Package 'regionReport'

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Type Package

Title Generate HTML reports for exploring a set of regions

Version 1.0.5

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Description Generate HTML reports to explore a set of regions such as the results from annotation-agnostic expression analysis of RNA-seq data at base-pair resolution performed by derfinder.

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LazyData true

URL https://github.com/lcolladotor/regionReport

BugReports https://github.com/lcolladotor/regionReport/issues

VignetteBuilder knitr

biocViews DifferentialExpression, Sequencing, RNASeq, Software, Visualization, Transcription, Coverage

Depends R(>= 3.1.1)

Imports derfinder (>= 1.0.0), derfinderPlot (>= 1.0.0), devtools (>= 1.6), GenomeInfoDb, GenomicRanges, ggbio (>= 1.13.13), ggplot2, grid, gridExtra, IRanges, knitcitations (>= 1.0.1), knitr (>= 1.6), knitrBootstrap (>= 0.9.0), mgcv, RColorBrewer, rmarkdown (>= 0.3.3)

Suggests biovizBase, Cairo, TxDb.Hsapiens.UCSC.hg19.knownGene

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R topics documented:

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regionReport-package   *Generate HTML reports for a aset of regions.*

Description

Generate an HTML reports to explore a set of regions such as the results from annotation-agnostic expression analysis of RNA-seq data at base-pair resolution performed by derfinder. The HTML report itself is generated using knitrBootstrap (https://github.com/jimhester/knitrBootstrap).

Author(s)

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derfinderReport   *Generate a HTML report exploring the basic results from derfinder*

Description

This function generates a HTML report exploring the basic results from derfinder (https://github.com/lcolladotor/derfinder). The HTML report itself is generated using knitrBoostrap which uses knitr (http://yihui.name/knitr/) behind the scenes. It works best after using mergeResults.

Usage

```
derfinderReport(prefix, outdir = "basicExploration",
  output = "basicExploration", project = prefix, browse = interactive(),
  nBestRegions = 100, makeBestClusters = TRUE, nBestClusters = 2,
  fullCov = NULL, hg19 = TRUE, p.ideos = NULL, txdb = NULL,
  device = "CairoPNG", ...)
```

Arguments

prefix	The main data directory path where mergeResults was run. It should be the same as mergeResults(prefix).
outdir	The name of output directory relative to prefix.
output	The name of output HTML file (without the html extension).
project	The title of the project.
browse	If TRUE the HTML report is opened in your browser once it's completed.
nBestRegions	The number of region plots to make, ordered by area.
makeBestClusters	
	If TRUE, plotCluster is used on the nBestClusters regions by area. Note that these plots take some time to make.
nBestClusters	The number of region cluster plots to make by taking the nBestClusters regions ranked by area of the cluster.

fullCov	A list where each element is the result from loadCoverage used with cutoff=NULL. Can be generated using fullCoverage.
hg19	If TRUE then the reference is assumed to be hg19 and chromosome lengths as well as the default transcription database (TxDb.Hsapiens.UCSC.hg19.knownGene) will be used.
p.ideos	A list where each element is the result of plotIdeogram. If it's NULL and hg19=TRUE then they are created for the hg19 human reference.
txdb	Specify the transcription database to use for making the plots for the top regions by area. If NULL and hg19=TRUE then TxDb.Hsapiens.UCSC.hg19.knownGene is used.
device	The graphical device used when knitting. See more at http://yihui.name/knitr/options (dev argument).
...	Arguments passed to other methods and/or advanced arguments.

Value

An HTML report with a basic exploration of the derfinder results.

Author(s)

Leonardo Collado-Torres

See Also

mergeResults, analyzeChr, fullCoverage

Examples

```
## Load derfinder
library(derfinder)

## The output will be saved in the derfinderReport-example directory
dir.create(derfinderReport-example, showWarnings = FALSE, recursive = TRUE)

## For convenience, the derfinder output has been pre-computed
file.copy(system.file(file.path(extdata, chr21), package=derfinder,
    mustWork=TRUE), derfinderReport-example, recursive = TRUE)

## Not run:
## If you prefer, you can generate the output from derfinder
initialPath <- getwd()
setwd(file.path(initialPath, derfinderReport-example))

## Collapse the coverage information
collapsedFull <- collapseFullCoverage(list(genomeData$coverage),
    verbose=TRUE)

## Calculate library size adjustments
sampleDepths <- sampleDepth(collapsedFull, probs=c(0.5), nonzero=TRUE,
    verbose=TRUE)
```

```
## Build the models
group <- genomeInfo$pop
adjustvars <- data.frame(genomeInfo$gender)
models <- makeModels(sampleDepths, testvars=group, adjustvars=adjustvars)

## Analyze chromosome 21
analyzeChr(chr=21, coverageInfo=genomeData, models=models,
    cutoffFstat=1, cutoffType=manual, seeds=20140330, groupInfo=group,
    mc.cores=1, writeOutput=TRUE, returnOutput=FALSE)

## Change the directory back to the original one
setwd(initialPath)

## End(Not run)

## Merge the results from the different chromosomes. In this case, theres
## only one: chr21
mergeResults(chrs = 21, prefix = derfinderReport-example,
    genomicState = genomicState$fullGenome)

## Load the options used for calculating the statistics
load(file.path(derfinderReport-example, chr21, optionsStats.Rdata))

## Generate the HTML report
report <- derfinderReport(prefix=derfinderReport-example, browse=FALSE,
    nBestRegions=1, makeBestClusters=FALSE,
    fullCov=list(21=genomeDataRaw$coverage), optionsStats=optionsStats)


if(interactive()) {
    ## Browse the report
    browseURL(report)
}

## Not run:
## Note that you can run the example using:
example(derfinderReport, regionReport, ask=FALSE)

## End(Not run)
```

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