# Package ‘systemPipeRdata’

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**Title** systemPipeRdata: NGS workflow templates and sample data

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**biocViews** Genetics, Infrastructure, DataImport, Sequencing, RNASeq, ChIPSeq, MethylSeq, SNP, GeneExpression, Coverage, GeneSetEnrichment, Alignment, QualityControl, ImmunoOncology

**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.

**Depends** methods

**Imports** BiocGenerics

**Suggests** RUnit, BiocStyle, knitr, rmarkdown, systemPipeR

**VignetteBuilder** knitr

**License** Artistic-2.0

**NeedsCompilation** no

**URL** `https://github.com/tgirke/systemPipeRdata`

**git_url** https://git.bioconductor.org/packages/systemPipeRdata

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## R topics documented:

## `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 here: http://bioconductor.org/packages/systemPipeR.

### Usage

```
genWorkenvir(workflow, mydirname=NULL, bam=FALSE, url=NULL, urlname=NULL)
```

### Arguments

| | |
|---|---|
| `workflow` | Can be assigned workflow type as character string. Supported values are: `rnaseq`, `riboseq`, `varseq` or `chipseq` |
| `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. |
| `url` | Specifies the location of a different version of the workflow template or other file to download. The default `NULL` copies the current version available in the ‘systemPipeRdata‘. Please check the available options [here](https://github.com/tgirke/systemPipeRdata/ |
| `urlname` | Specifies the name of the download file. The default `NULL` uses the name of the chosen workflow. An error is issued when the `url` is provided and only the default `urlname` is provided it. |

### 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

## 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")

## End(Not run)
```

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# `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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