systemPipeR: pipeline to run command-line NGS software

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1 Introduction

systemPipeR is a pipeline for running command-line software, such as NGS aligners, on both single machines or compute clusters. It supports interactive job submissions or batch submissions to queuing systems of clusters (currently tested only with Torque) (Chen and Reynolds, 2002).

2 Getting Started

2.1 Installation

The R software can be downloaded from CRAN (`http://cran.at.r-project.org/`) and the *systemPipeR* package from GitHub (`https://github.com/tgirke/systemPipeR`). The *systemPipeR* package can be installed from R using the `install.packages` command after downloading and uncompressing the package directory.

```
> # $ R CMD build systemPipeR # Builds package
> install.packages("systemPipeR.1.0.0.tar.gz", repos=NULL, type="source") # Installs the package
```

2.2 Loading the Package and Documentation

```
> library("systemPipeR") # Loads the package

> library(help="systemPipeR") # Lists all functions and classes
> vignette("systemPipeR") # Opens this PDF manual from R
```

3 Version Information

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

- R version 3.0.2 (2013-09-25), `x86_64-unknown-linux-gnu`
- Locale: `C`
- Base packages: base, datasets, grDevices, graphics, methods, parallel, stats, utils
- Other packages: BiocGenerics 0.8.0, Biostrings 2.30.1, GenomicRanges 1.14.2, IRanges 1.20.1, Rsamtools 1.14.2, ShortRead 1.20.0, XVector 0.2.0, lattice 0.20-24, systemPipeR 1.0
- Loaded via a namespace (and not attached): Biobase 2.22.0, BiocStyle 1.0.0, RColorBrewer 1.0-5, bitops 1.0-6, grid 3.0.2, hwriter 1.3, latticeExtra 0.6-26, stats4 3.0.2, tools 3.0.2, zlibbioc 1.8.0

4 Funding

5   References

X. Chen and C.H. Reynolds. Performance of Similarity Measures in 2D Fragment-Based Similarity Searching: Comparison of Structural Descriptors and Similarity Coefficients. *Journal of Chemical Information and Computer Sciences*, 42(6): 1407–1414, 2002.