# Package ‘LOLA’

**Version** 1.32.0  
**Date** 2021-11-20  
**Title** Locus overlap analysis for enrichment of genomic ranges  
**Description** Provides functions for testing overlap of sets of genomic regions with public and custom region set (genomic ranges) databases. This makes it possible to do automated enrichment analysis for genomic region sets, thus facilitating interpretation of functional genomics and epigenomics data.  
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**Depends** R (>= 2.10)  
**Imports** BiocGenerics, S4Vectors, IRanges, GenomicRanges, data.table, reshape2, utils, stats, methods  
**Suggests** parallel, testthat, knitr, BiocStyle, rmarkdown  
**Enhances** simpleCache, qvalue, ggplot2  
**VignetteBuilder** knitr  
**License** GPL-3  
**biocViews** GeneSetEnrichment, GeneRegulation, GenomeAnnotation, SystemsBiology, FunctionalGenomics, ChIPSeq, MethylSeq, Sequencing  
**URL** [http://code.databio.org/LOLA](http://code.databio.org/LOLA)  
**BugReports** [http://github.com/nsheff/LOLA](http://github.com/nsheff/LOLA)  
**RoxygenNote** 7.1.0  
**git_url** [https://git.bioconductor.org/packages/LOLA](https://git.bioconductor.org/packages/LOLA)  
**git_branch** RELEASE_3_18  
**git_last_commit** 148d0c1  
**git_last_commit_date** 2023-10-24  
**Repository** Bioconductor 3.18  
**Date/Publication** 2024-03-13
If you want to test for differential enrichment within your usersets, you can restrict the universe to only regions that are covered in at least one of your sets. This function helps you build just such a restricted universe.
checkUniverseAppropriateness

Description
If you want to test for differential enrichment within your usersets, you can restrict the universe to only regions that are covered in at least one of your sets. This function helps you build just such a restricted universe.

Usage
buildRestrictedUniverse(userSets)

Arguments
userSets The userSets you will pass to the enrichment calculation.

Value
A restricted universe

Examples
data("sample_input", package="LOLA") # load userSets
restrictedUniverse = buildRestrictedUniverse(userSets)

checkUniverseAppropriateness

Check universe appropriateness

Description
Checks to see if the universe is appropriate for the userSets. Anything in the userSets should be present in the universe. In addition, 2 different regions in the userSets should not overlap the same region in the universe.

Usage
checkUniverseAppropriateness(userSets, userUniverse, cores = 1, fast = FALSE)

Arguments
userSets Regions of interest
userUniverse Regions tested for inclusion in userSets
cores Number of processors
fast Skip the (slow) test for many-to-many relationships

Value
No return value.
Examples

data("sample_input", package="LOLA") # load userSet
data("sample_universe", package="LOLA") # load userUniverse
checkUniverseAppropriateness(userSets, userUniverse)

cleanws

cleanws takes multi-line, code formatted strings and just formats them as simple strings

Description

cleanws takes multi-line, code formatted strings and just formats them as simple strings

Usage

cleanws(string)

Arguments

string string to clean

Value

A string with all consecutive whitespace characters, including tabs and newlines, merged into a single space.

countOverlapsAnyRev

Just a reverser. Reverses the order of arguments and passes them untouched to countOverlapsAny – so you can use it with lapply.

Description

Just a reverser. Reverses the order of arguments and passes them untouched to countOverlapsAny – so you can use it with lapply.

Usage

countOverlapsAnyRev(subj, quer)

Arguments

subj Subject
quer Query

Value

Results from countOverlaps
extractEnrichmentOverlaps

Given a single row from an enrichment table calculation, finds the set of overlaps between the user set and the test set. You can then use these, for example, to get sequences for those regions.

Description

Given a single row from an enrichment table calculation, finds the set of overlaps between the user set and the test set. You can then use these, for example, to get sequences for those regions.

Usage

extractEnrichmentOverlaps(locResult, userSets, regionDB)

Arguments

locResult     Results from runLOLA function
userSets      User sets passed to the runLOLA function
regionDB      Region database used

Value

userSets overlapping the supplied database entry.

Examples

dbPath = system.file("extdata", "hg19", package="LOLA")
regionDB = loadRegionDB(dbLocation=dbPath)
data("sample_universe", package="LOLA")
data("sample_input", package="LOLA")

getRegionSet(regionDB, collections="ucsc_example", filenames="vistaEnhancers.bed")
getRegionSet(dbPath, collections="ucsc_example", filenames="vistaEnhancers.bed")
getRegionFile(dbPath, collections="ucsc_example", filenames="vistaEnhancers.bed")

res = runLOLA(userSets, userUniverse, regionDB, cores=1)
locResult = res[2,]
extractEnrichmentOverlaps(locResult, userSets, regionDB)
writeCombinedEnrichment(locResult, "temp_outfolder")

userSetsRedefined = redefineUserSets(userSets, userUniverse)
resRedefined = runLOLA(userSetsRedefined, userUniverse, regionDB, cores=1)

g = plotTopLOLAEncrichments(resRedefined)
getRegionFile

Grab the filename for a single region set from a database specified by filename.

Description

Like getRegionSet but returns a filename instead of a GRanges object. Given a local filename, returns a complete absolute path so you can read that file in.

Usage

getRegionFile(dbLocation, filenames, collections = NULL)

Arguments

dbLocation folder of regionDB
filenames Filename(s) of a particular region set to grab.
collections (optional) subset of collections to list

Value

A filename the specified file in the regionDB.

Examples

dbPath = system.file("extdata", "hg19", package="LOLA")
regionDB = loadRegionDB(dbLocation=dbPath)
data("sample_universe", package="LOLA")
data("sample_input", package="LOLA")

getRegionSet(regionDB, collections="ucsc_example", filenames="vistaEnhancers.bed")
getRegionSet(dbPath, collections="ucsc_example", filenames="vistaEnhancers.bed")
getRegionFile(dbPath, collections="ucsc_example", filenames="vistaEnhancers.bed")

res = runLOLA(userSets, userUniverse, regionDB, cores=1)
locResult = res[2,]
exttractEnrichmentOverlaps(locResult, userSets, regionDB)
writeCombinedEnrichment(locResult, "temp_outfolder")

userSetsRedefined = redefineUserSets(userSets, userUniverse)
resRedefined = runLOLA(userSetsRedefined, userUniverse, regionDB, cores=1)

g = plotTopLOLAEnrichments(resRedefined)
getRegionSet

Grab a single region set from a database, specified by filename.

Description
If you want to work with a LOLA regionDB region set individually, this function can help you. It can extract individual (or subsets of) region sets from either loaded regionDBs, loaded with loadRegionDB(), or from a database on disk, where only the region sets of interest will be loaded.

Usage
getRegionSet(regionDB, filenames, collections = NULL)

Arguments
- regionDB: A region database loaded with loadRegionDB().
- filenames: Filename(s) of a particular region set to grab.
- collections: (optional) subset of collections to list

Value
A GRanges object derived from the specified file in the regionDB.

Examples
```
dbPath = system.file("extdata", "hg19", package="LOLA")
regionDB = loadRegionDB(dbLocation=dbPath)
data("sample_universe", package="LOLA")
data("sample_input", package="LOLA")

getRegionSet(regionDB, collections="ucsc_example", filenames="vistaEnhancers.bed")
getRegionSet(dbPath, collections="ucsc_example", filenames="vistaEnhancers.bed")
gRegionFile(dbPath, collections="ucsc_example", filenames="vistaEnhancers.bed")
```

```
res = runLOLA(userSets, userUniverse, regionDB, cores=1)
locResult = res[2,]
extractEnrichmentOverlaps(locResult, userSets, regionDB)
writeCombinedEnrichment(locResult, "temp_outfolder")

userSetsRedefined = redefineUserSets(userSets, userUniverse)
resRedefined = runLOLA(userSetsRedefined, userUniverse, regionDB, cores=1)

g = plotTopLOLAEnrichments(resRedefined)
```
**lapplyAlias**

*Function to run lapply or mclapply, depending on the option set in `getOption("mc.cores"), which can be set with `setLapplyAlias()`.*

**Description**

Function to run lapply or mclapply, depending on the option set in `getOption("mc.cores"), which can be set with `setLapplyAlias()`.

**Usage**

```r
lapplyAlias(..., mc.preschedule = TRUE)
```

**Arguments**

- `...` Arguments passed `lapply()` or `mclapply()`
- `mc.preschedule` Argument passed to `mclapply`

**Value**

Result from `lapply` or `parallel::mclapply`

---

**listRegionSets**

*Lists the region sets for given collection(s) in a region database on disk.*

**Description**

Lists the region sets for given collection(s) in a region database on disk.

**Usage**

```r
listRegionSets(regionDB, collections = NULL)
```

**Arguments**

- `regionDB` File path to region database
- `collections` (optional) subset of collections to list

**Value**

a list of files in the given collections

**Examples**

```r
dbPath = system.file("extdata", "hg19", package="LOLA")
listRegionSets(dbPath)
```
**listToGRangesList**

converts a list of GRanges into a GRangesList; strips all metadata.

**Description**

converts a list of GRanges into a GRangesList; strips all metadata.

**Usage**

```r
listToGRangesList(lst)
```

**Arguments**

- `lst` a list of GRanges objects

**Value**

- a GRangesList object

**loadRegionDB**

Helper function to annotate and load a regionDB, a folder with subfolder collections of regions.

**Description**

Helper function to annotate and load a regionDB, a folder with subfolder collections of regions.

**Usage**

```r
loadRegionDB(dbLocation, useCache = TRUE, limit = NULL, collections = NULL)
```

**Arguments**

- `dbLocation` folder where your regionDB is stored, or list of such folders
- `useCache` uses simpleCache to cache and load the results
- `limit` You can limit the number of regions for testing. Default: NULL (no limit)
- `collections` Restrict the database loading to this list of collections

**Value**

- regionDB list containing database location, region and collection annotations, and regions GRangesList

**Examples**

```r
dbPath = system.file("extdata", "hg19", package="LOLA")
regionDB = loadRegionDB(dbLocation=dbPath)
```
mergeRegionDBs

LOLA  Genome locus overlap analysis.

Description

Run, Lola!

Author(s)

Nathan Sheffield

References

http://github.com/sheffien

mergeRegionDBs  Given two regionDBs, (lists returned from loadRegionDB()), This function will combine them into a single regionDB. This will enable you to combine, for example, LOLA Core databases with custom databases into a single analysis.

Description

Given two regionDBs, (lists returned from loadRegionDB()), This function will combine them into a single regionDB. This will enable you to combine, for example, LOLA Core databases with custom databases into a single analysis.

Usage

mergeRegionDBs(dbA, dbB)

Arguments

dbA  First regionDB database.

dbB  Second regionDB database.

Value

A combined regionDB.

Examples

dbPath = system.file("extdata", "hg19", package="LOLA")
regionDB = loadRegionDB(dbPath)
combinedRegionDB = mergeRegionDBs(regionDB, regionDB)
**nlist**

*Named list function.*

**Description**

This function is a drop-in replacement for the base list() function, which automatically names your list according to the names of the variables used to construct it. It seamlessly handles lists with some names and others absent, not overwriting specified names while naming any unnamed parameters. Took me awhile to figure this out.

**Usage**

```r
nlist(...)```

**Arguments**

... arguments passed to list()

**Value**

A named list object.

---

**plotTopLOLAEnrichments**

*Given some results (you grab the top ones on your own), this plots a barplot visualizing their odds ratios.*

**Description**

Given some results (you grab the top ones on your own), this plots a barplot visualizing their odds ratios.

**Usage**

```r
plotTopLOLAEnrichments(data)
```

**Arguments**

- **data** A results table returned from runLOLA()

**Value**

Returns a ggplot2 plot object.
Examples

dbPath = system.file("extdata", "hg19", package="LOLA")
regionDB = loadRegionDB(dbLocation=dbPath)
data("sample_universe", package="LOLA")
data("sample_input", package="LOLA")

getRegionSet(regionDB, collections="ucsc_example", filenames="vistaEnhancers.bed")
getRegionSet(dbPath, collections="ucsc_example", filenames="vistaEnhancers.bed")
getRegionFile(dbPath, collections="ucsc_example", filenames="vistaEnhancers.bed")

res = runLOLA(userSets, userUniverse, regionDB, cores=1)
locResult = res[2,]
extractEnrichmentOverlaps(locResult, userSets, regionDB)
writeCombinedEnrichment(locResult, "temp_outfolder")

userSetsRedefined = redefineUserSets(userSets, userUniverse)
resRedefined = runLOLA(userSetsRedefined, userUniverse, regionDB, cores=1)
g = plotTopLOLAEnrichments(resRedefined)

readBed

Imports bed files and creates GRanges objects, using the fread() function from data.table.

Description
Imports bed files and creates GRanges objects, using the fread() function from data.table.

Usage
readBed(file)

Arguments
file File name of bed file.

Value
GRanges Object

Examples
a = readBed(system.file("extdata", "examples/combined_regions.bed", package="LOLA"))
**readCollection**  

*Given a bunch of region set files, read in all those flat (bed) files and create a GRangesList object holding all the region sets. This function is used by readRegionGRL to process annotation objects.*

**Description**

Given a bunch of region set files, read in all those flat (bed) files and create a GRangesList object holding all the region sets. This function is used by readRegionGRL to process annotation objects.

**Usage**

```r
readCollection(filesToRead, limit = NULL)
```

**Arguments**

- `filesToRead`: a vector containing bed files
- `limit`: for testing purposes, limit the number of files read. NULL for no limit (default).

**Value**

A GRangesList with the GRanges in the filesToRead.

**Examples**

```r
files = list.files(system.file("extdata", "hg19/ucsc_example/regions", package="LOLA"), pattern="*.bed")
regionAnno = readCollection(files)
```

---

**readCollectionAnnotation**

*Read collection annotation*

**Description**

Read collection annotation

**Usage**

```r
readCollectionAnnotation(dbLocation, collections = NULL)
```

**Arguments**

- `dbLocation`: Location of the database
- `collections`: Restrict the database loading to this list of collections. Leave NULL to load the entire database (Default).
readCollectionFiles

Description
Given a database and a collection, this will create the region annotation data.table; either giving a generic table based on file names, or by reading in the annotation data.

Usage
readCollectionFiles(dbLocation, collection, refreshSizes = FALSE)

Arguments
- dbLocation: folder where your regionDB is stored.
- collection: Collection folder to load
- refreshSizes: should I recreate the sizes files documenting how many regions (lines) are in each region set?

Value
A data.table annotating the regions in the collections.

Examples

```r
dbPath = system.file("extdata", "hg19", package="LOLA")
collectionAnno = readCollectionAnnotation(dbLocation=dbPath)
```

```r
dbPath = system.file("extdata", "hg19", package="LOLA")
regionAnno = readCollectionFiles(dbLocation=dbPath, "ucsc_example")
```
readRegionGRL

This function takes a region annotation object and reads in the regions, returning a GRangesList object of the regions.

**Description**

This function takes a region annotation object and reads in the regions, returning a GRangesList object of the regions.

**Usage**

```r
readRegionGRL(
  dbLocation, 
  annoDT, 
  refreshCaches = FALSE, 
  useCache = TRUE, 
  limit = NULL
)
```

**Arguments**

- `dbLocation`: folder of regionDB
- `annoDT`: output of readRegionSetAnnotation().
- `refreshCaches`: should I recreate the caches?
- `useCache`: uses simpleCache to cache and load the results
- `limit`: for testing purposes, limit the number of files read. NULL for no limit (default).

**Value**

GRangesList object

**Examples**

```r
dbPath = system.file("extdata", "hg19", package="LOLA")
regionAnno = readRegionSetAnnotation(dbLocation=dbPath)
regionGRL = readRegionGRL(dbLocation= dbPath, regionAnno, useCache=FALSE)
```
readRegionSetAnnotation

*Description*

Given a folder containing region collections in subfolders, this function will either read the annotation file if one exists, or create a generic annotation file.

*Usage*

```r
readRegionSetAnnotation(
  dbLocation,
  collections = NULL,
  refreshCaches = FALSE,
  refreshSizes = TRUE,
  useCache = TRUE
)
```

*Arguments*

- `dbLocation`: folder where your regionDB is stored.
- `collections`: Restrict the database loading to this list of collections Leave NULL to load the entire database (Default).
- `refreshCaches`: should I recreate the caches? Default: FALSE
- `refreshSizes`: should I refresh the size files? Default: TRUE
- `useCache`: Use simpleCache to store results and load them?

*Value*

Region set annotation (data.table)

*Examples*

```r
dbPath = system.file("extdata", "hg19", package="LOLA")
regionAnno = readRegionSetAnnotation(dbLocation=dbPath)
```
redefineUserSets

This function will take the user sets, overlap with the universe, and redefine the user sets as the set of regions in the user universe that overlap at least one region in user sets. This makes for a more appropriate statistical enrichment comparison, as the user sets are actually exactly the same regions found in the universe otherwise, you can get some weird artifacts from the many-to-many relationship between user set regions and universe regions.

Description

This function will take the user sets, overlap with the universe, and redefine the user sets as the set of regions in the user universe that overlap at least one region in user sets. This makes for a more appropriate statistical enrichment comparison, as the user sets are actually exactly the same regions found in the universe otherwise, you can get some weird artifacts from the many-to-many relationship between user set regions and universe regions.

Usage

redefineUserSets(userSets, userUniverse, cores = 1)

Arguments

- userSets: Regions of interest
- userUniverse: Regions tested for inclusion in userSets
- cores: Number of processors

Value

userSets redefined in terms of userUniverse

Examples

dbPath = system.file("extdata", "hg19", package="LOLA")
regionDB = loadRegionDB(dbLocation=dbPath)
data("sample_universe", package="LOLA")
data("sample_input", package="LOLA")

getRegionSet(regionDB, collections="ucsc_example", filenames="vistaEnhancers.bed")
getRegionSet(dbPath, collections="ucsc_example", filenames="vistaEnhancers.bed")
getRegionFile(dbPath, collections="ucsc_example", filenames="vistaEnhancers.bed")

res = runLOLA(userSets, userUniverse, regionDB, cores=1)
locResult = res[2,]
extractEnrichmentOverlaps(locResult, userSets, regionDB)
writeCombinedEnrichment(locResult, "temp_outfolder")
userSetsRedefined = redefineUserSets(userSets, userUniverse)
resRedefined = runLOLA(userSetsRedefined, userUniverse, regionDB, cores=1)

g = plotTopLOLAEnrichments(resRedefined)

replaceFileExtension  This will change the string in filename to have a new extension

Description
This will change the string in filename to have a new extension

Usage
replaceFileExtension(filename, extension)

Arguments
filename  string to convert
extension  new extension

Value
Filename with original extension deleted, replaced by provided extension

runLOLA  Enrichment Calculation

Description
Workhorse function that calculates overlaps between userSets, and then uses a fisher’s exact test to rank them by significance of the overlap.

Usage
runLOLA(
    userSets,
    userUniverse,
    regionDB,
    minOverlap = 1,
    cores = 1,
    redefineUserSets = FALSE,
    direction = "enrichment"
    )
**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>userSets</td>
<td>Regions of interest</td>
</tr>
<tr>
<td>userUniverse</td>
<td>Regions tested for inclusion in userSets</td>
</tr>
<tr>
<td>regionDB</td>
<td>Region DB to check for overlap, from loadRegionDB()</td>
</tr>
<tr>
<td>minOverlap</td>
<td>(Default: 1) Minimum bases required to count an overlap</td>
</tr>
<tr>
<td>cores</td>
<td>Number of processors</td>
</tr>
<tr>
<td>redefineUserSets</td>
<td>run redefineUserSets() on your userSets?</td>
</tr>
<tr>
<td>direction</td>
<td>Defaults to &quot;enrichment&quot;, but may also accept &quot;depletion&quot;, which will swap the direction of the fisher test (use 'greater' or 'less' value passed to the 'alternative' option of fisher.test)</td>
</tr>
</tbody>
</table>

**Value**

Data.table with enrichment results. Rows correspond to individual pairwise fisher’s tests comparing a single userSet with a single databaseSet. The columns in this data.table are: userSet and dbSet: index into their respective input region sets. pvalueLog: -log10(pvalue) from the fisher’s exact result; oddsRatio: result from the fisher’s exact test; support: number of regions in userSet overlapping databaseSet; rnkPV, rnkOR, rnkSup: rank in this table of p-value, oddsRatio, and Support respectively. The –value is the negative natural log of the p-value returned from a one-sided fisher’s exact test. maxRnk, meanRnk: max and mean of the 3 previous ranks, providing a combined ranking system. b, c, d: 3 other values completing the 2x2 contingency table (with support). The remaining columns describe the dbSet for the row.

If you have the qvalue package installed from bioconductor, runLOLA will add a q-value transformation to provide FDR scores automatically.

**Examples**

```r
dbPath = system.file("extdata", "hg19", package="LOLA")
regionDB = loadRegionDB(dbLocation=dbPath)
data("sample_universe", package="LOLA")
data("sample_input", package="LOLA")

getRegionSet(regionDB, collections="ucsc_example", filenames="vistaEnhancers.bed")
getRegionSet(dbPath, collections="ucsc_example", filenames="vistaEnhancers.bed")
getRegionFile(dbPath, collections="ucsc_example", filenames="vistaEnhancers.bed")

res = runLOLA(userSets, userUniverse, regionDB, cores=1)
locResult = res[2,]
extractEnrichmentOverlaps(locResult, userSets, regionDB)
writeCombinedEnrichment(locResult, "temp_outfolder")

userSetsRedefined = redefineUserSets(userSets, userUniverse)
resRedefined = runLOLA(userSetsRedefined, userUniverse, regionDB, cores=1)

g = plotTopLOLAEnrichments(resRedefined)
```
sampleGRL

Function to sample regions from a GRangesList object, in specified proportion

Description
Function to sample regions from a GRangesList object, in specified proportion

Usage
sampleGRL(GRL, prop)

Arguments
- GRL: GRangesList from which to sample
- prop: vector with same length as GRL, of values between 0-1, proportion of the list to select

Value
A sampled subset of original GRangesList object.

setLapplyAlias

To make parallel processing a possibility but not required, I use an lapply alias which can point at either the base lapply (for no multicore), or it can point to mclapply, and set the options for the number of cores (what mclapply uses). With no argument given, returns instead the number of cpus currently selected.

Description
To make parallel processing a possibility but not required, I use an lapply alias which can point at either the base lapply (for no multicore), or it can point to mclapply, and set the options for the number of cores (what mclapply uses). With no argument given, returns instead the number of cpus currently selected.

Usage
setLapplyAlias(cores = 0)

Arguments
- cores: Number of cpus

Value
None
**setSharedDataDir**

Sets global variable specifying the default data directory.

**Description**

setSharedDataDir Sets global variable specifying the default data directory.

**Usage**

```r
setSharedDataDir(sharedDataDir)
```

**Arguments**

- `sharedDataDir` directory where the shared data is stored.

**Value**

No return value.

**Examples**

```r
setSharedDataDir("project/data")
```

---

**splitDataTable**

Efficiently split a data.table by a column in the table

**Description**

Efficiently split a data.table by a column in the table

**Usage**

```r
splitDataTable(DT, splitFactor)
```

**Arguments**

- `DT` Data.table to split
- `splitFactor` Column to split, which can be a character vector or an integer.

**Value**

List of data.table objects, split by column
splitFileIntoCollection

This function will take a single large bed file that is annotated with a column grouping different sets of similar regions, and split it into separate files for use with the LOLA collection format.

Description

This function will take a single large bed file that is annotated with a column grouping different sets of similar regions, and split it into separate files for use with the LOLA collection format.

Usage

splitFileIntoCollection(
  filename,
  splitCol,
  collectionFolder = NULL,
  filenamePrepend ="
)

Arguments

filename the file to split
splitCol factor column that groups the lines in the file by set. It should be an integer.
collectionFolder name of folder to place the new split files.
filenamePrepend string to prepend to the filenames. Defaults to blank.

Value

No return value.

Examples

combFile = system.file("extdata", "examples/combined_regions.bed", package="LOLA")
splitFileIntoCollection(combFile, 4)
userSets

An example set of regions, sampled from the example database.

Description

A dataset containing a few sample regions.

Usage

data(sample_input)

Format

A GRangesList object

Value

No return value.

Examples

## Not run:
This is how I produced the sample data sets:

```
dbPath = system.file("extdata", "hg19", package="LOLA")
regionDB = loadRegionDB(dbLocation= dbPath)
userSetA = reduce(do.call(c, (sampleGRL(regionDB$regionGRL,
prop=c(.1,.25,.05,.05,0)))))
userSetB = reduce(do.call(c, (sampleGRL(regionDB$regionGRL,
prop=c(.2,.05,.05,.05,0)))))

userSets = GRangesList(setA=userSetA, setB=userSetB)
userUniverse = reduce(do.call(c, regionDB$regionGRL))
save(userSets, file="sample_input.RData")
save(userUniverse, file="sample_universe.RData")
```

## End(Not run)

userUniverse

A reduced GRanges object from the example regionDB database

Description

A reduced GRanges object from the example regionDB database

Usage

data(sample_universe)
**Format**

A GRanges object

**Value**

No return value.

---

**write.tsv**

Wrapper of write.table that provides defaults to write a simple .tsv file. Passes additional arguments to write.table

---

**Description**

Wrapper of write.table that provides defaults to write a simple .tsv file. Passes additional arguments to write.table

**Usage**

write.tsv(...)

**Arguments**

... Additional arguments passed to write.table

**Value**

No return value

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**writeCombinedEnrichment**

Function for writing output all at once: combinedResults is an table generated by "locationEnrichment()" or by rbinding category/location results. Writes all enrichments to a single file, and also spits out the same data divided into groups based on userSets, and Databases, just for convenience. disable this with an option.

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**Description**

Function for writing output all at once: combinedResults is an table generated by "locationEnrichment()" or by rbinding category/location results. Writes all enrichments to a single file, and also spits out the same data divided into groups based on userSets, and Databases, just for convenience. disable this with an option.
Usage

writeCombinedEnrichment(
    combinedResults,
    outFolder = NULL,
    includeSplits = TRUE
)

Arguments

combinedResults
    enrichment results object
outFolder
    location to write results on disk
includeSplits
    also include individual files for each user set and database?

Value

No return value.

Examples

dbPath = system.file("extdata", "hg19", package="LOLA")
regionDB = loadRegionDB(dbLocation=dbPath)
data("sample_universe", package="LOLA")
data("sample_input", package="LOLA")

getRegionSet(regionDB, collections="ucsc_example", filenames="vistaEnhancers.bed")
getRegionSet(dbPath, collections="ucsc_example", filenames="vistaEnhancers.bed")
getRegionFile(dbPath, collections="ucsc_example", filenames="vistaEnhancers.bed")

res = runLOLA(userSets, userUniverse, regionDB, cores=1)
locResult = res[2,]
extractEnrichmentOverlaps(locResult, userSets, regionDB)
writeCombinedEnrichment(locResult, "temp_outfolder")

userSetsRedefined = redefineUserSets(userSets, userUniverse)
resRedefined = runLOLA(userSetsRedefined, userUniverse, regionDB, cores=1)

g = plotTopLOLAEEnrichments(resRedefined)
writeDataTableSplitByColumn

**Description**

Given a data table and a factor variable to split on, efficiently divides the table and then writes the different splits to separate files, named with filePrepend and numbered according to split.

**Usage**

```r
writeDataTableSplitByColumn(
  DT,
  splitFactor,
  filePrepend = "",
  orderColumn = NULL
)
```

**Arguments**

- `DT` _data.table to split_
- `splitFactor` _column of DT to split on_
- `filePrepend` _notation string to prepend to output files_
- `orderColumn` _column of DT to order on (defaults to the first column)_

**Value**

- number of splits written
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