

*systemPipeR*data: sample data for NGS workflows

Thomas Girke

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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 `vaseq`).

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

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-unknown-linux-gnu
- Locale: LC_CTYPE=en_US.UTF-8, LC_NUMERIC=C, LC_TIME=en_US.UTF-8, LC_COLLATE=C, 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, grDevices, graphics, methods, parallel, stats, stats4, utils
- Other packages: Biobase 2.29.1, BiocGenerics 0.15.3, BiocParallel 1.3.34, BiocStyle 1.7.4, Biostrings 2.37.2, DBI 0.3.1, GenomInfoDb 1.5.8, GenomicAlignments 1.5.11, GenomicRanges 1.21.16, IRanges 2.3.14, RSQLite 1.0.0, Rsamtools 1.21.14, S4Vectors 0.7.10, ShortRead 1.27.5, SummarizedExperiment 0.3.2, XVector 0.9.1, ggplot2 1.0.1, knitr 1.10.5, systemPipeR 1.3.16, systemPipeRdata 0.99.2
- Loaded via a namespace (and not attached): AnnotationDbi 1.31.17, AnnotationForge 1.11.12, BBmisc 1.9, BatchJobs 1.6, Category 2.35.1, GO.db 3.1.2, GOstats 2.35.1, GSEABase 1.31.3, MASS 7.3-43, Matrix 1.2-2, RBGL 1.45.1, RColorBrewer 1.1-2, Rcpp 0.11.6, XML 3.98-1.3, annotate 1.47.1, base64enc 0.1-2, bitops 1.0-6, brew 1.0-6, checkmate 1.6.1, codetools 0.2-14, colorspace 1.2-6, crayon 1.3.1, digest 0.6.8, edgeR 3.11.2, evaluate 0.7, fail 1.2, formatR 1.2, futile.logger 1.4.1, futile.options 1.0.0, genefilter 1.51.0, graph 1.47.2, grid 3.2.1, gtable 0.1.2, highr 0.5, htmltools 0.2.6, hwriter 1.3.2, lambda.r 1.1.7, lattice 0.20-33, latticeExtra 0.6-26, limma 3.25.13, magrittr 1.5, memoise 0.2.1, munsell 0.4.2, pheatmap 1.0.7, plyr 1.8.3, proto 0.3-10, reshape2 1.4.1, rjson 0.2.15, rmarkdown 0.7, scales 0.2.5, sendmailR 1.2-1, splines 3.2.1, stringi 0.5-5, stringr 1.0.0, survival 2.38-3, testthat 0.10.0, tools 3.2.1, xtable 1.7-4, yaml 2.1.13, zlibbioc 1.15.0

4 Funding

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5 References

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