Package 'OGRE'

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Type Package

Title Calculate, visualize and analyse overlap between genomic regions

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Description OGRE calculates overlap between user defined genomic region datasets.
Any regions can be supplied i.e. genes, SNPs, or reads from sequencing experiments.
Key numbers help analyse the extend of overlaps which can also be visualized at a genomic level.

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Contents

`OGRE-package` *OGRE package to calculate, analyze and visiualize overlap between annotated genomic region datasets*

Description

OGRE calculates overlap between user defined annotated genomic region datasets. Any regions can be supplied such as public annotations (genes), genetic variation (SNPs, mutations), regulatory elements (TFBS, promoters, CpG islands) and basically all types of NGS output from sequencing experiments. After overlap calculation, key numbers help analyse the extend of overlaps which can also be visualized at a genomic level.

Details

The main functions are:

OGREDataSetFromDir - build an OGRE dataset from a user defined directory with GRanges annotation files.

- loadAnnotations - Load dataset files containing genomic regions annotation information from hard drive

OGREDataSet - build an empty OGRE dataset to flexibly add datasets from other sources like AnnotationHub or custom GRanges objects.

- addDataSetFromHub - adds datasets from AnnotationHub
- addGRanges - adds user defined GenomicRanges datasets

fOverlaps - Finds all overlaps between query and subject datasets
sumPlot - calculates key numbers, tables and plots
gvizPlot - generates a genomic plot around query elements with overlapping subject hits.

For additional information, see the package vignette, by typing `vignette("OGRE")`. Software-related questions or issues can be posted to the Bioconductor Support Site:

https://support.bioconductor.org

or on github:

https://https://github.com/svenbioinf/OGRE

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addDataSetFromHub *Add dataSet from AnnotationHub*

Description

AnnotationHub offers a wide range of annotated datasets which can be manually aquired but need some parsing to work with OGRE as detailed in vignette section "Load datasets from AnnotationHub". For convienence `addDataSetFromHub()` adds one of the predefined human dataSets of `listPredefinedDataSets()` to a OGREDataSet.Those are taken from AnnotationHub and are ready to use for OGRE. Additional information on dataSets can be found here listPredefinedDataSets.

Usage

```
addDataSetFromHub(OGREDataSet, dataSet, type)
```

Arguments

OGREDataSet	OGREDataSet
dataSet	character Name of one predefined dataSets to add as query or subject to a OGREDataSet. Possible dataSets can be show with listPredefinedDataSets().
type	Type of dataSet, must be either query or subject. If query the dataSet will be added as query and at the first position of OGREDataSet.

Value

OGREDataSet.

Examples

```
myOGRE <- OGREDataSet()
myOGRE <- addDataSetFromHub(myOGRE,"protCodingGenes","query")
```

---

addGRanges *Add GenomicRanges*

Description

Add a GenomicRanges dataset to OGREDataSet

Usage

```
addGRanges(OGREDataSet, dataSet, type, label = NULL)
```

Arguments

OGREDataSet	An OGREDataSet
dataSet	A GRanges object. Each region needs chromosome, start, end and strand information. A unique ID and a name column must be present in the GenomicRanges object metadata. Avoid different chromosome naming conventions i.e. (chr1, CHR1, 1, I) among all datasets
type	Type of dataSet, must be either query or subject. If query the dataSet will be added as query and at the first position of OGREDataSet.
label	A character that will label your GRanges object. If not supplied, the label will be guessed from the dataset parameter.

Value

OGREDataSet.

Examples

```
myOGRE <- OGREDataSet()
myGRanges <- makeExampleGRanges()
myOGRE <- addGRanges(myOGRE,myGRanges,"query")
```

covPlot *Coverage plot*

Description

Generates coverage plots of all subject datasets and stores them as a list, that can be accessed by `metadata(OGREDataSet)$covPlot`

Usage

```
covPlot(
  OGREDataSet,
  datasets = names(OGREDataSet)[seq(2, length(OGREDataSet))],
  nbin = 100
)
```

Arguments

`OGREDataSet`	An OGREDataSet
`datasets`	`character vector` of subject dataset names. Default: Generates a coverage plots for all subjects
`nbin`	Number of bins

Value

OGREDataSet.

Examples

```
myOGRE <- makeExampleOGREDataSet()
myOGRE <- loadAnnotations(myOGRE)
myOGRE <- fOverlaps(myOGRE)
myOGRE <- covPlot(myOGRE)
metadata(myOGRE)$covPlot
```

extendGRanges *Extend a GRanges object*

Description

Extend(shrink) ranges of a GRanges object.

Usage

```
extendGRanges(OGREDataSet, name, upstream = 0, downstream = 0)
```

Arguments

OGREDataSet	An OGREDataSet
name	character Name of the GRanges object for extending
upstream	int (positive or negative number)
downstream	int (positive or negative number)

Value

OGREDataSet

Examples

```
myOGRE <- makeExampleOGREDataSet()
myOGRE <- loadAnnotations(myOGRE)
#extend range by shifting start 100 bp in upstream direction
myOGRE <- extendGRanges(myOGRE,"genes",upstream=100)
#shrinking range by shifting end 100 bp in upstream direction
myOGRE <- extendGRanges(myOGRE,"genes",downstream=-100)
#shrinking range by shifting from both sides to the center
myOGRE <- extendGRanges(myOGRE,"genes",upstream=-10,downstream=-10)
```

---

extractPromoters *Extract promoter*

Description

A wrapper of GenomicRanges::promoters() to extract promoter regions of a GRanges object stored in a OGREDataSet

Usage

```
extractPromoters(OGREDataSet, name, upstream = 2000, downstream = 200)
```

Arguments

OGREDataSet	An OGREDataSet
name	character Name of the GRanges object
upstream	int (positive) upstream=2000(default)
downstream	int (positive) downstream=200(default)

Value

OGREDataSet

Examples

```
myOGRE <- makeExampleOGREDataSet()
myOGRE <- loadAnnotations(myOGRE)
myOGRE <- extractPromoters(myOGRE,"genes", upstream=2000, downstream=200)
```

`fOverlaps` *Find overlaps*

Description

Finds all overlaps between query and subject(s) and stores each hit (overlap) in data table `detailDT`. Data table `sumDT` shows all overlaps of a certain subject type for all query elements. By default also partially overlaps are reported. Overlap calculation is done using `GenomicRanges::findOverlaps()` implementation.

Usage

```
fOverlaps(OGREDataSet, selfHits = FALSE, ignoreStrand = TRUE, ...)
```

Arguments

`OGREDataSet`	A OGREDataSet.
`selfHits`	`logical` if FALSE(default) ignores self hits of identical regions (with identical IDs) within datasets.
`ignoreStrand`	`logical` If TRUE (default) two regions with overlapping locations on different strands are considered an overlap hit.
`...`	Additional parameters, see `GenomicRanges::findOverlaps()`

Value

OGREDataSet.

Examples

```
myOGRE <- makeExampleOGREDataSet()
myOGRE <- loadAnnotations(myOGRE)
myOGRE <- fOverlaps(myOGRE)
```

gvizPlot *Generate Gviz plot*

Description

gvizPlot generates a plot around one or many given query elements with all overlapping subject hits. In addition, each generated plot can be stored in the gvizPlots folder get or set by gvizPlotsFolder. A maximum of 25 elements can be plotted per track.

Usage

```
gvizPlot(
  OGREDataSet,
  query,
  gvizPlotsFolder = metadata(OGREDataSet)$gvizPlotsFolder,
 trackRegionLabels = setNames(rep("ID", length(OGREDataSet)), names(OGREDataSet)),
 trackShapes = setNames(rep("fixedArrow", length(OGREDataSet)), names(OGREDataSet)),
  showPlot = FALSE,
  extendPlot = c(-300, 300),
  nElements = 25
)
```

Arguments

OGREDataSet	A OGREDataSet.
query	A character vector of one or many query elements ID's (i.e. Gene ID's).
gvizPlotsFolder	A character pointing to the plot(s) output directory. If not supplied a folder is automatically generated and can be accessed by metatdata(OGREDataSet)$gvizPlotsFolder.
trackRegionLabels	A labeled character vector that defines the type of label that is displayed for query and subject elements during plotting. Vector values represent the type of label and vector labels define the type of subject element. In the following example setNames(c("ID","name"),c("genes","CGI")) Value "ID" and label "genes" would annotate your genes with IDs taken from the ID column of your dataset. Datasets not defined in this vector are plotted without track labels.
trackShapes	A labeled character vector that defines the type of shape in which every dataset's elements are displayed. Vector values represent the type of shape and vector labels define the type of subject element. In the following example setNames(c("fixedArrow","box"),c(Value "fixedArrow" and label "genes" would display your genes in fixedArrow and CGI as box shape. Possible values: (box, arrow, fixedArrow, ellipse, and smallArrow) Default="fixedArrow"
showPlot	logical If FALSE(default) plots are only saved to gvizPlotsFolder. If TRUE plots are additionally send to the plotting window.

`extendPlot` `int vector` Integer vector of length two that extends the plot window to the left or right by adding the first value to query start and the second value to query end coordinates(bp). e.g. `c(-1000,1000)` zooms out, `c(1000,-1000)` zooms in and `c(-1000,0)` shifts the plot window to the left.

`nElements` `integer` Number of elements that are displayed in each track (Default=25). High n.elements can lead to overplotting. Use `nElements=FALSE` to display all elements.

Value

OGREDataSet.

Examples

```
myOGRE <- makeExampleOGREDataSet()
myOGRE <- loadAnnotations(myOGRE)
myOGRE <- fOverlaps(myOGRE)
myOGRE <- gvizPlot(myOGRE,query="ENSG00000142168")
```

---

listPredefinedDataSets

List predefined datasets

Description

Use `listPredefinedDataSets()` to receive a vector of names for predefined datasets that can be aquired from AnnotationHub that are already correctly parsed and formatted. Each of the listed names can be used as input for `addDataSetFromHub()`. Currently supported:

- protCodingGenes - Protein coding genes from HG19 (GRCh37) Ensembl For additional information use: `getInfoOnIds(AnnotationHub(), "AH10684")`
- CGI - CpG islands from HG19 UCSC For additional information use: `getInfoOnIds(AnnotationHub(), "AH5086")`
- SNP - Common Single Nucleotide Polymorphism from HG19 UCSC For additional information use: `getInfoOnIds(AnnotationHub(), "AH5105")`
- TFBS - Transcription Factor Binding Sites conserved from HG19 UCSC For additional information use: `getInfoOnIds(AnnotationHub(), "AH5090")`
- Promoters - Promoter and flanking regions from HG19 Ensembl (Note: This annotation is currently not included in AnnotationHub and is therefore downloaded from Ensembl's ftp site)

Usage

```
listPredefinedDataSets()
```

Value

character vector.

Examples

```
listPredefinedDataSets()
```

---

loadAnnotations *Load annotation datasets*

Description

Load dataset files containing genomic regions annotation information from hard drive. loadAnnotations calls readQuery and readSubject to read in genomic regions as GenomicRanges objects stored as .RDS / .rds files. Each region needs chromosome, start, end and strand information. A unique ID and a name column must be present in the GenomicRanges object metadata. OGRE searches for the query file in your query folder and any number of subject files in your subjects folder. Alternatively, .gff (v2&v3) files in the query or subject folder with attribute columns containing "ID" and "name" information are read in by OGRE.

Usage

```
loadAnnotations(OGREDataSet)
```

Arguments

OGREDataSet	A OGREDataSet.

Value

A OGREDataSet.

Examples

```
myOGRE <- makeExampleOGREDataSet()
myOGRE <- loadAnnotations(myOGRE)
```

makeExampleGRanges *Make an example GRanges dataset*

Description

makeExampleGRanges generates an example GRanges dataset.

Usage

```
makeExampleGRanges()
```

Value

OGREDataSet.

Examples

```
myGRanges <- makeExampleGRanges()
```

makeExampleOGREDataSet *Make a example OGRE dataset*

Description

makeExampleOGREDataSet generates a example OGREDataSet from dataset files stored in OGRE's extdata directory.

Usage

```
makeExampleOGREDataSet()
```

Value

OGREDataSet.

Examples

```
myOGRE <- makeExampleOGREDataSet()
```

OGREDataSet *BuildOGREDataSet*

Description

Builds a OGREDataset as a GenomicRangesList for storing and analysing datasets which can be added by addDataSetFromHub() or addGRanges(). Use BuildOGREDataSetFromDir for adding dataSets stored as files.

Usage

```
OGREDataSet()
```

Value

A OGREDataSet.

Examples

```
myOGRE <- OGREDataSet()
```

OGREDataSetFromDir *BuildOGREDataSetFromDir*

Description

Builds a OGREDataset from user specified directories containing datasets for which an overlap between query and subject is to be calculated. A OGREDataset is a GenomicRangesList which stores datasets in a list like structure and possible metadata information.

Usage

```
OGREDataSetFromDir(queryFolder, subjectFolder)
```

Arguments

queryFolder	A character path pointing to the directory where your query dataset is located.
subjectFolder	A character path pointing to the directory where your subject dataset(s) are located.

Value

A OGREDataSet.

Examples

```
myQueryFolder <- file.path(system.file('extdata', package = 'OGRE'),"query")
mySubjectFolder <- file.path(system.file('extdata', package = 'OGRE'),"subject")
myOGRE <- OGREDataSetFromDir(queryFolder=myQueryFolder,subjectFolder=mySubjectFolder)
```

`plotHist` *Plot histogram*

Description

Plots overlap histograms of all subject datasets and stores them as a list, that can be accessed by `metadata(myOGRE)$hist`

Usage

```
plotHist(OGREDataSet, plot0 = FALSE)
```

Arguments

`OGREDataSet`	An OGREDataSet
`plot0`	plot0=FALSE(default) plots a histogram of all dataset elements with overlaps, excluding elements without overlaps. plot0=FALSE also includes elements without overlaps.

Value

OGREDataSet.

Examples

```
myOGRE <- makeExampleOGREDataSet()
myOGRE <- loadAnnotations(myOGRE)
myOGRE <- fOverlaps(myOGRE)
myOGRE <- plotHist(myOGRE)
metadata(myOGRE)$hist
```

readDataSetFromFolder *Read dataset(s) from folder*

Description

readDataSetFromFolder() scanns queryFolder and subjectFolder for either .RDS/.rds or .CSV/.csv files and adds them to a OGREDataSet. Each region needs chromosome, start, end and strand information. (tabular file columns must be named accordingly). A unique ID and a name column must be present in the GenomicRanges object's metatdata and tabular file.

Usage

```
readDataSetFromFolder(OGREDataSet, type)
```

Arguments

OGREDataSet	A OGREDataSet.
type	character and one of query/subject.

Value

A OGREDataSet.

Examples

```
myOGRE <- makeExampleOGREDataSet()
myOGRE <- readDataSetFromFolder(myOGRE,type="query")
myOGRE <- readDataSetFromFolder(myOGRE,type="subject")
```

readQuery *Read query dataset*

Description

readQuery() scanns queryFolder for a GRanges object stored as .RDS/.rds or .gff .GFF file and attaches it to the OGREDataSet.

Usage

```
readQuery(OGREDataSet)
```

Arguments

OGREDataSet	A OGREDataSet.

Value

A OGREDataSet.

readSubject *Read subject datasets*

Description

readSubject() scanns SubjectFolder for GRanges objects stored as .RDS/.rds or .gff .GFF files and attaches them to the OGREDataSet.

Usage

```
readSubject(OGREDataSet)
```

Arguments

OGREDataSet	A OGREDataSet.

Value

A OGREDataSet.

SHREC *SHREC SHiny interface for REgion Comparison*

Description

SHREC() is a graphical user interface for OGRE

Usage

```
SHREC()
```

Value

Runs GUI, this function normally does not return

subsetGRanges *Subset a GRanges object*

Description

Subsets a GRanges object with reference to it's ID column using a ID vector.

Usage

```
subsetGRanges(OGREDataSet, IDs, name)
```

Arguments

OGREDataSet	An OGREDataSet
IDs	character vector with IDs used to subset the GRanges object defined in name
name	character Name of the GRanges object for subsetting. One of the GRanges objects in a OGREDataSet

Value

OGREDataSet.

Examples

```
myOGRE <- makeExampleOGREDataSet()
myOGRE <- loadAnnotations(myOGRE)
myOGRE <- subsetGRanges(myOGRE,c("ENSG00000142168","ENSG00000256715"),"genes")
```

summarizeOverlap *Calculates min/max/average overlap*

Description

Calculates min/max/average overlap for all datasets using summary(). Results can be accessed by metadata(OGREDataSet)$summaryDT which is a list() of two data.table objects. The first one includes elements without any overlap at all and the second provides summary numbers for all elements that have at least one overlap.

Usage

```
summarizeOverlap(OGREDataSet)
```

Arguments

OGREDataSet	An OGREDataSet

Value

OGREDataSet.

Examples

```
myOGRE <- makeExampleOGREDataSet()
myOGRE <- loadAnnotations(myOGRE)
myOGRE <- fOverlaps(myOGRE)
myOGRE <- summarizeOverlap(myOGRE)
metadata(myOGRE)$summaryDT
```

---

sumPlot *Generate summary plot*

Description

`sumPlot()` calculates key numbers i.e. (total number of overlaps, number of overlaps per subject...) to help with an exploratory data evaluation and displays them in an informative barplot.

Usage

```
sumPlot(OGREDataSet)
```

Arguments

`OGREDataSet`	A OGREDataSet.

Value

OGREDataSet.

Examples

```
myOGRE <- makeExampleOGREDataSet()
myOGRE <- loadAnnotations(myOGRE)
myOGRE <- fOverlaps(myOGRE)
myOGRE <- sumPlot(myOGRE)
```

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