Package 'regionReport'

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Type Package

Title Generate HTML reports for exploring a set of regions

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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/leekgroup/regionReport

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

VignetteBuilder knitr

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

Depends R(>= 3.2)

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

NeedsCompilation no

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R topics documented:

`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 = "png", significantVar = "qvalue", customCode = NULL,
  template = NULL, ...)
```

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).
significantVar	A character variable specifying whether to use the p-values, the FDR adjusted p-values or the FWER adjusted p-values to determine significance. Has to be either 'pvalue', 'qvalue' or 'fwer'.
customCode	An absolute path to a child R Markdown file with code to be evaluated before the reproducibility section. Its useful for users who want to customize the report by adding conclusions derived from the data and/or further quality checks and plots.
template	Template file to use for the report. If not provided, will use the default file found in basicExploration/basicExploration.Rmd within the package source.
...	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, there's
## 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)
```

`regionReport-deprecated` *Deprecated functions in package 'regionReport'*

Description

These functions are provided for compatibility with older versions of 'regionReport' only, and will be defunct at the next release.

Usage

```
derfinder_report()

render_report()
```

Details

The following functions are deprecated and will be made defunct; use the replacement indicated below:

- plot_cluster: `plotCluster`
- render_report: `render_report`

renderReport *Generate a HTML report exploring a set of genomic regions*

Description

This function generates a HTML report with quality checks, genome location exploration, and an interactive table with the results. Other output formats are possible such as PDF but lose the interactivity. Users can easily append to the report by providing a R Markdown file to `customCode`, or can customize the entire template by providing an R Markdown file to `template`.

Usage

```
renderReport(regions, project, pvalueVars = c(`P-values` = "pval"),
  densityVars = NULL, significantVar = mcols(regions)$pval <= 0.05,
  annotation = NULL, nBestRegions = 500, customCode = NULL,
  outdir = "regionExploration", output = "regionExploration",
  browse = interactive(), txdb = NULL, device = "png",
  densityTemplates = list(Pvalue = templatePvalueDensity, Common =
  templateDensity, Manhattan = templateManhattan), template = NULL, ...)

templatePvalueDensity

templateDensity

templateManhattan
```

Arguments

`regions`	The set of genomic regions of interest as a `GRanges` object. All sequence lengths must be provided.
`project`	The title of the project.
`pvalueVars`	The names of the variables with values between 0 and 1 to plot density values by chromosome and a table for commonly used cutoffs. Most commonly used to explore p-value distributions. If a named character vector is provided, the names are used in the plot titles.
`densityVars`	The names of variables to use for making density plots by chromosome. Commonly used to explore scores and other variables given by region. If a named character vector is provided, the names are used in the plot titles.
`significantVar`	A `logical` variable differentiating statistically significant regions from the rest. When provided, both types of regions are compared against each other to see differences in width, location, etc.
`annotation`	The output from matchGenes used on `regions`. Note that this can take time for a large set of regions so it's better to pre-compute this information and save it.
`nBestRegions`	The number of regions to include in the interactive table.

customCode	An absolute path to a child R Markdown file with code to be evaluated before the reproducibility section. Its useful for users who want to customize the report by adding conclusions derived from the data and/or further quality checks and plots.
outdir	The name of output directory.
output	The name of output HTML file (without the html extension).
browse	If TRUE the HTML report is opened in your browser once it's completed.
txdb	Specify the transcription database to use for identifying the closest genes via matchGenes. If NULL it will use TxDb.Hsapiens.UCSC.hg19.knownGene by default.
device	The graphical device used when knitting. See more at http://yihui.name/knitr/options (dev argument).
densityTemplates	A list of length 3 with templates for the p-value density plots (variables from pvalueVars), the continuous variables density plots (variables from densityVars), and Manhattan plots for the p-value variables (pvalueVars). These templates are processed by whisker.render. Check the default templates for more information. The densityTemplates argument is available for those users interested in customizing these plots. For example, to show histograms instead of density plots.
template	Template file to use for the report. If not provided, will use the default file found in regionExploration/regionExploration.Rmd within the package source.
...	Arguments passed to other methods and/or advanced arguments.

Format

```
chr "\n## {{{densityVarName}}}\n\n```{r density-{{{varName}}}, fig.width=10, fig.height=10, dev=devi
```

Value

An HTML report with a basic exploration for the given set of genomic regions.

Author(s)

Leonardo Collado-Torres

Examples

```
## Load derfinder for an example set of regions
library('derfinder')
regions <- genomeRegions$regions

## Assign chr length
library('GenomicRanges')
seqlengths(regions) <- c('chr21' = 48129895)

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

```
## Generate the HTML report
report <- renderReport(regions, 'Example run', pvalueVars = c(
    'Q-values' = 'qvalues', 'P-values' = 'pvalues'), densityVars = c(
    'Area' = 'area', 'Mean coverage' = 'meanCoverage'),
    significantVar = regions$qvalues <= 0.05, nBestRegions = 20,
    outdir = 'renderReport-example')

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

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

## End(Not run)

## Check the default templates. For users interested in customizing these
## plots.
## For p-value variables:
cat(templatePvalueDensity)

## For continous variables:
cat(templateDensity)

## For Manhattan plots
cat(templateManhattan)
```

`with_wd` *Temporarily evaluate an expression in a directory*

Description

Temporarily evaluate an expression in a directory, then set the directory back to the original.

Usage

```
with_wd(dir, expr)
```

Arguments

`dir`	a directory to perform an expression within
`expr`	expression to evaluate

Details

See here: http://plantarum.ca/code/setwd-part2/

Author(s)

Tyler Smith, contributed to regionReport by David Robinson https://github.com/dgrtwo

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