

# *systemPipeRdata*: sample data for NGS workflows

Thomas Girke

July 18, 2015

## Contents

---

<b>1</b>	<b>Introduction</b>	<b>1</b>
<b>2</b>	<b>Getting Started</b>	<b>1</b>
2.1	Installation . . . . .	1
2.2	Generate workflow template . . . . .	1
2.3	Run workflow . . . . .	2
<b>3</b>	<b>Version Information</b>	<b>2</b>
<b>4</b>	<b>Funding</b>	<b>2</b>
<b>5</b>	<b>References</b>	<b>2</b>

## 1 Introduction

---

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

---

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

The BioC 2015 vignette is available [here](#). It also can be opened with the following command.

```
vignette("systemPipeR_Presentation", package = "systemPipeRdata")
```

## 3 Version Information

---

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

- R version 3.2.1 (2015-06-18), x86\_64-pc-linux-gnu
- Locale: LC\_CTYPE=en\_US.UTF-8, LC\_NUMERIC=C, LC\_TIME=en\_US.UTF-8, LC\_COLLATE=en\_US.UTF-8, LC\_MONETARY=en\_US.UTF-8, LC\_MESSAGES=en\_US.UTF-8, LC\_PAPER=en\_US.UTF-8, LC\_NAME=C, LC\_ADDRESS=C, LC\_TELEPHONE=C, LC\_MEASUREMENT=en\_US.UTF-8, LC\_IDENTIFICATION=C
- 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

---

This project was supported by funds from the National Institutes of Health (NIH).

## 5 References

---

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