



## 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-to-date 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:* differential enrichment, KEGG REST API, R.

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## 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 abbreviations 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  $y_i$  ( $i = 1, \dots, n$ ) by assuming a Poisson distribution  $y_i \sim \text{Pois}(\mu_i)$ . The dependence of the conditional mean  $E[y_i | x_i] = \mu_i$  on the regressors  $x_i$  is then specified via a log link and a linear predictor

$$\log(\mu_i) = x_i^\top \beta, \quad (1)$$

where the regression coefficients  $\beta$  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, estimated by maximum likelihood (ML)
		Quasi	“Quasi-Poisson regression”: same mean function, estimated by quasi-ML (QML) or equivalently generalized estimating equations (GEE), inference adjustment via estimated 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  $\text{\LaTeX}$  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  $\text{\LaTeX}$  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)
```

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)
```

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

```
BIC(m_pois, m_nbin)

##          df          BIC
## m_pois 18 2046.851
## m_nbin 19 1157.235
```

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

```
summary(m_nbin)

##
## Call:
```

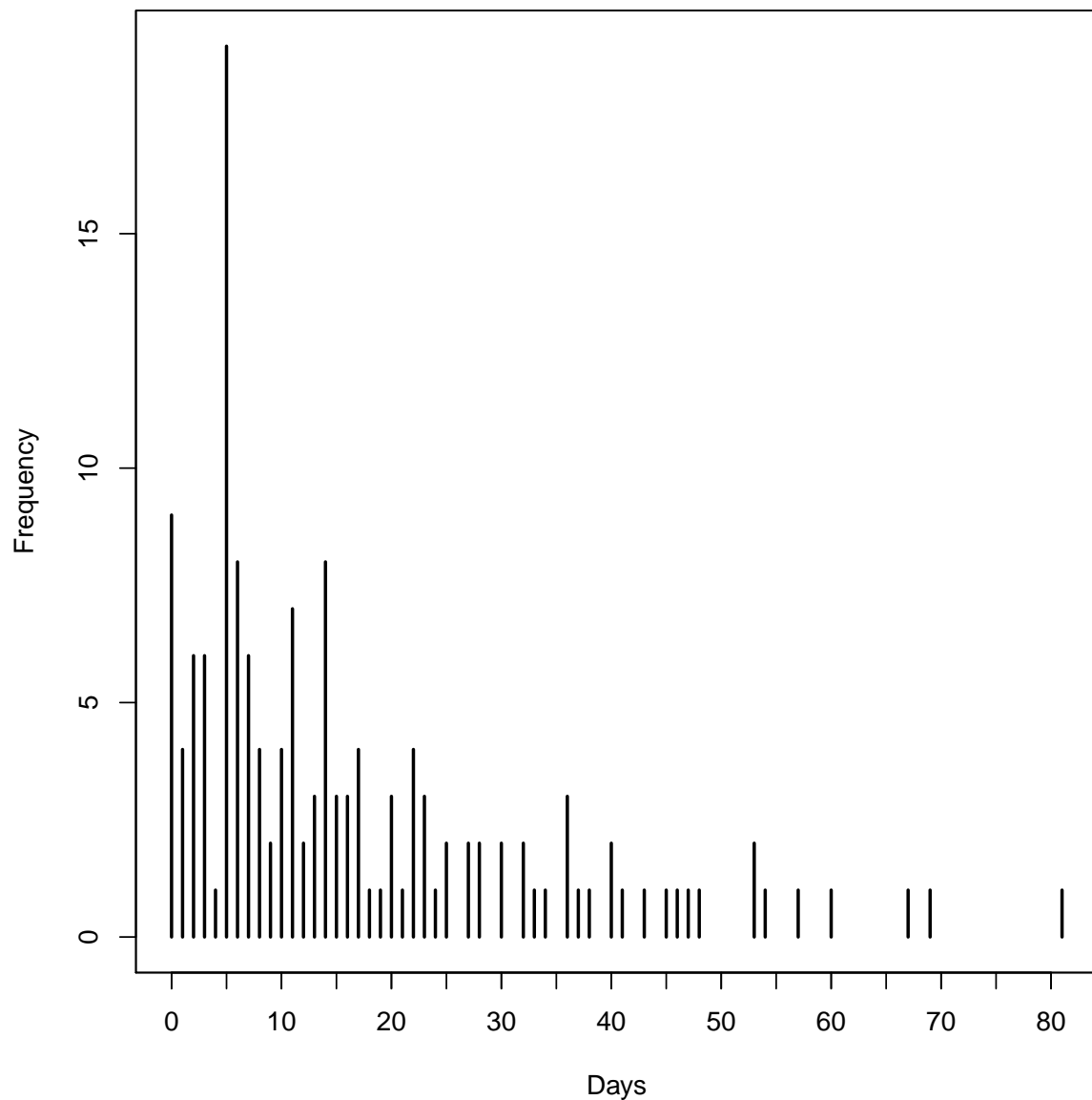


Figure 1: Frequency distribution for number of days absent from school.

```
## glm.nb(formula = Days ~ (Eth + Sex + Age + Lrn)^2, data = quine,
##       init.theta = 1.60364105, link = log)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      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
## AgeF3     -0.25735    0.40558   -0.635    0.52574
## LrnSL      0.38919    0.48421    0.804    0.42153
## 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
## SexM:AgeF1  0.02257    0.47360    0.048    0.96198
## 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
## AgeF2:LrnSL  0.52074    0.48567    1.072    0.28363
## AgeF3:LrnSL      NA          NA          NA          NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 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

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Cleaning up Bib<sub>T</sub><sub>E</sub>X files is a somewhat tedious task – especially when acquiring the entries automatically from mixed online sources. However, it is important that informations are complete and presented in a consistent style to avoid confusions. JSS requires the following format.

- JSS-specific markup (`\proglang`, `\pkg`, `\code`) should be used in the references.
- Titles should be in title case.
- 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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