linkSet
linkSetObj <- baitGInteractions(gi, geneGr, peakGr, geneSymbol = "geneSymbol")

# Print the linkSet object
print(linkSetObj)
```

---

character\_Or\_missing-class

*Character or Missing Class Union*

---

**Description**

A class union of character vectors and missing values used in `linkSet` package for optional character arguments.

**Details**

This class is used internally by the `linkSet` package to handle optional character arguments, particularly in the `linkSet` constructor and methods.

---

|               |                                                                    |
|---------------|--------------------------------------------------------------------|
| checkPackages | <i>Check if packages are installed for truncated distributions</i> |
|---------------|--------------------------------------------------------------------|

---

**Description**

Check if required packages are available for truncated distributions

**Usage**

```
checkPackages(distribution)
```

**Arguments**

`distribution`      Character string specifying the distribution type

**Value**

Logical indicating if packages are available, or stops with error

---

|                            |                                       |
|----------------------------|---------------------------------------|
| checkSplitDataNumericalFit | <i>check.split.data.numerical.fit</i> |
|----------------------------|---------------------------------------|

---

**Description**

Helper function to check if the chicane model can be fit on each element of a split data list.  
Check if split data has valid numerical fit for model fitting

**Usage**

```
checkSplitDataNumericalFit(split.data)
```

**Arguments**

`split.data`      Split data for model fitting

**Value**

Logical indicating if the model can be fit  
Check split data numerical fit  
None, stops with error if data is invalid

---

|                    |                             |
|--------------------|-----------------------------|
| cleanUnusedRegions | <i>Clean Unused Regions</i> |
|--------------------|-----------------------------|

---

### Description

This function removes unused regions from a linkSet object to minimize memory usage.

### Usage

```
cleanUnusedRegions(x)

clean_unused_regions(x)

## S4 method for signature 'linkSet'
cleanUnusedRegions(x)

## S4 method for signature 'linkSet'
clean_unused_regions(x)
```

### Arguments

x                      A linkSet object

### Value

A linkSet object with unused regions removed

### Examples

```
data(linkExample)
linkExample <- cleanUnusedRegions(linkExample)
```

---

|                              |                                         |
|------------------------------|-----------------------------------------|
| Convert,GInteractions-method | <i>Convert GInteractions to linkSet</i> |
|------------------------------|-----------------------------------------|

---

### Description

Convert other data formats to linkSet. Currently supported: GInteractions, data.frame.

### Usage

```
## S4 method for signature 'GInteractions'
Convert(x, baitCol = NULL, ...)

## S4 method for signature 'data.frame'
Convert(x, source = "data.frame", baitCol = "gene", oeCol = "peak", ...)

## S4 method for signature 'Pairs'
Convert(x, baitCol = NULL, ...)
```

```
## S4 method for signature 'ANY'
Convert(x, baitCol = NULL, ...)

readvalidPairs(file, njobs = 1, format = "validPairs")
```

### Arguments

|         |                                                                                                                                                                                                                                  |
|---------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| x       | An object of unsupported class                                                                                                                                                                                                   |
| baitCol | A character string specifying the column to use for bait naming                                                                                                                                                                  |
| ...     | Additional arguments (not used)                                                                                                                                                                                                  |
| source  | The source of the data frame, either "data.frame" or "chicane"                                                                                                                                                                   |
| oeCol   | The column name in the data frame that contains the other end information                                                                                                                                                        |
| file    | A character string specifying the path to the validPairs file or 4DN pairs file                                                                                                                                                  |
| njobs   | An integer specifying the number of threads to use for reading the file                                                                                                                                                          |
| format  | A character string specifying the format of the file, either "validPairs" or "pair". Pair format should be "readID chr1 pos1 chr2 pos2 strand1 strand2". And valid-Pairs should be "readID chr1 pos1 strand1 chr2 pos2 strand2". |

### Value

A linkSet object  
 A linkSet object  
 A linkSet object  
 Nothing, throws an error  
 A GInteractions object

### Examples

```
library(InteractionSet)
gi <- GInteractions(anchor1 = c(1, 2), anchor2 = c(3, 4),
  regions = GRanges(seqnames = c("chr1", "chr1", "chr2", "chr2"),
    ranges = IRanges(start = c(100, 200, 300, 400), width = 50)))
linkset_obj <- Convert(gi)
linkset_obj

df <- data.frame(
  gene = c("gene1", "gene2"),
  peak = c("chr1:1000-2000", "chr2:1500-2500"),
  score = c(5.5, 6.0)
)
linkset_obj <- Convert(df, source = "data.frame", baitCol = "gene", oeCol = "peak")
linkset_obj
```

---

|                 |                                            |
|-----------------|--------------------------------------------|
| convertToGrange | <i>Convert string intervals to GRanges</i> |
|-----------------|--------------------------------------------|

---

**Description**

Convert various interval formats to GRanges objects

**Usage**

```
convertToGrange(intervals)
```

**Arguments**

|           |                          |
|-----------|--------------------------|
| intervals | Interval data to convert |
|-----------|--------------------------|

**Value**

GRanges object

---

|                      |                                          |
|----------------------|------------------------------------------|
| countInteractibility | <i>Count bait and oe interactibility</i> |
|----------------------|------------------------------------------|

---

**Description**

This function calculates the number of trans interactions for each bait and oe. The word "interactibility" can refer to <https://doi.org/10.1038%2Fnature11279>.

**Usage**

```
countInteractibility(x, baitRegions = TRUE)
```

```
## S4 method for signature 'linkSet'
countInteractibility(x, baitRegions = TRUE)
```

**Arguments**

|             |                                               |
|-------------|-----------------------------------------------|
| x           | A linkSet object                              |
| baitRegions | Whether to count bait regions (default: TRUE) |

**Details**

Count Interaction Interactibility

**Value**

A linkSet object with counts for each unique interaction

**Examples**

```
data(linkExample)
linkSet = c(linkExample,linkExample)
linkSet = countInteractions(linkSet)
linkSet = countInteractibility(linkSet)
```

---

|                   |                                              |
|-------------------|----------------------------------------------|
| countInteractions | <i>Count Bait and Other End Interactions</i> |
|-------------------|----------------------------------------------|

---

**Description**

This function takes a linkSet object and counts the number of interactions for each bait and other end.

**Usage**

```
countInteractions(x, baitRegions = TRUE)

## S4 method for signature 'linkSet'
countInteractions(x, baitRegions = TRUE)
```

**Arguments**

|             |                                               |
|-------------|-----------------------------------------------|
| x           | A linkSet object                              |
| baitRegions | Whether to count bait regions (default: TRUE) |

**Value**

A linkSet object with counts for each unique interaction

**Examples**

```
data(linkExample)
linkSet = c(linkExample,linkExample)
linkSet = countInteractions(linkSet)
linkSet
```

---

|                     |                                     |
|---------------------|-------------------------------------|
| createSampleLinkSet | <i>Create sample linkSet object</i> |
|---------------------|-------------------------------------|

---

**Description**

Create a sample linkSet object for testing purposes

**Usage**

```
createSampleLinkSet()
```

**Value**

A linkSet object with sample data

---

crossGeneEnhancer,linkSet-method  
*Cross gene enhancer*

---

### Description

Cross gene enhancer

### Usage

```
## S4 method for signature 'linkSet'
crossGeneEnhancer(x, score_threshold = NULL)
```

### Arguments

x                      A linkSet object  
 score\_threshold            The minimum score to filter interactions

### Value

A linkSet object with filtered interactions

### Examples

```
data(linkExample)
linkSet = c(linkExample,linkExample)
linkSet = countInteractions(linkSet)
linkSet = filterLinks(linkSet, filter_intra = FALSE, filter_unannotate = FALSE, distance = 100000)
linkSet = crossGeneEnhancer(linkSet, score_threshold = 10)
```

---

diagnoseLinkSet,linkSet-method  
*Diagnose the linkSet object, return barplot of inter/intra interaction and distance distribution*

---

### Description

Diagnose the linkSet object, return barplot of inter/intra interaction and distance distribution

### Usage

```
## S4 method for signature 'linkSet'
diagnoseLinkSet(x)
```

### Arguments

x                      A linkSet object

**Value**

Returns the input linkSet object with additional metadata columns for inter/intra interaction types and distances. Also prints diagnostic plots showing distance distribution and inter/intra interaction proportions.

**Examples**

```
data(linkExample)
diagnoseLinkSet(linkExample)
```

---

|             |                             |
|-------------|-----------------------------|
| Embryo_body | <i>Embryo Body BED File</i> |
|-------------|-----------------------------|

---

**Description**

A compressed BED format file containing genomic regions from mouse embryo body. This dataset contains regulatory elements identified in mouse embryonic development and is provided as example data for demonstrating genomic interaction analysis workflows.

**Usage**

```
Embryo_body
```

**Format**

A BED format file with the following columns:

- chromosome: The chromosome name (e.g., chr1, chr2)
- start: The starting position of the feature
- end: The ending position of the feature
- name: Name of the feature
- score: Score between 0 and 1000
- strand: Strand orientation (+ or -)

The file contains 3,727 genomic intervals.

**Value**

This is a data object. When loaded with `data(Embryo_body)`, it provides access to the file path of the compressed BED file containing embryo body genomic regions.

**Source**

These data were derived from publicly available mouse embryonic development datasets, specifically from the embryo body, and processed to identify regulatory elements. The original data were processed to create this example dataset for demonstration purposes.

Examples

```
# Get the file path
file_path <- system.file("extdata", "Embryo_body.bed.gz", package = "linkSet")

# Read the file
if (file.exists(file_path)) {
  embryo_data <- read.table(gzfile(file_path),
                           header = FALSE,
                           sep = "\t",
                           stringsAsFactors = FALSE)

  head(embryo_data)
}
```

---

|              |                                 |
|--------------|---------------------------------|
| enforceOrder | <i>Enforce order of anchors</i> |
|--------------|---------------------------------|

---

Description

Ensure consistent ordering of anchor pairs

Usage

```
enforceOrder(anchor1, anchor2)
```

Arguments

- anchor1      First anchor indices
- anchor2      Second anchor indices

Value

List with ordered anchors

---

|                |                                          |
|----------------|------------------------------------------|
| exportInterBed | <i>Export linkSet to interBed format</i> |
|----------------|------------------------------------------|

---

Description

Exports a linkSet object to a tab-delimited interBed format file

Usage

```
exportInterBed(x, outfile)

## S4 method for signature 'linkSet'
exportInterBed(x, outfile)
```

Arguments

- x              A linkSet object
- outfile        Output file path

**Details**

Export linkSet to interBed Format

**Value**

None. The function writes to the specified file.

**Examples**

```
data(linkExample)
tmpfile <- tempfile(fileext = ".txt")
exportInterBed(linkExample, tmpfile)
cat(readLines(tmpfile), sep = "\n")
```

---

|                 |                                 |
|-----------------|---------------------------------|
| exportToLinkSet | <i>Export to linkSet format</i> |
|-----------------|---------------------------------|

---

**Description**

Export to linkSet format

**Usage**

```
exportToLinkSet(
  cd,
  scoreCol = "score",
  cutoff = 0,
  b2bcutoff = NULL,
  order = c("position", "score")[1],
  removeMT = TRUE
)
```

---

|             |                                               |
|-------------|-----------------------------------------------|
| exportWashU | <i>Export linkSet to WashU browser format</i> |
|-------------|-----------------------------------------------|

---

**Description**

Exports a linkSet object to a tab-delimited format compatible with the WashU genome browser

**Usage**

```
exportWashU(x, outfile)

## S4 method for signature 'linkSet'
exportWashU(x, outfile)
```

**Arguments**

|         |                  |
|---------|------------------|
| x       | A linkSet object |
| outfile | Output file path |

**Details**

Export linkSet to WashU Format

**Value**

None. The function writes to the specified file.

**Examples**

```
data(linkExample)
tmpfile <- tempfile(fileext = ".txt")
exportWashU(linkExample, tmpfile)
cat(readLines(tmpfile), sep = "\n")
```

---

filterLinks,linkSet-method

*Filter links for further analysis*

---

**Description**

Filter links for further analysis

**Usage**

```
## S4 method for signature 'linkSet'
filterLinks(x, filter_intra = TRUE, filter_unannotate = TRUE, distance = NULL)
```

**Arguments**

|                   |                                                  |
|-------------------|--------------------------------------------------|
| x                 | A linkSet object                                 |
| filter_intra      | Whether to filter intra-chromosomal interactions |
| filter_unannotate | Whether to filter unannotated interactions       |
| distance          | The maximum distance between bait and other end  |

**Value**

A linkSet object with filtered interactions

**Examples**

```
data(linkExample)
linkSet = c(linkExample,linkExample)
linkSet = countInteractions(linkSet)
linkSet = filterLinks(linkSet, filter_intra = FALSE, filter_unannotate = FALSE, distance = 100000)
```

---

geom\_linkset*Add Genome Links to Coverage Plot*

---

## Description

Creates a visualization of genomic links for a linkSet object

## Usage

```
geom_linkset(  
  linkSet,  
  score.col = "count",  
  score.threshold = NULL,  
  score.color = c("grey70", "#56B1F7", "#132B43"),  
  scale.range = 10,  
  plot.space = 0.1,  
  plot.height = 0.2,  
  arrow.size = 0.05,  
  remove_x_axis = FALSE,  
  link_plot_on_top = FALSE,  
  extend.base = 10000,  
  show.rect = FALSE,  
  x.range = NULL,  
  log.scale = TRUE  
)  
  
## S4 method for signature 'linkSet'  
geom_linkset(  
  linkSet,  
  score.col = "count",  
  score.threshold = NULL,  
  score.color = c("grey70", "#56B1F7", "#132B43"),  
  scale.range = 10,  
  plot.space = 0.1,  
  plot.height = 0.2,  
  arrow.size = 0.05,  
  remove_x_axis = FALSE,  
  link_plot_on_top = FALSE,  
  extend.base = 1e+06,  
  show.rect = FALSE,  
  x.range = NULL,  
  log.scale = TRUE  
)
```

## Arguments

|                 |                                                             |
|-----------------|-------------------------------------------------------------|
| linkSet         | A linkSet object                                            |
| score.col       | Column name containing score information (default: "count") |
| score.threshold | Score threshold for filtering links (default: NULL)         |

|                  |                                                                                   |
|------------------|-----------------------------------------------------------------------------------|
| score.color      | Color vector for score visualization (default: c("grey70", "#56B1F7", "#132B43")) |
| scale.range      | Scale factor for link height (default: 10)                                        |
| plot.space       | Top and bottom margin (default: 0.1)                                              |
| plot.height      | Relative height of link to coverage plot (default: 0.2)                           |
| arrow.size       | Size of arrow heads (default: 0.05)                                               |
| remove_x_axis    | Whether to remove x-axis (default: FALSE)                                         |
| link_plot_on_top | Whether to plot links above coverage (default: FALSE)                             |
| extend.base      | Base pair extension range (default: 10000)                                        |
| show.rect        | Whether to show rectangle borders (default: FALSE)                                |
| x.range          | Range for x-axis (default: NULL)                                                  |
| log.scale        | Whether to use log scale for scores (default: TRUE)                               |

## Details

Add Genome Links to Coverage Plot

## Value

A ggplot layer object

## Examples

```
# Create example linkSet data
gr1 <- GRanges(seqnames = "chr1",
               ranges = IRanges(start = c(1000, 2000), width = 100),
               strand = "+", symbol = c("Gene1", "Gene2"))
gr2 <- GRanges(seqnames = "chr1",
               ranges = IRanges(start = c(5000, 6000), width = 100),
               strand = "+")
linkset_obj <- linkSet(gr1, gr2, specificCol = "symbol")

# Add some metadata for visualization
mcols(linkset_obj)$count <- c(10, 20)

# Example plot (requires ggplot2)

library(ggplot2)
p <- ggplot() + geom_linkset(linkset_obj)
print(p)
```

---

getDistOutput

*Get distance output*

---

## Description

Calculate distance metrics for genomic interactions

**Usage**

```
getDistOutput(regs, ai1, ai2, type, inter_type)
```

**Arguments**

|            |                  |
|------------|------------------|
| regs       | Genomic regions  |
| ai1        | Anchor 1 indices |
| ai2        | Anchor 2 indices |
| type       | Distance type    |
| inter_type | Interaction type |

**Value**

Distance calculations

---

|             |                               |
|-------------|-------------------------------|
| linkExample | <i>Example linkSet Object</i> |
|-------------|-------------------------------|

---

**Description**

A dataset containing example genomic interactions in linkSet format. This example dataset was created to demonstrate the functionality of the linkSet package for representing and analyzing genomic interactions such as those from Hi-C or promoter-capture Hi-C experiments.

**Usage**

```
data(linkExample)
```

**Format**

A linkSet object with example interactions. The object contains:

- Bait regions (anchor1): GRanges object representing promoter regions
- Other end regions (anchor2): GRanges object representing potential enhancer regions
- Metadata columns including: count (interaction strength), baitID (unique identifiers for bait regions), and additional annotations

The data was simulated to reflect typical patterns seen in chromatin interaction data, including distance-dependent interaction frequencies and varying interaction strengths.

**Details**

The dataset represents simulated chromatin interactions between regulatory elements (enhancers) and promoters across several chromosomes. It includes interaction counts, genomic coordinates for both anchors of the interactions, and associated metadata.

**Value**

A linkSet object containing example genomic interactions. When loaded with `data(linkExample)`, it provides a linkSet object with simulated chromatin interactions for demonstration and testing purposes.

## Source

This is a synthetic dataset created specifically for the linkSet package to demonstrate various analysis workflows. The genomic coordinates are based on the human genome (hg38), but the interaction patterns were simulated.

## Examples

```
data(linkExample)
show(linkExample)

# Examine the structure
regions(linkExample)

# View metadata
head(mcols(linkExample))
```

---

linkSet

*linkSet: Base Classes for Storing Genomic Link Data*

---

## Description

The linkSet package provides tools for working with genomic link sets, which represent connections between different genomic regions. This package is designed for bioinformatics and genomic data analysis, offering various methods to manipulate and analyze linkSet objects.

## Details

The main class provided by this package is the linkSet class, which is designed to represent and analyze genomic interactions, particularly focusing on gene-enhancer relationships. Key features include:

- Representation of genomic interactions with two types of anchors: "bait" (typically genes) and "other end" (typically enhancers or other regulatory elements).
- Flexible input methods, supporting construction from various data types.
- Metadata storage for additional information about interactions.
- Integration with Bioconductor classes and tools.
- Methods for annotating promoters and distinguishing between inter- and intra-chromosomal interactions.

## Value

This is package documentation. The linkSet package provides classes and methods for working with genomic interaction data. See the individual function documentation for specific return values.

## References

Add any relevant references here.

**See Also**

Useful links:

- <https://github.com/GilbertHan1011/linkSet>
- Report bugs at <https://github.com/GilbertHan1011/linkSet/issues/new>

**Examples**

```
data(linkExample)
linkExample
```

---

```
linkSet, character, GRanges, character_Or_missing-method
  Create a linkSet object from input data
```

---

**Description**

Create a linkSet object from input data

**Usage**

```
## S4 method for signature 'character,GRanges,character_Or_missing'
linkSet(anchor1, anchor2, specificCol, metadata = list(), ...)
```

**Arguments**

|             |                                                                                                                                     |
|-------------|-------------------------------------------------------------------------------------------------------------------------------------|
| anchor1     | For the first method, a character vector of bait names. For the second method, a GRanges object containing anchor1 regions.         |
| anchor2     | A GRanges object containing anchor2 regions                                                                                         |
| specificCol | Optional character vector specifying names for the baits. Can be either a column name from anchor1's metadata or a vector of names. |
| metadata    | Optional list of metadata to store                                                                                                  |
| ...         | Additional columns to add to the linkSet's elementMetadata                                                                          |

**Value**

A linkSet object containing the interaction data

---

```
linkSet,GRanges,GRanges,character_Or_missing-method
```

*Create a linkSet object from input data*

---

### Description

Create a linkSet object from input data

### Usage

```
## S4 method for signature 'GRanges,GRanges,character_Or_missing'
linkSet(anchor1, anchor2, specificCol, metadata = list(), ...)
```

### Arguments

|             |                                                                                                                                     |
|-------------|-------------------------------------------------------------------------------------------------------------------------------------|
| anchor1     | For the first method, a character vector of bait names. For the second method, a GRanges object containing anchor1 regions.         |
| anchor2     | A GRanges object containing anchor2 regions                                                                                         |
| specificCol | Optional character vector specifying names for the baits. Can be either a column name from anchor1's metadata or a vector of names. |
| metadata    | Optional list of metadata to store                                                                                                  |
| ...         | Additional columns to add to the linkSet's elementMetadata                                                                          |

### Value

A linkSet object containing the interaction data

---

|               |                       |
|---------------|-----------------------|
| linkSet-class | <i>LinkSet object</i> |
|---------------|-----------------------|

---

### Description

The linkSet object is a container for storing gene-enhancer interactions.

### Details

The linkSet object is a vectors of paired gene-enhancer interactions.

### Slots

|                 |                                                |
|-----------------|------------------------------------------------|
| nameBait        | A character vector of the bait names.          |
| anchor1         | A integer vector of the first anchor indices.  |
| anchor2         | A integer vector of the second anchor indices. |
| regions         | A GenomicRanges object of the regions.         |
| NAMES           | A character vector of the region names.        |
| elementMetadata | A DataFrame of the element metadata.           |

**See Also**[linkSet](#)**Examples**

```

showClass("linkSet") # shows the known subclasses

set.seed(7000)
N <- 40
all.starts <- round(runif(N, 1, 100))
all.ends <- all.starts + round(runif(N, 5, 20))
all.regions <- GRanges(rep(c("chrA", "chrB"), c(N-10, 10)), IRanges(all.starts, all.ends))
genes = c(rep("SP7",4),rep("ASPN",10),rep("XBP1",6))
Np <- 20
all.anchor1 <- sample(N, Np)
gr1 <- all.regions[all.anchor1]
gr1$symbol <- genes
all.anchor2 <- setdiff(1:40,all.anchor1)
gr2 <- all.regions[all.anchor2]
x <- linkSet(gr1, gr2,specificCol = "symbol")
x
x2 <- linkSet(genes, gr2)
x2

```

oe&lt;-

*Set Other End (OE) Anchors***Description**

Replace the other end (oe) anchors of a linkSet object with new values

**Usage**

```
oe(x) <- value
```

**Arguments**

|       |                                                       |
|-------|-------------------------------------------------------|
| x     | A linkSet object                                      |
| value | A GRanges object containing the new other end anchors |

**Details**

Set Other End Anchors for linkSet Object

**Value**

The modified linkSet object

**Examples**

```
# Create example data
gr1 <- GRanges("chr1", IRanges(1:3, width=1))
gr2 <- GRanges("chr1", IRanges(4:6, width=1))
linkset_obj <- linkSet(gr1, gr2)

# Create new other end anchors
new_oe <- GRanges("chr1", IRanges(7:9, width=1))

# Replace other end anchors
oe(linkset_obj) <- new_oe
```

---

```
orderLinks,linkSet-method
      Order linkSet by mcols
```

---

**Description**

Order linkSet by mcols

**Usage**

```
## S4 method for signature 'linkSet'
orderLinks(x, by = "count", decreasing = TRUE)
```

**Arguments**

|            |                                     |
|------------|-------------------------------------|
| x          | A linkSet object                    |
| by         | The column name to order by         |
| decreasing | Whether to sort in decreasing order |

**Value**

A linkSet object with ordered interactions

**Examples**

```
data(linkExample)
linkSet = c(linkExample,linkExample)
linkSet = countInteractions(linkSet)
linkSet = filterLinks(linkSet, filter_intra = FALSE, filter_unannotate = FALSE, distance = 100000)
linkSet = orderLinks(linkSet, by = "count", decreasing = TRUE)
```

---

pairdist,linkSet-method

*Calculate the distance between bait and the other end*

---

### Description

Outputs an integer vector specifying the distance between the interacting bins, depending on the type of distance specified.

Example:

```

rangeA:  |-----|
rangeB:           |-----|
mid:      <----->
gap:      <-->
span:     <----->

```

- mid: Half the distance between the end of first range and start of second range
- gap: Distance between the end of first range and start of second range
- span: Total span from start of first range to end of second range

### Usage

```

## S4 method for signature 'linkSet'
pairdist(x, type = "mid")

```

### Arguments

|      |                                                                   |
|------|-------------------------------------------------------------------|
| x    | A linkSet object                                                  |
| type | The type of distance to calculate, either "mid", "gap", or "span" |

### Value

A linkSet object with a new metadata column "distance"

### Examples

```

data(linkExample)
linkExample <- pairdist(linkExample, type="mid")

```

---

pasteAnchor

*Format anchor information for display*

---

### Description

Format anchor information for display

### Usage

```

pasteAnchor(x, append)

```

---

plotBaits

*Plot Baits*


---

## Description

Plot baits in a linkSet object

## Usage

```
plotBaits(
  linkset,
  scoreCol = "score",
  countCol = "count",
  n = 4,
  baits = NULL,
  plotBaitNames = TRUE,
  plevel1 = 5,
  plevel2 = 3,
  outfile = NULL,
  width = 20,
  height = 20,
  extend.base = 1e+06,
  bgCol = "black",
  lev2Col = "blue",
  lev1Col = "red",
  ...
)
```

## Arguments

|               |                                                                        |
|---------------|------------------------------------------------------------------------|
| linkset       | A linkSet object                                                       |
| scoreCol      | Column name containing scores for coloring points                      |
| countCol      | Column name containing counts for y-axis values                        |
| n             | Number of random baits to plot if baits parameter is NULL              |
| baits         | Vector of specific baits to plot. If NULL, n random baits are selected |
| plotBaitNames | Logical indicating whether to show bait names in plot titles           |
| plevel1       | Upper threshold for score coloring (red)                               |
| plevel2       | Lower threshold for score coloring (blue)                              |
| outfile       | Output file path. If NULL, plot is displayed rather than saved         |
| width         | Width of output plot in inches                                         |
| height        | Height of output plot in inches                                        |
| extend.base   | Base pairs to extend view range on either side of bait                 |
| bgCol         | Color for points below plevel2 threshold                               |
| lev2Col       | Color for points between plevel2 and plevel1 thresholds                |
| lev1Col       | Color for points above plevel1 threshold                               |
| ...           | Additional plotting parameters                                         |

**Value**

A ggplot object

**Examples**

```
# Create example linkSet object
library(GenomicRanges)
gr1 <- GRanges(seqnames = c("chr1", "chr1", "chr2"),
               ranges = IRanges(start = c(1000, 2000, 3000), width = 100),
               strand = "+", symbol = c("Gene1", "Gene2", "Gene3"))
gr2 <- GRanges(seqnames = c("chr1", "chr2", "chr2"),
               ranges = IRanges(start = c(5000, 6000, 7000), width = 100),
               strand = "+")
linkset_obj <- linkSet(gr1, gr2, specificCol = "symbol")

# Add score and count metadata for plotting
mcols(linkset_obj)$score <- c(2.5, 4.2, 6.1)
mcols(linkset_obj)$count <- c(10, 25, 15)

# Plot baits (requires annotated bait regions)

# Note: This requires regionsBait to be annotated
# plotBaits(linkset_obj, n = 2)
```

---

|                   |                            |
|-------------------|----------------------------|
| plotGenomicRanges | <i>Plot Genomic Ranges</i> |
|-------------------|----------------------------|

---

**Description**

Creates a visualization of genomic ranges and interactions from a linkSet object

**Usage**

```
plotGenomicRanges(
  linkset,
  showBait = NULL,
  showOE = NULL,
  x.range = NULL,
  score.col = "count",
  show.rect = TRUE,
  extend.base = 10000,
  ...,
  bait_col = "red",
  oe_col = "DeepSkyBlue3",
  default_col = "grey",
  vjust = NULL,
  linejoin = "mitre",
  na.rm = FALSE,
  minimal_width = 0.01,
  show.legend = NA,
  inherit.aes = TRUE,
```

```

    link_plot_on_top = FALSE,
    arrow.size = 0.05,
    remove_x_axis = FALSE,
    plot.height = 0.4,
    plot.space = 0.1,
    log.scale = TRUE
  )

```

```

plot_genomic_ranges(
  linkset,
  showBait = NULL,
  showOE = NULL,
  x.range = NULL,
  score.col = "count",
  show.rect = TRUE,
  extend.base = 10000,
  ...,
  bait_col = "red",
  oe_col = "DeepSkyBlue3",
  default_col = "grey",
  vjust = NULL,
  linejoin = "mitre",
  na.rm = FALSE,
  minimal_width = 0.01,
  show.legend = NA,
  inherit.aes = TRUE,
  link_plot_on_top = FALSE,
  arrow.size = 0.05,
  remove_x_axis = FALSE,
  plot.height = 0.4,
  plot.space = 0.1,
  log.scale = TRUE
)

```

```

## S4 method for signature 'linkSet'
plot_genomic_ranges(
  linkset,
  showBait = NULL,
  showOE = NULL,
  x.range = NULL,
  score.col = "count",
  show.rect = TRUE,
  extend.base = 10000,
  ...,
  bait_col = "red",
  oe_col = "DeepSkyBlue3",
  default_col = "grey",
  vjust = NULL,
  linejoin = "mitre",
  na.rm = FALSE,
  minimal_width = 0.01,
  show.legend = NA,

```

```

    inherit.aes = TRUE,
    link_plot_on_top = FALSE,
    arrow.size = 0.05,
    remove_x_axis = FALSE,
    plot.height = 0.4,
    plot.space = 0.1,
    log.scale = TRUE
  )

```

## Arguments

|                  |                                                                      |
|------------------|----------------------------------------------------------------------|
| linkset          | A linkSet object                                                     |
| showBait         | Logical indicating whether to show bait regions (default: NULL)      |
| showOE           | Logical indicating whether to show other end regions (default: NULL) |
| x.range          | Range for x-axis (default: NULL)                                     |
| score.col        | Column name containing score information (default: "count")          |
| show.rect        | Whether to show rectangle borders (default: TRUE)                    |
| extend.base      | Base pair extension range (default: 10000)                           |
| ...              | Additional plotting parameters                                       |
| bait_col         | Color for bait regions (default: "red")                              |
| oe_col           | Color for other end regions (default: "DeepSkyBlue3")                |
| default_col      | Default color (default: "grey")                                      |
| vjust            | Vertical adjustment (default: NULL)                                  |
| linejoin         | Line join style (default: "mitre")                                   |
| na.rm            | Whether to remove NA values (default: FALSE)                         |
| minimal_width    | Minimal width for plotting (default: 0.01)                           |
| show.legend      | Whether to show legend (default: NA)                                 |
| inherit.aes      | Whether to inherit aesthetics (default: TRUE)                        |
| link_plot_on_top | Whether to plot links on top (default: FALSE)                        |
| arrow.size       | Size of arrow heads (default: 0.05)                                  |
| remove_x_axis    | Whether to remove x-axis (default: FALSE)                            |
| plot.height      | Relative height of plot (default: 0.4)                               |
| plot.space       | Plot spacing (default: 0.1)                                          |
| log.scale        | Whether to use log scale (default: TRUE)                             |

## Details

Plot Genomic Ranges from linkSet Object

## Value

A ggplot object

## Examples

```
# Create example linkSet object
library(GenomicRanges)
gr1 <- GRanges(seqnames = c("chr1", "chr1", "chr2"),
               ranges = IRanges(start = c(1000, 2000, 3000), width = 100),
               strand = "+", symbol = c("Gene1", "Gene2", "Gene3"))
gr2 <- GRanges(seqnames = c("chr1", "chr2", "chr2"),
               ranges = IRanges(start = c(5000, 6000, 7000), width = 100),
               strand = "+")
linkset_obj <- linkSet(gr1, gr2, specificCol = "symbol")

# Add count metadata for plotting
mcols(linkset_obj)$count <- c(10, 25, 15)

# Plot genomic ranges (requires annotated bait regions)

# Note: This requires regionsBait to be annotated
# plotGenomicRanges(linkset_obj, extend.base = 1000)
```

---

plotGenomicRanges,linkSet-method

*Plot genomic ranges for linkSet objects*

---

## Description

This function visualizes the genomic interactions in a linkSet object, showing the bait and other end regions as well as the links between them.

## Usage

```
## S4 method for signature 'linkSet'
plotGenomicRanges(
  linkset,
  showBait = NULL,
  showOE = NULL,
  x.range = NULL,
  score.col = "count",
  show.rect = TRUE,
  extend.base = 10000,
  ...,
  bait_col = "red",
  oe_col = "DeepSkyBlue3",
  default_col = "grey",
  vjust = NULL,
  linejoin = "mitre",
  na.rm = FALSE,
  minimal_width = 0.01,
  show.legend = NA,
  inherit.aes = TRUE,
  link_plot_on_top = FALSE,
  arrow.size = 0.05,
```

```

    remove_x_axis = FALSE,
    plot.height = 0.4,
    plot.space = 0.1,
    log.scale = TRUE
  )

```

### Arguments

|                  |                                                       |
|------------------|-------------------------------------------------------|
| linkset          | A linkSet object to plot                              |
| showBait         | Vector of bait regions to display (NULL for all)      |
| showOE           | Vector of other end regions to display (NULL for all) |
| x.range          | Range of x-axis to display                            |
| score.col        | Column name for coloring links                        |
| show.rect        | Whether to show rectangles for regions                |
| extend.base      | Base pairs to extend the plot                         |
| ...              | Additional arguments                                  |
| bait_col         | Color for bait regions                                |
| oe_col           | Color for other end regions                           |
| default_col      | Default color                                         |
| vjust            | Vertical justification                                |
| linejoin         | Line join style                                       |
| na.rm            | Whether to remove NA values                           |
| minimal_width    | Minimal width for regions                             |
| show.legend      | Whether to show legend                                |
| inherit.aes      | Whether to inherit aesthetics                         |
| link_plot_on_top | Whether to draw links on top                          |
| arrow.size       | Size of arrows                                        |
| remove_x_axis    | Whether to remove x axis                              |
| plot.height      | Height of the plot                                    |
| plot.space       | Space between plots                                   |
| log.scale        | Whether to use log scale for colors                   |

### Value

A ggplot object

### Examples

```

data(linkExample)
plotGenomicRanges(linkExample, extend.base = 10)

```

---

|               |                                           |
|---------------|-------------------------------------------|
| reduceRegions | <i>Reduce Regions in a linkSet Object</i> |
|---------------|-------------------------------------------|

---

**Description**

This function reduces the bait and/or oe regions of a linkSet object and optionally counts interactions, while maintaining the original length of the linkSet.

**Usage**

```
reduceRegions(x, region = "both", countInteractions = TRUE, ...)
```

```
## S4 method for signature 'linkSet'
reduceRegions(x, region = "both", countInteractions = TRUE, ...)
```

**Arguments**

|                   |                                                                                          |
|-------------------|------------------------------------------------------------------------------------------|
| x                 | A linkSet object                                                                         |
| region            | Character, specifying which regions to reduce: "both", "bait", or "oe" (default: "both") |
| countInteractions | Logical, whether to count interactions after reducing (default: TRUE)                    |
| ...               | Additional arguments passed to GenomicRanges::reduce                                     |

**Details**

Reduce a linkSet Object

**Value**

A reduced linkSet object with the same length as the input

**Examples**

```
data(linkExample)
reduced_linkset <- reduceRegions(linkExample, region = "both", countInteractions = TRUE)
reduced_linkset
```

---

|               |                         |
|---------------|-------------------------|
| regionsBait<- | <i>Set Bait Regions</i> |
|---------------|-------------------------|

---

**Description**

Replace the regions corresponding to the bait anchors of a linkSet object

**Usage**

```
regionsBait(x) <- value
```

**Arguments**

x                    A linkSet object  
 value                A GRanges object containing the new bait regions

**Details**

Set Bait Regions for linkSet Object

**Value**

The modified linkSet object

**Examples**

```
# Create example data
gr1 <- GRanges("chr1", IRanges(1:3, width=1))
gr2 <- GRanges("chr1", IRanges(4:6, width=1))
linkset_obj <- linkSet(gr1, gr2)

# Create new bait regions
new_bait <- GRanges("chr1", IRanges(7:9, width=1))

# Replace bait regions
regionsBait(linkset_obj) <- new_bait
```

---

|             |                             |
|-------------|-----------------------------|
| run_chicane | <i>Run ChICANE Analysis</i> |
|-------------|-----------------------------|

---

**Description**

This function adapts the `chicane` function from the `ChICANE` package to work with the `linkSet` object format. It runs the full method for detecting significant interactions in capture Hi-C experiments.

**Usage**

```
run_chicane(linkSet, ...)

## S4 method for signature 'linkSet'
run_chicane(
  linkSet,
  replicate.merging.method = "sum",
  distribution = "negative-binomial",
  include.zeros = "none",
  bait.filters = c(0, 1),
  target.filters = c(0, 1),
  distance.bins = NULL,
  multiple.testing.correction = c("bait-level", "global"),
  adjustment.terms = NULL,
  remove.adjacent = FALSE,
  temp.directory = NULL,
  keep.files = FALSE,
```

```

    maxit = 100,
    epsilon = 1e-08,
    cores = 1,
    trace = FALSE,
    verbose = FALSE
  )

```

## Arguments

|                                          |                                                                      |
|------------------------------------------|----------------------------------------------------------------------|
| <code>linkSet</code>                     | A linkSet object containing interaction data                         |
| <code>...</code>                         | Additional arguments passed to methods                               |
| <code>replicate.merging.method</code>    | Method for merging replicates (default: 'sum')                       |
| <code>distribution</code>                | Distribution to use for modeling (default: 'negative-binomial')      |
| <code>include.zeros</code>               | How to handle zero counts (default: 'none')                          |
| <code>bait.filters</code>                | Vector of length 2 for bait filtering thresholds (default: c(0,1))   |
| <code>target.filters</code>              | Vector of length 2 for target filtering thresholds (default: c(0,1)) |
| <code>distance.bins</code>               | Number of distance bins (default: NULL)                              |
| <code>multiple.testing.correction</code> | Method for multiple testing correction (default: 'bait-level')       |
| <code>adjustment.terms</code>            | Additional terms for model adjustment (default: NULL)                |
| <code>remove.adjacent</code>             | Whether to remove adjacent fragments (default: FALSE)                |
| <code>temp.directory</code>              | Directory for temporary files (default: NULL)                        |
| <code>keep.files</code>                  | Whether to keep temporary files (default: FALSE)                     |
| <code>maxit</code>                       | Maximum iterations for model fitting (default: 100)                  |
| <code>epsilon</code>                     | Convergence threshold (default: 1e-8)                                |
| <code>cores</code>                       | Number of CPU cores to use (default: 1)                              |
| <code>trace</code>                       | Whether to print trace information (default: FALSE)                  |
| <code>verbose</code>                     | Whether to print progress information (default: FALSE)               |

## Details

Run ChICANE Analysis on linkSet Object

## Value

A linkSet object with additional columns:

- `expected` The expected number of reads linking fragments under the fitted model
- `p.value` P-value for test of observed vs expected read counts
- `q.value` FDR-corrected p-value

**Examples**

```
# Create example data
gr1 <- GRanges(seqnames = c("chr1", "chr3", "chr3"),
               ranges = IRanges(start = c(1000, 2000, 3000), width = 100),
               strand = "+", symbol = c("BRCA1", "TP53", "NONEXISTENT"))
gr2 <- GRanges(seqnames = c("chr1", "chr2", "chr3"),
               ranges = IRanges(start = c(5000, 6000, 7000), width = 100),
               strand = "+")
ls <- linkSet(gr1, gr2, specificCol = "symbol")

# Annotate and prepare data
annotated_ls <- suppressWarnings(
  annotatePromoter(ls, genome = "hg38", upstream = 500, overwrite = TRUE)
)
annotated_ls <- countInteractability(annotated_ls)
annotated_ls <- linkSet::pairdist(annotated_ls)

# Run analysis
result_ls <- run_chicane(
  annotated_ls,
  replicate.merging.method = 'sum',
  bait.filters = c(0, 1),
  target.filters = c(0, 1),
  distance.bins = NULL,
  multiple.testing.correction = 'bait-level',
  verbose = TRUE
)
```

---

|                     |                                                            |
|---------------------|------------------------------------------------------------|
| show,linkSet-method | <i>Display detailed information about a linkSet object</i> |
|---------------------|------------------------------------------------------------|

---

**Description**

Display detailed information about a linkSet object

**Usage**

```
## S4 method for signature 'linkSet'
show(object)
```

**Arguments**

object                    A linkSet object to display

**Value**

Invisibly returns NULL. This method is called for its side effect of printing detailed information about the linkSet object to the console.

## Examples

```
# Example usage of show method for linkSet object
gr1 <- GRanges(seqnames = c("chr1", "chr2", "chr3"),
               ranges = IRanges(start = c(1000, 2000, 3000), width = 100),
               strand = "+", symbol = c("BRCA1", "TP53", "NONEXISTENT"))
gr2 <- GRanges(seqnames = c("chr1", "chr2", "chr3"),
               ranges = IRanges(start = c(5000, 6000, 7000), width = 100),
               strand = "+")
ls <- linkSet(gr1, gr2, specificCol = "symbol")
show(ls)
```

---

showLinkSet

*Show linkSet Object Details*


---

## Description

Displays detailed information about a linkSet object, including regions, metadata, and optionally sequence information.

## Usage

```
showLinkSet(
  object,
  margin = "",
  print.seqinfo = FALSE,
  print.classinfo = FALSE,
  baitRegion = FALSE,
  ...
)

## S4 method for signature 'linkSet'
showLinkSet(
  object,
  margin = "",
  print.seqinfo = FALSE,
  print.classinfo = FALSE,
  baitRegion = FALSE
)
```

## Arguments

|                 |                                                                 |
|-----------------|-----------------------------------------------------------------|
| object          | A linkSet object to display                                     |
| margin          | Character string for display margin (default: "")               |
| print.seqinfo   | Logical, whether to print sequence information (default: FALSE) |
| print.classinfo | Logical, whether to print class information (default: FALSE)    |
| baitRegion      | Logical, whether to display bait regions (default: FALSE)       |
| ...             | Additional arguments                                            |

**Details**

Display Detailed Information About a linkSet Object

**Value**

None (invisible NULL)

**Examples**

```
gr1 <- GRanges(seqnames = c("chr1", "chr2", "chr3"),
               ranges = IRanges(start = c(1000, 2000, 3000), width = 100),
               strand = "+", symbol = c("BRCA1", "TP53", "NONEXISTENT"))
gr2 <- GRanges(seqnames = c("chr1", "chr2", "chr3"),
               ranges = IRanges(start = c(5000, 6000, 7000), width = 100),
               strand = "+")
linkset_obj <- linkSet(gr1, gr2, specificCol = "symbol")
showLinkSet(linkset_obj)
```

---

subsetBait,linkSet-method

*Subset linkSet object based on bait names*

---

**Description**

Subset linkSet object based on bait names

Subset linkSet object based on bait regions

Subset linkSet object based on other end (oe) regions

**Usage**

```
## S4 method for signature 'linkSet'
subsetBait(x, subset)
```

```
## S4 method for signature 'linkSet'
subsetBaitRegion(x, subset)
```

```
## S4 method for signature 'linkSet'
subsetOE(x, subset)
```

**Arguments**

x                    A linkSet object

subset              A GRanges object specifying the regions to keep

**Value**

A new linkSet object containing only the specified bait interactions

A new linkSet object containing only the interactions with bait regions overlapping the subset

A new linkSet object containing only the interactions with oe regions overlapping the subset

**Examples**

```

data(linkExample)
subset_bait_names <- c("bait1", "bait2")
subsetting_linkSet <- subsetBait(linkExample, subset_bait_names)
data(linkExample)
subset_bait_regions <- GRanges(seqnames = "chr1",
                             ranges = IRanges(start = c(100, 200), end = c(150, 250)))
subsetting_linkSet <- subsetBaitRegion(linkExample, subset_bait_regions)
data(linkExample)
subset_oe_regions <- GRanges(seqnames = "chr1",
                             ranges = IRanges(start = c(300, 400), end = c(350, 450)))
subsetting_linkSet <- subsetOE(linkExample, subset_oe_regions)

```

---

|              |                                |
|--------------|--------------------------------|
| themeLinkset | <i>Theme for linkSet plots</i> |
|--------------|--------------------------------|

---

**Description**

Theme for linkSet plots

**Usage**

```
themeLinkset(x.range, margin.len, show.rect)
```

**Arguments**

|            |                           |
|------------|---------------------------|
| x.range    | The x-axis range          |
| margin.len | Margin length             |
| show.rect  | Whether to show rectangle |

**Value**

A ggplot2 theme

---

|            |                                      |
|------------|--------------------------------------|
| themeRange | <i>Theme for genomic range plots</i> |
|------------|--------------------------------------|

---

**Description**

Theme for genomic range plots

**Usage**

```
themeRange(x.range, show.rect)
```

**Arguments**

|           |                           |
|-----------|---------------------------|
| x.range   | The x-axis range          |
| show.rect | Whether to show rectangle |

**Value**

A ggplot2 theme

---

|                     |                               |
|---------------------|-------------------------------|
| trim,linkSet-method | <i>linkSet-GRange-Methods</i> |
|---------------------|-------------------------------|

---

**Description**

This man page documents intra range transformations of a [linkSet](#) object.

**Usage**

```
## S4 method for signature 'linkSet'
trim(x, use.names = TRUE, ...)

## S4 method for signature 'linkSet'
resize(x, width, fix = "start", use.names = TRUE, ...)

## S4 method for signature 'linkSet'
resizeRegions(
  x,
  width = 1000,
  fix = "start",
  use.names = TRUE,
  region = "both",
  ...
)

## S4 method for signature 'linkSet'
narrow(x, start = NA, end = NA, width = NA, use.names = TRUE)

## S4 method for signature 'linkSet'
narrowRegions(
  x,
  start = NA,
  end = NA,
  width = NA,
  use.names = TRUE,
  region = "both"
)

## S4 method for signature 'linkSet'
shift(x, shift = 0L, use.names = TRUE)

## S4 method for signature 'linkSet'
shiftRegions(x, shift = 0L, use.names = TRUE, region = "both")

## S4 method for signature 'linkSet'
flank(
  x,
```

```

    width,
    start = TRUE,
    both = FALSE,
    use.names = TRUE,
    ignore.strand = FALSE
  )

## S4 method for signature 'linkSet'
flankRegions(
  x,
  width,
  start = TRUE,
  both = FALSE,
  use.names = TRUE,
  ignore.strand = FALSE,
  region = "both"
)

## S4 method for signature 'linkSet'
promoters(x, upstream = 2000, downstream = 200, use.names = TRUE)

## S4 method for signature 'linkSet'
promoterRegions(
  x,
  upstream = 2000,
  downstream = 200,
  use.names = TRUE,
  region = "both"
)

## S4 method for signature 'linkSet'
width(x)

## S4 method for signature 'linkSet'
reduce(x, drop.empty.ranges = FALSE, ...)

```

## Arguments

|                            |                                                                                                    |
|----------------------------|----------------------------------------------------------------------------------------------------|
| <code>x</code>             | A linkSet object                                                                                   |
| <code>use.names</code>     | A logical indicating whether to use names                                                          |
| <code>...</code>           | Additional arguments passed to the GenomicRanges trim method                                       |
| <code>width</code>         | The desired width of the output ranges                                                             |
| <code>fix</code>           | The anchor point for resizing operations ("start", "end", or "center")                             |
| <code>region</code>        | Which regions to modify ("both", "bait", or "oe")                                                  |
| <code>start, end</code>    | The desired start and end coordinates for narrowing                                                |
| <code>shift</code>         | The number of positions to shift                                                                   |
| <code>both</code>          | Whether to get flanking regions on both sides                                                      |
| <code>ignore.strand</code> | TRUE or FALSE. Whether the strand of the input ranges should be ignored or not. See details below. |

upstream, downstream  
 Number of bases upstream/downstream for promoter regions  
 drop.empty.ranges  
 Whether to drop empty ranges when reducing

**Value**

A linkSet object

**Author(s)**

Gilbert Han

**Examples**

```
data(linkExample)
resize_bait <- resizeRegions(linkExample, width = 75, fix = "start", region = "bait")
resize_bait

narrow_bait <- narrowRegions(linkExample, start = 1, width = 5, region = "bait")
narrow_bait

shift_oe <- shiftRegions(linkExample, shift = 10, region = "oe")
shift_oe

flank_bait <- flankRegions(linkExample, width = 100, start = TRUE, both = FALSE,
                           use.names = TRUE, ignore.strand = FALSE, region = "bait")
flank_bait

width(linkExample)
```

---

unchecked\_anchor1<-     *Set unchecked anchor1*

---

**Description**

Set unchecked anchor1

**Usage**

```
unchecked_anchor1(x) <- value
```

---

unchecked\_anchor2<-     *Set unchecked anchor2*

---

**Description**

Set unchecked anchor2

**Usage**

```
unchecked_anchor2(x) <- value
```

---

 verifyLinkSet

*verify.linkSet*


---

## Description

Verify that linkSet object is in expected format. Throws an error if object does not fit requirements.

Check if an error matches the error raised by `glm.nb` due to an inflated theta estimate.

This happens when the variance of the negative binomial does not exceed the mean (i.e. there is no overdispersion). In such cases, the Poisson distribution may be a suitable alternative.

Check if chicane model can be fit on a given dataset.

`glm.nb` does not work when all responses are constant, or there are only two unique values and a covariate is a perfect predictor.

Perform multiple testing correction on p-values from interaction test. By default, multiple testing correction is applied per bait. To change this to a global multiple testing correction, set `bait.level = FALSE`.

Split a data frame into a prespecified number of bins, using `split` and `cut`. Unlike the default R functions, this does not fail when asked to split the data into a single bin.

Verify that interaction.data object is in expected format. Throws an error if object does not fit requirements.

Fit GLM according to a specified distribution. This needs to be done separately from `glm` in order to include negative binomial and truncated distributions as options.

Check that the model fit contains the same number of rows as the data used to fit it,

and throw an error if not

Check if a warning object is an iteration limit reached warning from `glm.nb`

Check if a warning matches the square root warning raised by `glm.nb` due to an inflated theta estimate

This happens when the variance of the negative binomial does not exceed the mean (i.e. there is no overdispersion). In such cases, the Poisson distribution may be a suitable alternative.

## Usage

```
verifyLinkSet(linkSet)
```

```
isGlmNbThetaError(e)
```

```
checkModelNumericalFit(interaction.data)
```

```
multipleTestingCorrect(interaction.data, bait.level = TRUE)
```

```
smartSplit(dat, bins)
```

```

verifyInteractionData(interaction.data)

fitGlm(
  formula,
  data,
  distribution = c("negative-binomial", "poisson", "truncated-poisson",
    "truncated-negative-binomial"),
  start = NULL,
  init.theta = NULL,
  maxit = 100,
  epsilon = 1e-08,
  trace = FALSE
)

modelRowsSanityCheck(model.data, model)

isGlmNbMaxiterWarning(w)

isGlmNbThetaWarning(w)

```

### Arguments

|                  |                                                                                                                                        |
|------------------|----------------------------------------------------------------------------------------------------------------------------------------|
| linkSet          | Object to be verified.                                                                                                                 |
| e                | Error object                                                                                                                           |
| interaction.data | Object to be verified.                                                                                                                 |
| bait.level       | Logical indicating whether multiple testing correction should be performed per bait.                                                   |
| dat              | Data frame or data table to be split                                                                                                   |
| bins             | Number of bins to split data into                                                                                                      |
| formula          | Formula specifying model of interest                                                                                                   |
| data             | Data frame containing variables specified in formula                                                                                   |
| distribution     | Name of distribution of the counts. Options are 'negative-binomial', 'poisson', 'truncated-poisson', and 'truncated-negative-binomial' |
| start            | Starting values for model coefficients                                                                                                 |
| init.theta       | Initial value of theta if fitting the negative binomial distribution                                                                   |
| maxit            | Maximum number of IWLS iterations for fitting the model (passed to glm.control)                                                        |
| epsilon          | Positive convergence tolerance for Poisson and negative binomial models. Passed to glm.control                                         |
| trace            | Logical indicating if output should be produced for each of model fitting procedure. Passed to glm.control or gamlss.control           |
| model.data       | Data used to fit model                                                                                                                 |
| model            | Resulting negative binomial model object                                                                                               |
| w                | Warning object                                                                                                                         |

**Value**

None

Boolean indicating if error matches

boolean indicating if model can be fit

Original data table with new column

q.value                      FDR-corrected p-value

List with bins elements. Each element corresponds to one portion of the data

None

List with elements

model                      model object

expected.values

vector of expected values for each element in original data

p.values                      vector of p-values for test of significantly higher response than expected

None

Logical indicating if warning matches iteration limit reached warning

Boolean indicating if warning matches

---

withTxDb*Database Operation with Connection Management*

---

**Description**

Executes a database operation while managing the connection lifecycle automatically.

**Usage**`withTxDb(x, expr, ...)``## S4 method for signature 'character,function'``withTxDb(x, expr, ...)`**Arguments**

x                      Character string specifying the genome ("hg38", "hg19", or "mm10")

expr                      Function to execute with database connection

...                      Additional arguments passed to expr

**Details**

Execute Database Operation with Automatic Connection Management

**Value**

Result of the database operation

**Examples**

```
# Example 1: Get genes from hg38
result <- withTxDb("hg38", function(src) {
  genes <- Organism.dplyr::genes(src)
  return(head(genes))
})

# Example 2: Get transcripts
result2 <- withTxDb("hg38", function(src) {
  transcripts <- Organism.dplyr::transcripts(src)
  return(head(transcripts))
})
```

# Index

- \* **Convert**
  - convertToGrange, [14](#)
- \* **GRanges**
  - convertToGrange, [14](#)
- \* **datasets**
  - Embryo\_body, [17](#)
  - linkExample, [23](#)
- \* **internal**
  - checkPackages, [11](#)
  - checkSplitDataNumericalFit, [11](#)
  - convertToGrange, [14](#)
  - createSampleLinkSet, [15](#)
  - enforceOrder, [18](#)
  - exportToLinkSet, [19](#)
  - getDistOutput, [22](#)
  - linkSet-package, [3](#)
  - pasteAnchor, [29](#)
  - unchecked\_anchor1<-, [45](#)
  - unchecked\_anchor2<-, [45](#)
  - verifyLinkSet, [46](#)
- \* **intervals**
  - convertToGrange, [14](#)
- \* **to**
  - convertToGrange, [14](#)
- \$ (bait<-), [6](#)
- \$, linkSet-method (bait<-), [6](#)
- \$<-, linkSet-method (bait<-), [6](#)
- anchor1 (bait<-), [6](#)
- anchor1, linkSet-method (bait<-), [6](#)
- anchor1<- (bait<-), [6](#)
- anchor2 (bait<-), [6](#)
- anchor2, linkSet-method (bait<-), [6](#)
- anchor2<- (bait<-), [6](#)
- anchorIds (bait<-), [6](#)
- anchorIds, linkSet-method (bait<-), [6](#)
- anchors (bait<-), [6](#)
- anchors, linkSet-method (bait<-), [6](#)
- annotateInter
  - (annotateInter, linkSet-method), [4](#)
- annotateInter, linkSet-method, [4](#)
- annotatePromoter
  - (annotatePromoter, linkSet-method), [4](#)
- annotatePromoter, linkSet-method, [4](#)
- as.data.frame, linkSet-method, [5](#)
- as.GInteractions, [6](#)
- as.GInteractions, linkSet-method (as.GInteractions), [6](#)
- bait (bait<-), [6](#)
- bait, linkSet-method (bait<-), [6](#)
- bait<-, [6](#)
- bait<-, linkSet-method (bait<-), [6](#)
- baitGInteractions, [9](#)
- baitGInteractions, GInteractions, GRanges, GRanges-method (baitGInteractions), [9](#)
- character\_or\_missing-class, [10](#)
- checkModelNumericalFit (verifyLinkSet), [46](#)
- checkPackages, [11](#)
- checkSplitDataNumericalFit, [11](#)
- clean\_unused\_regions
  - (cleanUnusedRegions), [12](#)
- clean\_unused\_regions, linkSet-method (cleanUnusedRegions), [12](#)
- cleanUnusedRegions, [12](#)
- cleanUnusedRegions, linkSet-method (cleanUnusedRegions), [12](#)
- Convert (Convert, GInteractions-method), [12](#)
- Convert, ANY-method (Convert, GInteractions-method), [12](#)
- Convert, data.frame-method (Convert, GInteractions-method), [12](#)
- Convert, GInteractions-method, [12](#)
- Convert, Pairs-method (Convert, GInteractions-method), [12](#)
- convertToGrange, [14](#)
- countBait0e (countInteractions), [15](#)
- countInteractability, [14](#)
- countInteractability, linkSet-method (countInteractability), [14](#)

- countInteractions, 15
- countInteractions, linkSet-method
  - (countInteractions), 15
- createSampleLinkSet, 15
- crossGeneEnhancer
  - (crossGeneEnhancer, linkSet-method), 16
- crossGeneEnhancer, linkSet-method, 16
- diagnoseLinkSet
  - (diagnoseLinkSet, linkSet-method), 16
- diagnoseLinkSet, linkSet-method, 16
- Embryo\_body, 17
- enforceOrder, 18
- exportInterBed, 18
- exportInterBed, linkSet-method
  - (exportInterBed), 18
- exportToLinkSet, 19
- exportWashU, 19
- exportWashU, linkSet-method
  - (exportWashU), 19
- filterLinks
  - (filterLinks, linkSet-method), 20
- filterLinks, linkSet-method, 20
- first (bait<-), 6
- first, linkSet-method (bait<-), 6
- fitGlm (verifyLinkSet), 46
- flank (trim, linkSet-method), 43
- flank, linkSet-method
  - (trim, linkSet-method), 43
- flankRegions (trim, linkSet-method), 43
- flankRegions, linkSet-method
  - (trim, linkSet-method), 43
- geom\_linkset, 21
- geom\_linkset, linkSet-method
  - (geom\_linkset), 21
- getDistOutput, 22
- isGlmNbMaxiterWarning (verifyLinkSet), 46
- isGlmNbThetaError (verifyLinkSet), 46
- isGlmNbThetaWarning (verifyLinkSet), 46
- linkExample, 23
- LinkSet (linkSet-class), 26
- linkSet, 24, 27, 43
- linkSet, character, GRanges, character\_Or\_missing-method, 25
- linkSet, GRanges, GRanges, character\_Or\_missing-method, 26
- linkSet-class, 26
- linkSet-package, 3
- modelRowsSanityCheck (verifyLinkSet), 46
- multipleTestingCorrect (verifyLinkSet), 46
- names (bait<-), 6
- names, linkSet-method (bait<-), 6
- names<- (bait<-), 6
- names<-, linkSet-method (bait<-), 6
- narrow (trim, linkSet-method), 43
- narrow, linkSet-method
  - (trim, linkSet-method), 43
- narrowRegions (trim, linkSet-method), 43
- narrowRegions, linkSet-method
  - (trim, linkSet-method), 43
- oe (bait<-), 6
- oe, linkSet-method (bait<-), 6
- oe<-, 27
- oe<-, linkSet-method (bait<-), 6
- orderLinks (orderLinks, linkSet-method), 28
- orderLinks, linkSet-method, 28
- pairdist (pairdist, linkSet-method), 29
- pairdist, linkSet-method, 29
- pasteAnchor, 29
- plot\_genomic\_ranges
  - (plotGenomicRanges), 31
- plot\_genomic\_ranges, linkSet-method
  - (plotGenomicRanges), 31
- plotBaits, 30
- plotGenomicRanges, 31
- plotGenomicRanges, linkSet-method, 34
- promoterRegions (trim, linkSet-method), 43
- promoterRegions, linkSet-method
  - (trim, linkSet-method), 43
- promoters (trim, linkSet-method), 43
- promoters, linkSet-method
  - (trim, linkSet-method), 43
- readvalidPairs
  - (Convert, GInteractions-method), 12
- reduce (trim, linkSet-method), 43
- reduce, linkSet-method
  - (trim, linkSet-method), 43
- reduceRegions, 36

reduceRegions, linkSet-method  
     (reduceRegions), 36  
 regions (bait<-), 6  
 regions, linkSet-method (bait<-), 6  
 regions<- (bait<-), 6  
 regions<-, linkSet-method (bait<-), 6  
 regionsBait (bait<-), 6  
 regionsBait, linkSet-method (bait<-), 6  
 regionsBait<- , 36  
 regionsBait<-, linkSet-method (bait<-), 6  
 resize (trim, linkSet-method), 43  
 resize, linkSet-method  
     (trim, linkSet-method), 43  
 resizeRegions (trim, linkSet-method), 43  
 resizeRegions, linkSet-method  
     (trim, linkSet-method), 43  
 run\_chicane, 37  
 run\_chicane, linkSet-method  
     (run\_chicane), 37  
  
 second (bait<-), 6  
 second, linkSet-method (bait<-), 6  
 seqinfo (bait<-), 6  
 seqinfo, linkSet-method (bait<-), 6  
 shift (trim, linkSet-method), 43  
 shift, linkSet-method  
     (trim, linkSet-method), 43  
 shiftRegions (trim, linkSet-method), 43  
 shiftRegions, linkSet-method  
     (trim, linkSet-method), 43  
 show, linkSet-method, 39  
 showLinkSet, 40  
 showLinkSet, linkSet-method  
     (showLinkSet), 40  
 smartSplit (verifyLinkSet), 46  
 subsetBait (subsetBait, linkSet-method),  
     41  
 subsetBait, linkSet-method, 41  
 subsetBaitRegion  
     (subsetBait, linkSet-method), 41  
 subsetBaitRegion, linkSet-method  
     (subsetBait, linkSet-method), 41  
 subsetOE (subsetBait, linkSet-method), 41  
 subsetOE, linkSet-method  
     (subsetBait, linkSet-method), 41  
  
 themeLinkset, 42  
 themeRange, 42  
 trim (trim, linkSet-method), 43  
 trim, linkSet-method, 43  
  
 unchecked\_anchor1 (bait<-), 6  
 unchecked\_anchor1<- , 45  
 unchecked\_anchor1<- , linkSet-method  
     (bait<-), 6  
 unchecked\_anchor2 (bait<-), 6  
 unchecked\_anchor2<- , 45  
 unchecked\_anchor2<- , linkSet-method  
     (bait<-), 6  
 unchecked\_regions (bait<-), 6  
 unchecked\_regions<- (bait<-), 6  
 unchecked\_regions<- , linkSet-method  
     (bait<-), 6  
  
 verifyInteractionData (verifyLinkSet),  
     46  
 verifyLinkSet, 46  
  
 width (trim, linkSet-method), 43  
 width, linkSet-method  
     (trim, linkSet-method), 43  
 withTxDb, 48  
 withTxDb, character, function-method  
     (withTxDb), 48