

Package ‘systemPipeRdata’

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Title Sample data for workflows of systemPipeR package

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Description systemPipeRdata is a helper package to generate with a single command NGS workflow templates that are indented 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, ChIP-Seq, VAR-Seq and many others. Detailed examples for using systemPipeRdata are given in systemPipeR's overview vignette.

Depends methods

Imports BiocGenerics

Suggests RUnit, BiocStyle, knitr, rmarkdown, systemPipeR

VignetteBuilder knitr

License Artistic-2.0

NeedsCompilation no

URL <https://github.com/tgirke/systemPipeRdata>

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`genWorkenvir`*Generate workflow templates*

Description

Generates workflow templates for `systemPipeR` package. The template environments contain a predefined directory structure along with run parameter files and sample data. The structure of the workflow templates and the sample data are described in all details in the Overview Vignette of the `systemPipeR` package here: <http://bioconductor.org/packages/systemPipeR>.

Usage

```
genWorkenvir(workflow, mydirname=NULL)
```

Arguments

<code>workflow</code>	Can be assigned workflow type as character string. Supported values are: <code>rnaseq</code> , <code>vaseq</code> or <code>chipseq</code>
<code>mydirname</code>	Specifies the name of the workflow directory. The default <code>NULL</code> uses the name of the chosen workflow. An error is issued if a directory of the same name and path exists already.

Value

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

<code>param/</code>	stores parameter files
<code>data/</code>	stores input data
<code>results/</code>	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

Examples

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

## End(Not run)
```

<code>pathList</code>	<i>Return location of sample data</i>
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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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