

Statistical analysis of RNA-Seq pseudocounts (Jaffe *et al.*)

Nima Hejazi

2016 Oct 31 (Mon), 14:44:23

Abstract

Basic description goes here...

Contents

I. Introduction	1
II. Methodology	1
III. Results	1
IV. Reproducibility Notice	2
V. References	3

I. Introduction

II. Methodology

III. Results

IV. Reproducibility Notice

What follows is the *session information* associated with the R session in which this report was compiled:

R version 3.3.1 (2016-06-21)

****Platform:**** x86_64-apple-darwin16.0.0 (64-bit)

locale: en_US.UTF-8|en_US.UTF-8|en_US.UTF-8|C|en_US.UTF-8|en_US.UTF-8

attached base packages: *stats*, *graphics*, *grDevices*, *utils*, *datasets*, *methods* and *base*

other attached packages: *pander*(v.0.6.0), *nima*(v.0.3.5), *tibble*(v.1.2), *devtools*(v.1.12.0), *ggplot2*(v.2.1.0), *dplyr*(v.0.5.0) and *colorout*(v.1.1-2)

loaded via a namespace (and not attached): *Rcpp*(v.0.12.7), *knitr*(v.1.14), *magrittr*(v.1.5), *splines*(v.3.3.1), *munSELL*(v.0.4.3), *colorspace*(v.1.2-7), *lattice*(v.0.20-34), *R6*(v.2.2.0), *stringr*(v.1.1.0), *plyr*(v.1.8.4), *tools*(v.3.3.1), *grid*(v.3.3.1), *gtable*(v.0.2.0), *DBI*(v.0.5-1), *withr*(v.1.0.2), *htmltools*(v.0.3.5), *ggthemes*(v.3.2.0), *yaml*(v.2.1.13), *survival*(v.2.39-5), *assertthat*(v.0.1), *digest*(v.0.6.10), *Matrix*(v.1.2-7.1), *gridExtra*(v.2.2.1), *formatR*(v.1.4), *memoise*(v.1.0.0), *evaluate*(v.0.10), *rmarkdown*(v.1.1), *stringi*(v.1.1.2) and *scales*(v.0.4.0)

V. References

- Law, Charity W., Yunshun Chen, Wei Shi, and Gordon K. Smyth. 2014. “Voom: Precision Weights Unlock Linear Model Analysis Tools for RNA-Seq Read Counts.” *Genome Biology* 15 (2): 1–17.
- Robles, José A, Sumaira E Qureshi, Stuart J Stephen, Susan R Wilson, Conrad J Burden, and Jennifer M Taylor. 2012. “Efficient Experimental Design and Analysis Strategies for the Detection of Differential Expression Using RNA-Sequencing.” *BMC Genomics* 13 (1). BioMed Central: 1.
- Smyth, Gordon K. 2004. “Linear Models and Empirical Bayes Methods for Assessing Differential Expression in Microarray Experiments.” *Statistical Applications in Genetics and Molecular Biology* 3 (1). bepress: Article-3.
- Soneson, Charlotte, and Mauro Delorenzi. 2013. “A Comparison of Methods for Differential Expression Analysis of RNA-Seq Data.” *BMC Bioinformatics* 14 (1). BioMed Central: 1.