

# *systemPipeRdata*: sample data for NGS workflows

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## 1 Introduction

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This package provides sample data for running the NGS workflows of the *systemPipeR* package (Girke, 2014). The source and usage of the data is described in the overview vignette [here](#).

## 2 Getting Started

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### 2.1 Installation

The R software for running *systemPipeR* and *systemPipeRdata* can be downloaded from CRAN (<http://cran.at.r-project.org/>). The *systemPipeR* environment can be installed from R using the `biocLite` install command.

```
source("http://bioconductor.org/biocLite.R") # Sources the biocLite.R installation script
biocLite("systemPipeR") # Installs systemPipeR from Bioconductor
biocLite("tgirke/systemPipeRdata", build_vignettes=TRUE, dependencies=TRUE) # From github
```

### 2.2 Generate workflow template

Load one of the available NGS workflows into your current working directory (here for varseq).

```
genWorkenvir(workflow="varseq")
setwd("varseq")
```

## 2.3 Run workflow

Next, run the chosen sample workflow by executing from command-line 'make -B' within 'varseq' directory. Alternatively, one can run the code from the provided \*.Rnw template file from within R interactively. Much more detailed information is provided in *systemPipeR*'s overview and workflow vignettes available [here](#).

## 3 Version Information

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```
toLatex(sessionInfo())
```

- R version 3.2.1 (2015-06-18), x86\_64-apple-darwin13.4.0
- Locale: en\_US.UTF-8/en\_US.UTF-8/en\_US.UTF-8/C/en\_US.UTF-8/en\_US.UTF-8
- Base packages: base, datasets, graphics, grDevices, methods, stats, utils
- Other packages: knitr 1.10.5
- Loaded via a namespace (and not attached): BiocStyle 1.7.4, evaluate 0.7, formatR 1.2, highr 0.5, magrittr 1.5, stringi 0.5-5, stringr 1.0.0, tools 3.2.1

## 4 Funding

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## 5 References

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Thomas Girke. systemPipeR: NGS workflow and report generation environment, 28 June 2014. URL <https://github.com/tgirke/systemPipeR>.