Package 'systemPipeRdata'

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Title systemPipeRdata: Workflow templates and sample data

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Description systemPipeRdata is a helper package to generate with a single command NGS workflow templates that are intended to be used by its parent package systemPipeR. The latter is an environment for building end-to-end analysis pipelines with automated report generation for next generation sequence (NGS) applications such as RNA-Seq, RIBO-Seq, ChIP-Seq, VAR-Seq and many others. Detailed examples for using systemPipeRdata are given in systemPipeR's overview vignette.

Imports methods, Biostrings, BiocGenerics, jsonlite, remotes

Suggests GenomicFeatures, GenomicRanges, IRanges, Rsamtools, ShortRead, rtracklayer, RUnit, BiocStyle, knitr, rmarkdown, systemPipeR

VignetteBuilder knitr

License Artistic-2.0

NeedsCompilation no

URL https://github.com/tgirke/systemPipeRdata, https://systempipe.org/

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R topics documented:

`availableWF` *List Available Workflows Templates at* `systemPipeRdata` *package*

Description

This function checks the workflow templates availability from `systemPipeRdata` package and also from systemPipeR Organization on GitHub.

Usage

```
availableWF(github = FALSE)
```

Arguments

`github`	logical. If `TRUE`, it will return current workflow templates available on `systemPipeR` Organization.

Details

Internally, this function uses the GitHub API, and there is an access limit per hour. For more details, please check: `system("curl -i https://api.github.com/users/<username>")`.

Value

Return a list with the names of the workflows templates availabe at `systemPipeRdata` package. If `github = TRUE`, it will return an addicional `data.frame` with current workflow templates available on `systemPipeR` Organization.

Note

We are assuming that workflow templates repositories under systemPipeR Organization content the keyword "Workflow Template" on the Description section and "Topics" section, we expected "systempiper" and "release" or "development" words.

Author(s)

Daniela Cassol

See Also

`genWorkenvir`.

Examples

```
availableWF()
## Not run:
## List Workflow Templates from \code{systemPipeR} Organization
availableWF(github = TRUE)

## End(Not run)
```

---

genWorkenvir *Generate workflow templates*

Description

Generates workflow templates for systemPipeR package. The template environemts contain a predifined directory structure along with run parameter files and sample data. The strucutre of the workflow templates and the sample data are described in all details in the Overview Vignette of the systemPipeR package.

Usage

```
genWorkenvir(workflow, mydirname=NULL, bam=FALSE, ref="master", subdir=NULL, url=NULL, urlname=NULL)
```

Arguments

workflow	character string of workflow templates to be generated. Supported values can be checked with the \link{availableWF}() function. Workflow name containing a '/' are treated as GitHub repositories and installed using BiocManager::\link{install_gi For Github workflow templates, the format systemPipeR/repo is required. See Details.
mydirname	Specifies the name of the workflow directory. The default NULL uses the name of the chosen workflow. An error is issued if a directory of the same name and path exists already.
bam	If bam=TRUE pregenerated short read alignment (BAM) files will be included in the results directory of the workflow environment. Note, these BAM files have been generated with the HISAT2 aligner using the FASTQ files provided in the data directory. The default bam=FALSE omits this step meaning no BAM files will be copied into the results directory.
ref	Desired GitHub reference for the branch name. Default to master branch.
subdir	subdirectory within GitHub repo that contains the R package, if it is required.
url	character string of a specifies the URL of a different version of the R Markdown workflow template or other file to download. The default NULL copies the current version available in the 'systemPipeRdata' or the workflow template on GitHub being selected.
urlname	character string with the name where the downloaded file is saved. This is argument is required when the url is provided.

Details

When installing GitHub Workflow Packages under systemPipeR Organization, it is requested to the remotes package function `BiocManager::\link{install_github}()` to build vignettes and also install all the dependencies, via `dependencies=TRUE`, `build_vignettes=TRUE`.

Check the output of `\link{availableWF}()` to the current workflow templates available on `systemPipeR` Organization. The argument

For an `interactive()` session, the `readline()` function provides the option choose between proceeding or not, through options: `yes` or `no`. For non-interactive use, if there is no package install, the option `yes` will be selected.

Value

Workflow directory containing sample data and parameter files along with the following subdirectories:

`param/`	stores parameter files
`data/`	stores input data
`results/`	stores output results

For more details, please consult the Overview Vignette (HTML) of the systemPipeR package (http://bioconductor.org/packages/systemPipeR).

Author(s)

Thomas Girke and Daniela Cassol

Examples

```
## Return location of sample data
samplepaths <- pathList()
## Not run:
## Generate varseq workflow environment
genWorkenvir(workflow="varseq", mydirname=NULL, url=NULL, urlname=NULL)
setwd("varseq")

## List Workflow Templates from \code{systemPipeRdata} package and \code{systemPipeR} Organization
availableWF(github = TRUE)
## Generate 'systemPipeR/systemPipeChIPseq' workflow environment
genWorkenvir(workflow="systemPipeR/systemPipeChIPseq", mydirname=NULL, ref="master", subdir=NULL)
setwd("systemPipeChIPseq")

## Download a specific R Markdown file
genWorkenvir(workflow="systemPipeR/systemPipeRNAseq", mydirname="rnaseq", url = "https://raw.githubusercontent.c

## End(Not run)
```

getSubsetReads *Subsetting fastq data*

Description

Returns subsets of fastq files data based on specific mapping regions or list of genes or GRanges object.

Usage

```
getSubsetReads(args,
  geneList = NULL,
  gr = NULL,
  MappingRegion = 1:1e+05,
  sample_range = 90000:1e+05,
  truncate_refs = TRUE,
  id_read_number = TRUE,
  annotation = "data/tair10.gff",
  reference = "data/tair10.fasta",
  annot_outname = "tair10_sub.gff",
  ref_outname = "tair10_sub.fasta",
  outdir = "data/subset/",
  silent = FALSE
)
```

Arguments

args	object of class SYSargs2.
geneList	selected genes list to retrieve the reads from the fastq file.
gr	an object containing genomic ranges to retrieve the reads from the fastq file.
MappingRegion	integers ranges of start and end of chromosome position to retrieve the reads from the fastq file.
sample_range	random range to subsetted the fastq file.
truncate_refs	logical. If TRUE it will generate reference genome and annotation subset file.
id_read_number	if fastq file contains sequence name with read number (`$ri - --defline-seq '@$sn[_$rn]/$ri'`).
annotation	path to annotation file.
reference	path to reference genome.
annot_outname	character name of the annotation output file.
ref_outname	character name of the reference genome output file.
outdir	path to output directory.
silent	if set to TRUE, all messages returned by the function will be suppressed.

Value

Workflow directory containing sample data and parameter files along with the following subdirectories:

`param/`	stores parameter files
`data/`	stores input data
`results/`	stores output results

For more details, please consult the Overview Vignette (HTML) of the systemPipeR package (http://bioconductor.org/packages/systemPipeR).

Author(s)

Thomas Girke, Shiyuan Guo and Daniela Cassol

Examples

```
## Not run:
getSubsetReads(args, MappingRegion = 1:900, sample_range = 800:900, outdir = "data/subset/", silent = FALSE)
getSubsetReads(args, MappingRegion = 1:900, sample_range = NULL, outdir = "data/subset/", silent = FALSE)

## End(Not run)
```

---

pathList *Return location of sample data*

Description

Function to return paths to sample data provided by `sytemPipeRdata` package.

Usage

```
pathList()
```

Value

`list`

Author(s)

Thomas Girke

Examples

```
samplepaths <- pathList()
```

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