

Journal of Statistical Software

MMMMMM YYYY, Volume VV, Issue II.

doi: 10.18637/jss.v000.i00

diffEnrich: An R Package to Compare Functional Enrichment Between Two Experimentally-derived Groups of Genes by Connecting to the KEGG REST API

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Abstract

Motivation: To aid in the biological interpretation of a list of candidate genes and proteins generated as part of omics studies, researchers quantitate the enrichment of known pathways or biological functions among the genes of interest. With the advent of new technologies and new experimental designs, it is often of interest to compare enrichment of a particular pathway between two gene lists (i.e., differential enrichment). Results: This package provides a number of functions that are intended to be used in a pipeline. Briefly, a function within the package will map species-specific ENTREZ gene IDs to their respective Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways by accessing the KEGG REST API. The KEGG API is used to guarantee the most up-todate pathway data from KEGG. Next, another function will identify significantly enriched pathways in two gene sets independently. The user can then identify pathways that are differentially enriched between the two gene sets using a third function. This package also provides a plotting function. Availability and implementation: diffEnrich is freely available on the Comprehensive R Archive Network (CRAN). Issues and bug reports can be submitted to the GitHub page https://github.com/SabaLab/diffEnrich/issues. Supplementary information: A step-by-step tutorial is provided on the diffEnrich GitHub page https://github.com/SabaLab/diffEnrich, and example data are included in the package.

Keywords: JSS, style guide, comma-separated, not capitalized, R.

1. Introduction: Count data regression in R

The introduction is in principle "as usual". However, it should usually embed both the implemented *methods* and the *software* into the respective relevant literature. For the latter both competing and complementary software should be discussed (within the same software environment and beyond), bringing out relative (dis)advantages. All software mentioned should be properly \cite{}d. (See also Appendix B for more details on BibTeX.)

For writing about software JSS requires authors to use the markup \proglang{} (programming languages and large programmable systems), \pkg{} (software packages), \code{} (functions, commands, arguments, etc.). If there is such markup in (sub)section titles (as above), a plain text version has to be provided in the LATEX command as well. Below we also illustrate how abbrevations should be introduced and citation commands can be employed. See the LATEX code for more details.

Modeling count variables is a common task in economics and the social sciences. The classical Poisson regression model for count data is often of limited use in these disciplines because empirical count data sets typically exhibit overdispersion and/or an excess number of zeros. The former issue can be addressed by extending the plain Poisson regression model in various directions: e.g., using sandwich covariances or estimating an additional dispersion parameter (in a so-called quasi-Poisson model). Another more formal way is to use a negative binomial (NB) regression. All of these models belong to the family of generalized linear models (GLMs). However, although these models typically can capture overdispersion rather well, they are in many applications not sufficient for modeling excess zeros. Since Mullahy (1986) there is increased interest in zero-augmented models that address this issue by a second model component capturing zero counts. An overview of count data models in econometrics, including hurdle and zero-inflated models, is provided in Cameron and Trivedi (2013).

In R (R Core Team 2017), GLMs are provided by the model fitting functions glm() in the stats package and glm.nb() in the MASS package (Venables and Ripley 2002, Chapter 7.4) along with associated methods for diagnostics and inference. The manuscript that this document is based on (Zeileis, Kleiber, and Jackman 2008) then introduced hurdle and zero-inflated count models in the functions hurdle() and zeroinfl() in the pscl package (Jackman 2015). Of course, much more software could be discussed here, including (but not limited to) generalized additive models for count data as available in the R packages mgcv Wood (2006), gamlss (Stasinopoulos and Rigby 2007), or VGAM (Yee 2010).

2. Models and software

The basic Poisson regression model for count data is a special case of the GLM framework McCullagh and Nelder (1989). It describes the dependence of a count response variable y_i (i = 1, ..., n) by assuming a Poisson distribution $y_i \sim \text{Pois}(\mu_i)$. The dependence of the conditional mean $\mathsf{E}[y_i \mid x_i] = \mu_i$ on the regressors x_i is then specified via a log link and a linear predictor

$$\log(\mu_i) = x_i^{\top} \beta, \tag{1}$$

where the regression coefficients β are estimated by maximum likelihood (ML) using the iterative weighted least squares (IWLS) algorithm.

Type	Distribution	Method	Description
GLM	Poisson	ML	Poisson regression: classical GLM, esti-
			mated by maximum likelihood (ML)
		Quasi	"Quasi-Poisson regression": same mean
			function, estimated by quasi-ML (QML)
			or equivalently generalized estimating equa-
			tions (GEE), inference adjustment via esti-
			mated dispersion parameter
		Adjusted	"Adjusted Poisson regression": same mean
			function, estimated by QML/GEE, inference
			adjustment via sandwich covariances
	NB	ML	NB regression: extended GLM, estimated by
			ML including additional shape parameter
Zero-augmented	Poisson	ML	Zero-inflated Poisson (ZIP), hurdle Poisson
	NB	ML	Zero-inflated NB (ZINB), hurdle NB

Table 1: Overview of various count regression models. The table is usually placed at the top of the page ([t!]), centered (centering), has a caption below the table, column headers and captions are in sentence style, and if possible vertical lines should be avoided.

Note that around the {equation} above there should be no spaces (avoided in the LATEX code by % lines) so that "normal" spacing is used and not a new paragraph started.

R provides a very flexible implementation of the general GLM framework in the function glm() (Chambers and Hastie 1992) in the stats package. Its most important arguments are

```
glm(formula, data, subset, na.action, weights, offset,
  family = gaussian, start = NULL, control = glm.control(...),
  model = TRUE, y = TRUE, x = FALSE, ...)
```

where formula plus data is the now standard way of specifying regression relationships in R/S introduced in Chambers and Hastie (1992). The remaining arguments in the first line (subset, na.action, weights, and offset) are also standard for setting up formula-based regression models in R/S. The arguments in the second line control aspects specific to GLMs while the arguments in the last line specify which components are returned in the fitted model object (of class 'glm' which inherits from 'lm'). For further arguments to glm() (including alternative specifications of starting values) see ?glm. For estimating a Poisson model family = poisson has to be specified.

As the synopsis above is a code listing that is not meant to be executed, one can use either the dedicated {Code} environment or a simple {verbatim} environment for this. Again, spaces before and after should be avoided.

Finally, there might be a reference to a {table} such as Table 1. Usually, these are placed at the top of the page ([t!]), centered (\centering), with a caption below the table, column headers and captions in sentence style, and if possible avoiding vertical lines.

3. Illustrations

For a simple illustration of basic Poisson and NB count regression the quine data from the MASS package is used. This provides the number of Days that children were absent from school in Australia in a particular year, along with several covariates that can be employed as regressors. The data can be loaded by

```
data("quine", package = "MASS")
```

and a basic frequency distribution of the response variable is displayed in Figure 1.

For code input and output, the style files provide dedicated environments. Either the "agnostic" {CodeInput} and {CodeOutput} can be used or, equivalently, the environments {Sinput} and {Soutput} as produced by Sweave() or knitr when using the render_sweave() hook. Please make sure that all code is properly spaced, e.g., using y = a + b * x and not y=a+b*x. Moreover, code input should use "the usual" command prompt in the respective software system. For R code, the prompt "R> " should be used with "+ " as the continuation prompt. Generally, comments within the code chunks should be avoided – and made in the regular LATEX text instead. Finally, empty lines before and after code input/output should be avoided (see above).

As a first model for the quine data, we fit the basic Poisson regression model. (Note that JSS prefers when the second line of code is indented by two spaces.)

```
m_pois <- glm(Days ~ (Eth + Sex + Age + Lrn)^2, data = quine,
family = poisson)</pre>
```

To account for potential overdispersion we also consider a negative binomial GLM.

```
library("MASS")
m_nbin <- glm.nb(Days ~ (Eth + Sex + Age + Lrn)^2, data = quine)</pre>
```

In a comparison with the BIC the latter model is clearly preferred.

Hence, the full summary of that model is shown below.

```
summary(m_nbin)

##
## Call:
```

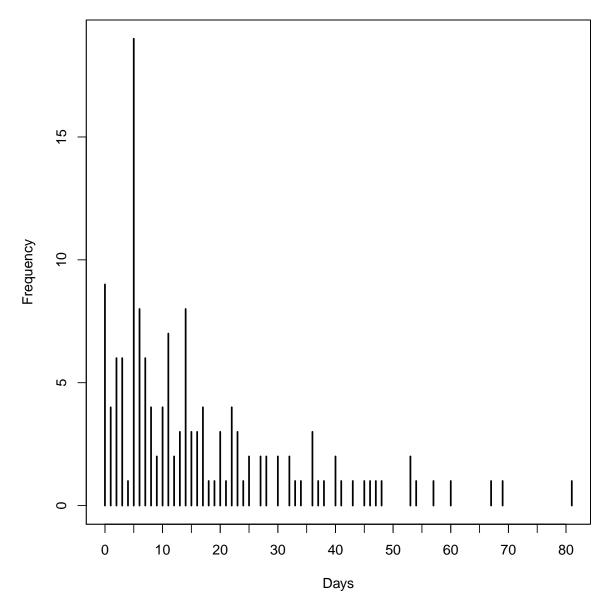


Figure 1: Frequency distribution for number of days absent from school.

```
## glm.nb(formula = Days ~ (Eth + Sex + Age + Lrn)^2, data = quine,
##
       init.theta = 1.60364105, link = log)
##
## Deviance Residuals:
                                   3Q
##
       Min
                 1Q
                      Median
                                           Max
  -3.0857 -0.8306 -0.2620
                               0.4282
                                        2.0898
##
##
## Coefficients: (1 not defined because of singularities)
              Estimate Std. Error z value Pr(>|z|)
## (Intercept) 3.00155
                           0.33709
                                   8.904 < 2e-16 ***
```

```
## EthN
       -0.24591 0.39135 -0.628 0.52977
## SexM
              -0.77181
                         0.38021 -2.030 0.04236 *
## AgeF1
              -0.02546
                         0.41615 -0.061 0.95121
## AgeF2
             -0.54884 0.54393 -1.009 0.31296
             -0.25735
## AgeF3
                         0.40558 -0.635 0.52574
## LrnSL
             ## EthN:SexM 0.36240 0.29430 1.231 0.21818
## EthN:AgeF1 -0.70000 0.43646 -1.604 0.10876
## EthN:AgeF2 -1.23283 0.42962 -2.870 0.00411 **
## EthN:AgeF3 0.04721 0.44883 0.105 0.91622
## EthN:LrnSL 0.06847 0.34040 0.201 0.84059
                       0.47360 0.048 0.96198
## SexM:AgeF1 0.02257
## SexM:AgeF2 1.55330 0.51325 3.026 0.00247 **
## SexM:AgeF3 1.25227 0.45539 2.750 0.00596 **
## SexM:LrnSL 0.07187 0.40805 0.176 0.86019
## AgeF1:LrnSL -0.43101
                       0.47948 -0.899 0.36870
                       0.48567 1.072 0.28363
## AgeF2:LrnSL 0.52074
## AgeF3:LrnSL
                              NA
                                    NA
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## (Dispersion parameter for Negative Binomial(1.6036) family taken to be 1)
##
      Null deviance: 235.23 on 145 degrees of freedom
##
## Residual deviance: 167.53 on 128 degrees of freedom
## AIC: 1100.5
##
## Number of Fisher Scoring iterations: 1
##
##
##
                Theta: 1.604
##
            Std. Err.: 0.214
##
## 2 x log-likelihood: -1062.546
```

4. Summary and discussion

As usual ...

Computational details

If necessary or useful, information about certain computational details such as version numbers, operating systems, or compilers could be included in an unnumbered section. Also, auxiliary packages (say, for visualizations, maps, tables, ...) that are not cited in the main text can be credited here.

The results in this paper were obtained using R 3.6.1 with the MASS 7.3.51.4 package. R itself and all packages used are available from the Comprehensive R Archive Network (CRAN) at https://CRAN.R-project.org/.

Acknowledgments

All acknowledgments (note the AE spelling) should be collected in this unnumbered section before the references. It may contain the usual information about funding and feedback from colleagues/reviewers/etc. Furthermore, information such as relative contributions of the authors may be added here (if any).

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A. More technical details

Appendices can be included after the bibliography (with a page break). Each section within the appendix should have a proper section title (rather than just Appendix).

For more technical style details, please check out JSS's style FAQ at https://www.jstatsoft.org/pages/view/style#frequently-asked-questions which includes the following topics:

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- Turning JSS manuscripts into R package vignettes.
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- Many other potentially helpful details...

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- JSS-specific markup (\proglang, \pkg, \code) should be used in the references.
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- Journal titles should not be abbreviated and in title case.
- DOIs should be included where available.
- Software should be properly cited as well. For R packages citation("pkgname") typically provides a good starting point.

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