

# Package ‘statmod’

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**Author** Gordon Smyth [cre, aut], Yifang Hu [ctb], Peter Dunn [ctb], Belinda Phipson [ctb], Yunshun Chen [ctb]

**Maintainer** Gordon Smyth <smyth@wehi.edu.au>

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**Imports** stats, graphics

**Suggests** MASS, tweedie

**Description** A collection of algorithms and functions to aid statistical modeling. Includes limiting dilution analysis (aka ELDA), growth curve comparisons, mixed linear models, heteroscedastic regression, inverse-Gaussian probability calculations, Gauss quadrature and a secure convergence algorithm for nonlinear models. Also includes a number of advanced generalized linear model functions including new Tweedie and Digamma glm families and a secure convergence algorithm.

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 statmod-package

*Introduction to the StatMod Package*


---

## Description

This package includes a variety of functions for numerical analysis and statistical modelling. The functions are briefly summarized by type of application below.

### Generalized Linear Models

The function [tweedie](#) defines a large class of generalized linear model families with power variance functions. It used in conjunction with the `glm` function, and widens the class of families that can be fitted.

[qresiduals](#) implements randomized quantile residuals for generalized linear models.

The functions `canonic.digamma`, `unitdeviance.digamma`, `varfun.digamma`, `cumulant.digamma`, `d2cumulant.digamma`, `meanval.digamma` and `logmdigamma` are used to fit double-generalized models, in which a link-linear model is fitted to the dispersion as well as to the mean. Specifically they are used to fit the dispersion submodel associated with a gamma glm.

### Growth Curves

[compareGrowthCurves](#), `compareTwoGrowthCurves` and `meanT` are functions to test for differences between growth curves with repeated measurements on subjects.

### Limiting Dilution Analysis

The `limdil` function is used in the analysis of stem cell frequencies. It implements limiting dilution analysis using complementary log-log binomial generalized linear model regression, with some improvements on previous programs.

### Probability Distributions

The functions `qinvgauss`, `dinvgauss`, `pinvgauss` and `rinvgauss` provide probability calculations for the inverse Gaussian distribution.

`gauss.quad` and `gauss.quad.prob` compute Gaussian Quadrature with probability distributions.

### Tests

`hommel.test` performs Hommel's multiple comparison tests.

`power.fisher.test` computes the power of Fisher's Exact Test for comparing proportions.

`sage.test` is a fast approximation to Fisher's exact test for each tag for comparing two Serial Analysis of Gene Expression (SAGE) libraries.

`permp` computes p-values for permutation tests when the permutations are randomly drawn.

### Variance Models

`mixedModel2`, `mixedModel2Fit` and `glmGam.fit` fit mixed linear models.

`remlscore` and `remlscoregamma` fit heteroscedastic and varying dispersion models by REML. `welding` is an example data set.

### Matrix Computations

`matvec` and `vecmat` facilitate multiplying matrices by vectors.

### Author(s)

Gordon Smyth

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Digamma

*Digamma generalized linear model family*

---

### Description

Produces a Digamma generalized linear model family object. The Digamma distribution is the distribution of the unit deviance for a gamma response.

**Usage**

```

Digamma(link = "log")
unitdeviance.digamma(y, mu)
cumulant.digamma(theta)
meanval.digamma(theta)
d2cumulant.digamma(theta)
varfun.digamma(mu)
canonic.digamma(mu)

```

**Arguments**

link	character string, number or expressing specifying the link function. See quasi for specification of this argument.
y	numeric vector of (positive) response values
mu	numeric vector of (positive) fitted values
theta	numeric vector of values of the canonical variable, equal to $-1/\phi$ where $\phi$ is the dispersion parameter of the gamma distribution

**Details**

This family is useful for dispersion modelling with gamma generalized linear models. The Digamma distribution describes the distribution of the unit deviances for a gamma family, in the same way that the gamma distribution itself describes the distribution of the unit deviances for Gaussian or inverse Gaussian families. The Digamma distribution is so named because it is dual to the gamma distribution in the above sense, and because the digamma function appears in its mean function.

Suppose that  $y$  follows a gamma distribution with mean  $\mu$  and dispersion parameter  $\phi$ , so the variance of  $y$  is  $\phi\mu^2$ . Write  $d(y, \mu)$  for the gamma distribution unit deviance. Then `meanval.digamma(-1/phi)` gives the mean of  $d(y, \mu)$  and `2*d2cumulant.digamma(-1/phi)` gives the variance.

**Value**

Digamma produces a glm family object, which is a list of functions and expressions used by glm in its iteratively reweighted least-squares algorithm. See `family` for details.

The other functions take vector arguments and produce vector values of the same length and called by Digamma. `unitdeviance.digamma` gives the unit deviances of the family, equal to the squared deviance residuals. `cumulant.digamma` is the cumulant function. If the dispersion is unity, then successive derivatives of the cumulant function give successive cumulants of the Digamma distribution. `meanvalue.digamma` gives the first derivative, which is the expected value. `d2cumulant.digamma` gives the second derivative, which is the variance. `canonic.digamma` is the inverse of `meanvalue.digamma` and gives the canonical parameter as a function of the mean parameter. `varfun.digamma` is the variance function of the Digamma family, the variance as a function of the mean.

**Author(s)**

Gordon Smyth

**References**

Smyth, G. K. (1989). Generalized linear models with varying dispersion. *J. R. Statist. Soc. B*, **51**, 47-61.

**See Also**

[quasi](#), [make.link](#)

**Examples**

```
# Test for log-linear dispersion trend in gamma regression
y <- rchisq(20,df=1)
x <- 1:20
out.gam <- glm(y~x,family=Gamma(link="log"))
d <- residuals(out.gam)^2
out.dig <- glm(d~x,family=Digamma(link="log"))
summary(out.dig,dispersion=2)
```

---

 elda

*Extreme Limiting Dilution Analysis*


---

**Description**

Fit single-hit model to a dilution series using complementary log-log binomial regression.

**Usage**

```
elda(response, dose, tested=rep(1,length(response)), group=rep(1,length(response)),
      observed=FALSE, confidence=0.95, test.unit.slope=FALSE)
limdil(response, dose, tested=rep(1,length(response)), group=rep(1,length(response)),
        observed=FALSE, confidence=0.95, test.unit.slope=FALSE)
eldaOneGroup(response, dose, tested, observed=FALSE, confidence=0.95,
              tol=1e-8, maxit=100, trace=FALSE)
```

**Arguments**

response	numeric vector giving number of positive cases out of tested trials. Should take non-negative integer values.
dose	numeric vector of expected number of cells in assay. Values must be positive.
tested	numeric vector giving number of trials at each dose. Should take integer values.
group	vector or factor giving group to which the response belongs.
observed	logical, is the actual number of cells observed?
confidence	numeric level for confidence interval. Should be strictly between 0 and 1.
test.unit.slope	logical, should the adequacy of the single-hit model be tested?
tol	convergence tolerance.
maxit	maximum number of Newton iterations to perform.
trace	logical, if TRUE then iterim results are output at each iteration.

## Details

elda and limdil are alternative names for the same function. (limdil was the older name before the 2009 paper by Hu and Smyth.) eldaOneGroup is a lower-level function that does the computations when there is just one group, using a globally convergent Newton iteration. It is called by the other functions.

These functions implement maximum likelihood analysis of limiting dilution data using methods proposed by Hu and Smyth (2009). The functions gracefully accommodate situations where 0% or 100% of the assays give positive results, which is why we call it "extreme" limiting dilution analysis. The functions provide the ability to test for differences in stem cell frequencies between groups, and to test goodness of fit in a number of ways. The methodology has been applied to the analysis of stem cell assays (Shackleton et al, 2006).

The statistical method is explained by Hu and Smyth (2009). A binomial generalized linear model is fitted for each group with cloglog link and offset  $\log(\text{dose})$ . If `observed=FALSE`, a classic Poisson single-hit model is assumed, and the Poisson frequency of the stem cells is the exp of the intercept. If `observed=TRUE`, the values of dose are treated as actual cell numbers rather than expected values. This doesn't change the generalized linear model fit, but it does change how the frequencies are extracted from the estimated model coefficient (Hu and Smyth, 2009).

The confidence interval is a Wald confidence interval, unless the responses are all negative or all positive, in which case Clopper-Pearson intervals are computed.

If `group` takes several values, then separate confidence intervals are computed for each group. In this case a likelihood ratio test is conducted for differences in active cell frequencies between the groups.

These functions compute a number of different tests of goodness of fit. One test is based on the coefficient for  $\log(\text{dose})$  in the generalized linear model. The nominal slope is 1. A slope greater than one suggests a multi-hit model in which two or more cells are synergistically required to produce a positive response. A slope less than 1 suggests some sort of cell interference. Slopes less than 1 can also be due to heterogeneity of the stem cell frequency between assays. elda conducts likelihood ratio and score tests that the slope is equal to one.

Another test is based on the coefficient for dose. This idea is motivated by a suggestion of Gart and Weiss (1967), who suggest that heterogeneity effects are more likely to be linear in dose than  $\log(\text{dose})$ . These functions conducts score tests that the coefficient for dose is non-zero. Negative values for this test suggest heterogeneity.

These functions produce objects of class "limdil". There are `print` and `plot` methods for "limdil" objects.

## Value

elda and limdil produce an object of class "limdil". This is a list with the following components:

CI	numeric matrix giving estimated stem cell frequency and lower and upper limits of Wald confidence interval for each group
test.difference	numeric vector giving chisquare likelihood ratio test statistic and p-value for testing the difference between groups
test.slope.wald	numeric vector giving wald test statistics and p-value for testing the slope of the offset equal to one

test.slope.lr    numeric vector giving chisquare likelihood ratio test statistics and p-value for testing the slope of the offset equal to one

test.slope.score.logdose  
                  numeric vector giving score test statistics and p-value for testing multi-hit alternatives

test.slope.score.dose  
                  numeric vector giving score test statistics and p-value for testing heterogeneity

response        numeric of integer counts of positive cases, out of tested trials

tested          numeric vector giving number of trials at each dose

dose            numeric vector of expected number of cells in assay

group          vector or factor giving group to which the response belongs

num.group      number of groups

### Author(s)

Yifang Hu and Gordon Smyth

### References

Hu, Y, and Smyth, GK (2009). ELDA: Extreme limiting dilution analysis for comparing depleted and enriched populations in stem cell and other assays. *Journal of Immunological Methods* 347, 70-78. <http://dx.doi.org/10.1016/j.jim.2009.06.008> <http://www.statsci.org/smyth/pubs/ELDApreprint.pdf>

Shackleton, M., Vaillant, F., Simpson, K. J., Stingl, J., Smyth, G. K., Asselin-Labat, M.-L., Wu, L., Lindeman, G. J., and Visvader, J. E. (2006). Generation of a functional mammary gland from a single stem cell. *Nature* 439, 84-88. <http://www.nature.com/nature/journal/v439/n7072/abs/nature04372.html>

Gart, JJ, and Weiss, GH (1967). Graphically oriented tests for host variability in dilution experiments. *Biometrics* 23, 269-284.

### See Also

[plot.limdil](#) and [print.limdil](#) are methods for `limdil` class objects.

A webpage interface to this function is available at <http://bioinf.wehi.edu.au/software/elda>.

### Examples

```
# When there is one group
Dose <- c(50,100,200,400,800)
Responses <- c(2,6,9,15,21)
Tested <- c(24,24,24,24,24)
out <- elda(Responses,Dose,Tested,test.unit.slope=TRUE)
out
plot(out)

# When there are four groups
```

```
Dose <- c(30000,20000,4000,500,30000,20000,4000,500,30000,20000,4000,500,30000,20000,4000,500)
Responses <- c(2,3,2,1,6,5,6,1,2,3,4,2,6,6,6,1)
Tested <- c(6,6,6,6,6,6,6,6,6,6,6,6,6,6,6,6)
Group <- c(1,1,1,1,2,2,2,2,3,3,3,3,4,4,4,4)
elda(Responses,Dose,Tested,Group,test.unit.slope=TRUE)
```

---

fitNBP	<i>Negative Binomial Model for SAGE Libraries with Pearson Estimation of Dispersion</i>
--------	---

---

### Description

Fit a multi-group negative-binomial model to SAGE data, with Pearson estimation of the common overdispersion parameter.

### Usage

```
fitNBP(y, group=NULL, lib.size=colSums(y), tol=1e-5, maxit=40, verbose=FALSE)
```

### Arguments

y	numeric matrix giving counts. Rows correspond to tags (genes) and columns to SAGE libraries.
group	factor indicating which library belongs to each group. If NULL then one group is assumed.
lib.size	vector giving total number of tags in each library.
tol	small positive numeric tolerance to judge convergence
maxit	maximum number of iterations permitted
verbose	logical, if TRUE then iteration progress information is output.

### Details

The overdispersion parameter is estimated equating the Pearson goodness of fit to its expectation. The variance is assumed to be of the form  $\text{Var}(y)=\mu*(1+\phi*\mu)$  where  $E(y)=\mu$  and  $\phi$  is the dispersion parameter. All tags are assumed to share the same dispersion.

For given dispersion, the model for each tag is a negative-binomial generalized linear model with log-link and  $\log(\text{lib.size})$  as offset. The coefficient parametrization used is that corresponding to the formula  $\sim 0 + \text{group} + \text{offset}(\log(\text{lib.size}))$ .

Except for the dispersion being common rather than genewise, the model fitted by this function is equivalent to that proposed by Lu et al (2005). The numeric algorithm used is that of alternating iterations (Smyth, 1996) using Newton's method as the outer iteration for the dispersion parameter starting at  $\phi=0$ . This iteration is monotonically convergent for the dispersion.



**Value**

List with components

coefficients    numeric matrix of rates for each tag (gene) and each group  
fitted.values    numeric matrix of fitted values  
dispersion      estimated dispersion parameter

**Note**

This function has been made obsolete by the edgeR package on Bioconductor, see <https://bioconductor.org/packages/edgeR>.

**Author(s)**

Gordon Smyth

**References**

Lu, J, Tomfohr, JK, Kepler, TB (2005). Identifying differential expression in multiple SAGE libraries: an overdispersed log-linear model approach. *BMC Bioinformatics* 6,165.

Smyth, G. K. (1996). Partitioned algorithms for maximum likelihood and other nonlinear estimation. *Statistics and Computing*, 6, 201-216.

**See Also**

[sage.test](#)

The edgeR package on Bioconductor provides new and better functions to fit negative-binomial GLMs to SAGE or RNA-seq data. See particularly the `glmFit` and `mglmOneWay` functions.

**Examples**

```
# True value for dispersion is 1/size=2/3
# Note the Pearson method tends to under-estimate the dispersion
y <- matrix(rnbinom(10*4,mu=4,size=1.5),10,4)
lib.size <- rep(50000,4)
group <- c(1,1,2,2)
fit <- fitNBP(y,group=group,lib.size=lib.size)
logratio <- fit$coef %*% c(-1,1)
```

---

forward

*Forward Selection of Covariates for Multiple Regression*

---

### Description

Fit a multi-group negative-binomial model to SAGE data, with Pearson estimation of the common overdispersion parameter.

### Usage

```
forward(y, x, xkept=NULL, intercept=TRUE, nvar=ncol(x))
```

### Arguments

y	numeric response vector.
x	numeric matrix of covariates, candidates to be added to the regression.
xkept	numeric matrix of covariates to be included in the starting regression.
intercept	logical, should an intercept be added to xkept?
nvar	integer, number of covariates from x to add to the regression.

### Details

This function has the advantage that x can have many more columns than the length of y.

### Value

Integer vector of length nvar, giving the order in which columns of x are added to the regression.

### Author(s)

Gordon Smyth

### See Also

[step](#)

### Examples

```
y <- rnorm(10)
x <- matrix(rnorm(10*5), 10, 5)
forward(y, x)
```

---

gauss.quad	<i>Gaussian Quadrature</i>
------------	----------------------------

---

**Description**

Calculate nodes and weights for Gaussian quadrature.

**Usage**

```
gauss.quad(n,kind="legendre",alpha=0,beta=0)
```

**Arguments**

n	number of nodes and weights
kind	kind of Gaussian quadrature, one of "legendre", "chebyshev1", "chebyshev2", "hermite", "jacobi" or "laguerre"
alpha	parameter for Jacobi or Laguerre quadrature, must be greater than -1
beta	parameter for Jacobi quadrature, must be greater than -1

**Details**

The integral from a to b of  $w(x)*f(x)$  is approximated by  $\sum(w*f(x))$  where x is the vector of nodes and w is the vector of weights. The approximation is exact if  $f(x)$  is a polynomial of order no more than  $2n-1$ . The possible choices for  $w(x)$ , a and b are as follows:

Legendre quadrature:  $w(x)=1$  on  $(-1, 1)$ .

Chebyshev quadrature of the 1st kind:  $w(x)=1/\sqrt{1-x^2}$  on  $(-1, 1)$ .

Chebyshev quadrature of the 2nd kind:  $w(x)=\sqrt{1-x^2}$  on  $(-1, 1)$ .

Hermite quadrature:  $w(x)=\exp(-x^2)$  on  $(-\text{Inf}, \text{Inf})$ .

Jacobi quadrature:  $w(x)=(1-x)^\alpha(1+x)^\beta$  on  $(-1, 1)$ . Note that Chebyshev quadrature is a special case of this.

Laguerre quadrature:  $w(x)=x^\alpha\exp(-x)$  on  $(0, \text{Inf})$ .

The algorithm used to generate the nodes and weights is explained in Golub and Welsch (1969).

**Value**

A list containing the components

nodes	vector of values at which to evaluate the function
weights	vector of weights to give the function values

**Author(s)**

Gordon Smyth, using Netlib Fortran code <http://www.netlib.org/go/gaussq.f>, and including a suggestion from Stephane Laurent

## References

- Golub, G. H., and Welsch, J. H. (1969). Calculation of Gaussian quadrature rules. *Mathematics of Computation* **23**, 221-230.
- Golub, G. H. (1973). Some modified matrix eigenvalue problems. *Siam Review* **15**, 318-334.
- Smyth, G. K. (1998). Numerical integration. In: *Encyclopedia of Biostatistics*, P. Armitage and T. Colton (eds.), Wiley, London, pages 3088-3095. <http://www.statsci.org/smyth/pubs/NumericalIntegration-Preprint.pdf>
- Smyth, G. K. (1998). Polynomial approximation. In: *Encyclopedia of Biostatistics*, P. Armitage and T. Colton (eds.), Wiley, London, pages 3425-3429. <http://www.statsci.org/smyth/pubs/PolyApprox-Preprint.pdf>
- Stroud, AH, and Secrest, D (1966). *Gaussian Quadrature Formulas*. Prentice-Hall, Englewood Cliffs, N.J.

## See Also

[gauss.quad.prob](#), [integrate](#)

## Examples

```
# mean of gamma distribution with alpha=6
out <- gauss.quad(10,"laguerre",alpha=5)
sum(out$weights * out$nodes) / gamma(6)
```

---

gauss.quad.prob

*Gaussian Quadrature with Probability Distributions*

---

## Description

Calculate nodes and weights for Gaussian quadrature in terms of probability distributions.

## Usage

```
gauss.quad.prob(n,dist="uniform",l=0,u=1,mu=0,sigma=1,alpha=1,beta=1)
```

## Arguments

n	number of nodes and weights
dist	distribution that Gaussian quadrature is based on, one of "uniform", "normal", "beta" or "gamma"
l	lower limit of uniform distribution
u	upper limit of uniform distribution
mu	mean of normal distribution
sigma	standard deviation of normal distribution
alpha	positive shape parameter for gamma distribution or first shape parameter for beta distribution
beta	positive scale parameter for gamma distribution or second shape parameter for beta distribution

**Details**

This is a rewriting and simplification of `gauss.quad` in terms of probability distributions. The probability interpretation is explained by Smyth (1998). For details on the underlying quadrature rules, see [gauss.quad](#).

The expected value of  $f(X)$  is approximated by  $\sum(w*f(x))$  where  $x$  is the vector of nodes and  $w$  is the vector of weights. The approximation is exact if  $f(x)$  is a polynomial of order no more than  $2n-1$ . The possible choices for the distribution of  $X$  are as follows:

Uniform on  $(1, u)$ .

Normal with mean  $\mu$  and standard deviation  $\sigma$ .

Beta with density  $x^{(\alpha-1)}*(1-x)^{(\beta-1)}/B(\alpha, \beta)$  on  $(0, 1)$ .

Gamma with density  $x^{(\alpha-1)}*exp(-x/\beta)/\beta^\alpha/\text{gamma}(\alpha)$ .

**Value**

A list containing the components

nodes	vector of values at which to evaluate the function
weights	vector of weights to give the function values

**Author(s)**

Gordon Smyth, using Netlib Fortran code <http://www.netlib.org/go/gaussq.f>, and including corrections suggested by Spencer Graves

**References**

Smyth, G. K. (1998). Polynomial approximation. In: *Encyclopedia of Biostatistics*, P. Armitage and T. Colton (eds.), Wiley, London, pages 3425-3429. <http://www.statsci.org/smyth/pubs/PolyApprox-Preprint.pdf>

**See Also**

[gauss.quad](#), [integrate](#)

**Examples**

```
# the 4th moment of the standard normal is 3
out <- gauss.quad.prob(10, "normal")
sum(out$weights * out$nodes^4)

# the expected value of log(X) where X is gamma is digamma(alpha)
out <- gauss.quad.prob(32, "gamma", alpha=5)
sum(out$weights * log(out$nodes))
```

---

 glm.scoretest

*Score Test for Adding a Covariate to a GLM*


---

### Description

Computes score test statistics (z-statistics) for adding covariates to a generalized linear model.

### Usage

```
glm.scoretest(fit, x2, dispersion=NULL)
```

### Arguments

fit	generalized linear model fit object, of class <code>glm</code> .
x2	vector or matrix with each column a covariate to be added.
dispersion	the dispersion for the generalized linear model family.

### Details

Rao's score test is a type of asymptotic test that is an alternative to Wald tests or likelihood ratio tests (LRTs) (Dunn and Smyth, 2018). Wald tests are computed by dividing parameter estimates by their standard errors. LRTs are computed from differences in the log-likelihoods between the null and alternative hypotheses. Score tests are computed from log-likelihood derivatives. All three types of tests (Wald, score and LRT) are asymptotically equivalent under ideal circumstances, but the score and LRT tests are invariant under-reparametrization whereas Wald tests are not.

One of the main differences between the tests is the need for estimation of parameters under the null and alternative hypotheses. Wald tests require maximum likelihood estimates (MLEs) to be computed only under the alternative hypothesis, LRT tests require both the null and alternative models to be fitted, while score tests require only the null hypothesis to be fitted.

When a generalized linear model (GLM) is fitted in R using the `glm` function, the `summary()` function presents Wald tests for all the coefficients in the linear model while `anova()` is able to compute likelihood ratio tests. GLM output in R has historically not included score tests, although score tests can be a very computationally coefficient choice when one wants to test for many potential additional covariates being added to a relatively simple null model.

A number of well known Pearson chisquare statistics, including goodness of fit statistics and the Pearson test for independence in a contingency table can be derived as score tests (Smyth, 2003; Dunn and Smyth, 2018).

This function computes score test statistics for adding a single numerical covariate to a GLM, given the `glm` output for the null model. It makes very efficient use of the quantities already stored in the GLM fit object. A computational formula for the score test statistics is given in Section 7.2.6 of Dunn and Smyth (2018).

The dispersion parameter is treated as for `summary.glm`. If `NULL`, the Pearson estimator is used, except for the binomial, Poisson and negative binomial families, for which the dispersion is one.

Note that the `anova.glm` function in the stats package has offered a Rao score test option since 2011, but it requires model fits under the alternative as well as the null hypothesis, which does not

take advantage of the computational advantage of score test. The `glm.scoretest` is more efficient as it does not require a full model fit. On the other hand, `anova.glm` can compute score tests for factors and multiple covariates, which `glm.scoretest` does not currently do.

### Value

numeric vector containing the z-statistics, one for each covariate. The z-statistics can be treated as standard normal under the null hypothesis.

### Author(s)

Gordon Smyth

### References

- Dunn, PK, and Smyth, GK (2018). *Generalized linear models with examples in R*. Springer, New York, NY. <https://doi.org/10.1007/978-1-4419-0118-7>
- Lovison, G (2005). On Rao score and Pearson  $X^2$  statistics in generalized linear models. *Statistical Papers*, 46, 555-574.
- Pregibon, D (1982). Score tests in GLIM with applications. In *GLIM82: Proceedings of the International Conference on Generalized Linear Models*, R Gilchrist (ed.), Lecture Notes in Statistics, Volume 14, Springer, New York, pages 87-97.
- Smyth, G. K. (2003). Pearson's goodness of fit statistic as a score test statistic. In: *Science and Statistics: A Festschrift for Terry Speed*, D. R. Goldstein (ed.), IMS Lecture Notes - Monograph Series, Volume 40, Institute of Mathematical Statistics, Beachwood, Ohio, pages 115-126. <http://www.statsci.org/smyth/pubs/goodness.pdf>

### See Also

[glm](#), [add1](#), [anova.glm](#)

### Examples

```
# Pearson's chisquare test for independence
# in a contingency table is a score test.

# First the usual test

y <- c(20,40,40,30)
chisq.test(matrix(y,2,2), correct=FALSE)

# Now same test using glm.scoretest

a <- gl(2,1,4)
b <- gl(2,2,4)
fit <- glm(y~a+b, family=poisson)
x2 <- c(0,0,0,1)
z <- glm.scoretest(fit, x2)
z^2
```

---

glmGamFit	<i>Fit Gamma Generalized Linear Model by Fisher Scoring with Identity Link</i>
-----------	--

---

### Description

Fit a generalized linear model with secure convergence.

### Usage

```
glmGamFit(X, y, coef.start = NULL, tol = 1e-6, maxit = 50, trace = FALSE)
```

### Arguments

X	design matrix, assumed to be of full column rank. Missing values not allowed.
y	numeric vector of responses. Negative or missing values not allowed.
coef.start	numeric vector of starting values for the regression coefficients
tol	small positive numeric value giving convergence tolerance
maxit	maximum number of iterations allowed
trace	logical value. If TRUE then output diagnostic information at each iteration.

### Details

This function implements a modified Fisher scoring algorithm for generalized linear models, similar to the Levenberg-Marquardt algorithm for nonlinear least squares. The Levenberg-Marquardt modification checks for a reduction in the deviance at each step, and avoids the possibility of divergence. The result is a very secure algorithm that converges for almost all datasets.

glmGamFit is in principle equivalent to `glm.fit(X, y, family=Gamma(link="identity"))` but with much more secure convergence.

### Value

List with the following components:

coefficients	numeric vector of regression coefficients
fitted	numeric vector of fitted values
deviance	residual deviance
iter	number of iterations used to convergence. If convergence was not achieved then iter is set to maxit+1.

### Author(s)

Gordon Smyth and Yunshun Chen



## References

Dunn, PK, and Smyth, GK (2018). *Generalized linear models with examples in R*. Springer, New York, NY. <https://doi.org/10.1007/978-1-4419-0118-7>

## See Also

glnGam.fit is called by [mixedModel2Fit](#).

[glm](#) is the standard glm fitting function in the stats package.

## Examples

```
y <- rgamma(10, shape=5)
X <- cbind(1, 1:10)
fit <- glnGam.fit(X, y, trace=TRUE)
```

---

glmnb.fit

*Fit Negative Binomial Generalized Linear Model with Log-Link*


---

## Description

Fit a generalized linear model with secure convergence.

## Usage

```
glmnb.fit(X, y, dispersion, weights = NULL, offset = 0, coef.start = NULL,
          start.method = "mean", tol = 1e-6, maxit = 50L, trace = FALSE)
```

## Arguments

X	design matrix, assumed to be of full column rank. Missing values not allowed.
y	numeric vector of responses. Negative or missing values not allowed.
dispersion	numeric vector of dispersion parameters for the negative binomial distribution. If of length 1, then the same dispersion is assumed for all observations.
weights	numeric vector of positive weights, defaults to all one.
offset	offset vector for linear model
coef.start	numeric vector of starting values for the regression coefficients
start.method	method used to find starting values, possible values are "mean" or "log(y)"
tol	small positive numeric value giving convergence tolerance
maxit	maximum number of iterations allowed
trace	logical value. If TRUE then output diagnostic information at each iteration.

**Details**

This function implements a modified Fisher scoring algorithm for generalized linear models, analogous to the Levenberg-Marquardt algorithm for nonlinear least squares. The Levenberg-Marquardt modification checks for a reduction in the deviance at each step, and avoids the possibility of divergence. The result is a very secure algorithm that converges for almost all datasets.

`glmnb.fit` is in principle equivalent to `glm.fit(X,y,family=negative.binomial(link="log",theta=1/dispersion))` but with more secure convergence. Here `negative.binomial` is a function in the MASS package.

The dispersion parameter is the same as `1/theta` for the MASS::`negative.binomial` function or `1/size` for the stats::`rnbinom` function. `dispersion=0` corresponds to the Poisson distribution.

**Value**

List with the following components:

<code>coefficients</code>	numeric vector of regression coefficients
<code>fitted</code>	numeric vector of fitted values
<code>deviance</code>	residual deviance
<code>iter</code>	number of iterations used to convergence. If convergence was not achieved then <code>iter</code> is set to <code>maxit+1</code> .

**Author(s)**

Gordon Smyth and Yunshun Chen

**References**

Dunn, PK, and Smyth, GK (2018). *Generalized linear models with examples in R*. Springer, New York, NY. <https://doi.org/10.1007/978-1-4419-0118-7>

**See Also**

The `glmFit` function in the edgeR package on Bioconductor is a high-performance version of `glmnb.fit` for many `y` vectors at once.

`glm` is the standard glm fitting function in the stats package. `negative.binomial` in the MASS package defines a negative binomial family for use with `glm`.

**Examples**

```
y <- rnbinom(10, mu=1:10, size=5)
X <- cbind(1, 1:10)
fit <- glmnb.fit(X, y, dispersion=0.2, trace=TRUE)
```

**Description**

Do all pairwise comparisons between groups of growth curves using a permutation test.

**Usage**

```
compareGrowthCurves(group, y, levels=NULL, nsim=100, fun=meanT, times=NULL,
                      verbose=TRUE, adjust="holm")
compareTwoGrowthCurves(group, y, nsim=100, fun=meanT)
plotGrowthCurves(group, y, levels=sort(unique(group)), times=NULL, col=NULL,...)
```

**Arguments**

group	vector or factor indicating group membership. Missing values are allowed in <code>compareGrowthCurves</code> but not in <code>compareTwoGrowthCurves</code> .
y	matrix of response values with rows for individuals and columns for times. The number of rows must agree with the length of <code>group</code> . Missing values are allowed.
levels	a character vector containing the identifiers of the groups to be compared. By default all groups with two or more members will be compared.
nsim	number of permutations to estimate p-values.
fun	a function defining the statistic used to measure the distance between two groups of growth curves. Defaults to <code>meanT</code> .
times	a numeric vector containing the column numbers on which the groups should be compared. By default all the columns are used.
verbose	should progress results be printed?
adjust	method used to adjust for multiple testing, see <code>p.adjust</code> .
col	vector of colors corresponding to distinct groups
...	other arguments passed to <code>plot()</code>

**Details**

`compareTwoGrowthCurves` performs a permutation test of the difference between two groups of growth curves. `compareGrowthCurves` does all pairwise comparisons between two or more groups of growth curves. Accurate p-values can be obtained by setting `nsim` to some large value, `nsim=10000` say.

**Value**

compareTwoGrowthCurves returns a list with two components, stat and p.value, containing the observed statistics and the estimated p-value. compareGrowthCurves returns a data frame with components

Group1	name of first group in a comparison
Group2	name of second group in a comparison
Stat	observed value of the statistic
P.Value	estimated p-value
adj.P.Value	p-value adjusted for multiple testing

**Author(s)**

Gordon Smyth

**References**

Elso, C. M., Roberts, L. J., Smyth, G. K., Thomson, R. J., Baldwin, T. M., Foote, S. J., and Handman, E. (2004). Leishmaniasis host response loci (Imr13) modify disease severity through a Th1/Th2-independent pathway. *Genes and Immunity* 5, 93-100.

Baldwin, T., Sakhianandeswaren, A., Curtis, J., Kumar, B., Smyth, G. K., Foote, S., and Handman, E. (2007). Wound healing response is a major contributor to the severity of cutaneous leishmaniasis in the ear model of infection. *Parasite Immunology* 29, 501-513.

**See Also**

[meanT](#), [compareGrowthCurves](#), [compareTwoGrowthCurves](#)

**Examples**

```
# A example with only one time
data(PlantGrowth)
compareGrowthCurves(PlantGrowth$group,as.matrix(PlantGrowth$weight))
# Can make p-values more accurate by nsim=10000
```

---

hommel.test

*Test Multiple Comparisons Using Hommel's Method*

---

**Description**

Given a set of p-values and a test level, returns vector of test results for each hypothesis.

**Usage**

```
hommel.test(p, alpha=0.05)
```

**Arguments**

p                    numeric vector of p-values  
alpha                numeric value, desired significance level

**Details**

This function implements the multiple testing procedure of Hommel (1988). Hommel's method is also implemented as an adjusted p-value method in the function `p.adjust` but the accept/reject approach used here is faster.

**Value**

logical vector indicating whether each hypothesis is accepted

**Author(s)**

Gordon Smyth

**References**

Hommel, G. (1988). A stagewise rejective multiple test procedure based on a modified Bonferroni test. *Biometrika*, **75**, 383-386.  
Shaffer, J. P. (1995). Multiple hypothesis testing. *Annual Review of Psychology* **46**, 561-576. (An excellent review of the area.)

**See Also**

[p.adjust](#)

**Examples**

```
p <- sort(runif(100))[1:10]
cbind(p,p.adjust(p,"hommel"),hommel.test(p))
```

---

invgauss

*Inverse Gaussian Distribution*

---

**Description**

Density, cumulative probability, quantiles and random generation for the inverse Gaussian distribution.

**Usage**

```
dinvgauss(x, mean=1, shape=NULL, dispersion=1, log=FALSE)
pinvgauss(q, mean=1, shape=NULL, dispersion=1, lower.tail=TRUE, log.p=FALSE)
qinvgauss(p, mean=1, shape=NULL, dispersion=1, lower.tail=TRUE, log.p=FALSE,
          maxit=200L, tol=1e-14, trace=FALSE)
rinvgauss(n, mean=1, shape=NULL, dispersion=1)
```

**Arguments**

<code>x, q</code>	vector of quantiles.
<code>p</code>	vector of probabilities.
<code>n</code>	sample size. If <code>length(n)</code> is larger than 1, then <code>length(n)</code> random values are returned.
<code>mean</code>	vector of (positive) means.
<code>shape</code>	vector of (positive) shape parameters.
<code>dispersion</code>	vector of (positive) dispersion parameters. Ignored if <code>shape</code> is not NULL, in which case <code>dispersion=1/shape</code> .
<code>lower.tail</code>	logical; if TRUE, probabilities are $P(X < q)$ otherwise $P(X > q)$ .
<code>log</code>	logical; if TRUE, the log-density is returned.
<code>log.p</code>	logical; if TRUE, probabilities are on the log-scale.
<code>maxit</code>	maximum number of Newton iterations used to find <code>q</code> .
<code>tol</code>	small positive numeric value giving the convergence tolerance for the quantile.
<code>trace</code>	logical, if TRUE then the working estimate for <code>q</code> from each iteration will be output.

**Details**

The inverse Gaussian distribution takes values on the positive real line. It is somewhat more right skew than the gamma distribution, with variance given by `dispersion*mean^3`. The distribution has applications in reliability and survival analysis and is one of the response distributions used in generalized linear models.

Giner and Smyth (2016) show that the inverse Gaussian distribution is asymptotically equal to an inverse chisquare distribution as the mean becomes large.

The functions provided here implement numeric algorithms developed by Giner and Smyth (2016) that achieve close to full machine accuracy for all possible parameter values. Giner and Smyth (2016) show that the probability calculations provided by these functions are considerably more accurate, and in most cases faster, than previous implementations of inverse Gaussian functions. The improvement in accuracy is most noticeable for extreme probability values and for large parameter values.

The `shape` and `dispersion` parameters are alternative parametrizations for the variability, with `dispersion=1/shape`. Only one of these two arguments needs to be specified. If both are set, then `shape` takes precedence.

**Value**

Output values give density (`dinvgauss`), probability (`pinvgauss`), quantile (`qinvgauss`) or random sample (`rinvgauss`) for the inverse Gaussian distribution with mean `mean` and dispersion `dispersion`. Output is a vector of length equal to the maximum length of any of the arguments `x`, `q`, `mean`, `shape` or `dispersion`. If the first argument is the longest, then all the attributes of the input argument are preserved on output, for example, a matrix `x` will give a matrix on output. Elements of input vectors that are missing will cause the corresponding elements of the result to be missing, as will non-positive values for `mean` or `dispersion`.

**Author(s)**

Gordon Smyth.

Paul Bagshaw (Centre National d'Etudes des Telecommunications, France) and Trevor Park (Department of Statistics, University of Florida) made suggestions on a much earlier versions of the code.

**References**

Giner, G., and Smyth, G. K. (2016). statmod: Probability calculations for the inverse Gaussian distribution. *R Journal* 8(1), 339-351. <https://journal.r-project.org/archive/2016-1/giner-smyth.pdf>

**Examples**

```
q <- rinvgauss(10, mean=1, disp=0.5) # generate vector of 10 random numbers
p <- pinvgauss(q, mean=1, disp=0.5) # p should be uniformly distributed

# Quantile for small right tail probability:
qinvgauss(1e-20, mean=1.5, disp=0.7, lower.tail=FALSE)

# Same quantile, but represented in terms of left tail probability on log-scale
qinvgauss(-1e-20, mean=1.5, disp=0.7, lower.tail=TRUE, log.p=TRUE)
```

---

logmdigamma

*Log Minus Digamma Function*

---

**Description**

The difference between the log and digamma functions.

**Usage**

```
logmdigamma(x)
```

**Arguments**

x                    numeric vector or array of positive values. Negative or zero values will return NA.

**Details**

digamma(x) is asymptotically equivalent to log(x). logmdigamma(x) computes log(x) - digamma(x) without subtractive cancellation for large x.

**Author(s)**

Gordon Smyth

## References

Abramowitz, M., and Stegun, I. A. (1970). *Handbook of mathematical functions*. Dover, New York.

## See Also

[digamma](#)

## Examples

```
log(10^15) - digamma(10^15) # returns 0
logmdigamma(10^15) # returns value correct to 15 figures
```

---

matvec

*Multiply a Matrix by a Vector*

---

## Description

Multiply the rows or columns of a matrix by the elements of a vector.

## Usage

```
matvec(M, v)
vecmat(v, M)
```

## Arguments

M	numeric matrix, or object which can be coerced to a matrix.
v	numeric vector, or object which can be coerced to a vector. Length should match the number of columns of M (for matvec) or the number of rows of M (for vecmat)

## Details

matvec(M,v) is equivalent to `M %*% diag(v)` but is faster to execute. Similarly `vecmat(v,M)` is equivalent to `diag(v) %*% M` but is faster to execute.

## Value

A matrix of the same dimensions as M.

## Author(s)

Gordon Smyth

## Examples

```
A <- matrix(1:12,3,4)
A
matvec(A,c(1,2,3,4))
vecmat(c(1,2,3),A)
```



---

`meanT`*Mean t-Statistic Between Two Groups of Growth Curves*

---

**Description**

The mean-t statistic of the distance between two groups of growth curves.

**Usage**

```
meanT(y1, y2)
```

**Arguments**

`y1` matrix of response values for the first group, with a row for each individual and a column for each time. Missing values are allowed.

`y2` matrix of response values for the second group. Must have the same number of columns as `y1`. Missing values are allowed.

**Details**

This function computes the pooled two-sample t-statistic between the response values at each time, and returns the mean of these values weighted by the degrees of freedom. This function is used by `compareGrowthCurves`.

**Value**

numeric vector of length one containing the mean t-statistic.

**Author(s)**

Gordon Smyth

**See Also**

[compareGrowthCurves](#), [compareTwoGrowthCurves](#)

**Examples**

```
y1 <- matrix(rnorm(4*3),4,3)
y2 <- matrix(rnorm(4*3),4,3)
meanT(y1,y2)

data(PlantGrowth)
compareGrowthCurves(PlantGrowth$group,as.matrix(PlantGrowth$weight))
# Can make p-values more accurate by nsim=10000
```

mixedModel2

*Fit Mixed Linear Model with 2 Error Components***Description**

Fits a mixed linear model by REML. The linear model contains one random factor apart from the unit errors.

**Usage**

```
mixedModel2(formula, random, weights=NULL, only.varcomp=FALSE, data=list(),
             subset=NULL, contrasts=NULL, tol=1e-6, maxit=50, trace=FALSE)
mixedModel2Fit(y, X, Z, w=NULL, only.varcomp=FALSE, tol=1e-6, maxit=50, trace=FALSE)
randomizedBlock(formula, random, weights=NULL, only.varcomp=FALSE, data=list(),
                 subset=NULL, contrasts=NULL, tol=1e-6, maxit=50, trace=FALSE)
randomizedBlockFit(y, X, Z, w=NULL, only.varcomp=FALSE, tol=1e-6, maxit=50, trace=FALSE)
```

**Arguments**

The arguments `formula`, `weights`, `data`, `subset` and `contrasts` have the same meaning as in `lm`. The arguments `y`, `X` and `w` have the same meaning as in `lm.wfit`.

`formula` specifying the fixed model.

<code>formula</code>	vector or factor specifying the blocks corresponding to random effects.
<code>weights</code>	optional vector of prior weights.
<code>only.varcomp</code>	logical value, if TRUE computation of standard errors and fixed effect coefficients will be skipped
<code>data</code>	an optional data frame containing the variables in the model.
<code>subset</code>	an optional vector specifying a subset of observations to be used in the fitting process.
<code>contrasts</code>	an optional list. See the <code>contrasts.arg</code> argument of <code>model.matrix.default</code> .
<code>tol</code>	small positive numeric tolerance, passed to <code>glmGam.fit</code>
<code>maxit</code>	maximum number of iterations permitted, passed to <code>glmGam.fit</code>
<code>trace</code>	logical value, passed to <code>glmGam.fit</code> . If TRUE then working estimates will be printed at each iteration.
<code>y</code>	numeric response vector
<code>X</code>	numeric design matrix for fixed model
<code>Z</code>	numeric design matrix for random effects
<code>w</code>	optional vector of prior weights

## Details

Note that `randomizedBlock` and `mixedModel2` are alternative names for the same function.

This function fits the model  $y = Xb + Zu + e$  where  $b$  is a vector of fixed coefficients and  $u$  is a vector of random effects. Write  $n$  for the length of  $y$  and  $q$  for the length of  $u$ . The random effect vector  $u$  is assumed to be normal, mean zero, with covariance matrix  $\sigma_u^2 I_q$  while  $e$  is normal, mean zero, with covariance matrix  $\sigma^2 I_n$ . If  $Z$  is an indicator matrix, then this model corresponds to a randomized block experiment. The model is fitted using an eigenvalue decomposition which transforms the problem into a Gamma generalized linear model.

Note that the block variance component `varcomp[2]` is not constrained to be non-negative. It may take negative values corresponding to negative intra-block correlations. However the correlation `varcomp[2]/sum(varcomp)` must lie between -1 and 1.

Missing values in the data are not allowed.

This function is equivalent to `lme(fixed=formula,random=~1|random)`, except that the block variance component is not constrained to be non-negative, but is faster and more accurate for small to moderate size data sets. It is slower than `lme` when the number of observations is large.

This function tends to be fast and reliable, compared to competitor functions which fit randomized block models, when then number of observations is small, say no more than 200. However it becomes quadratically slow as the number of observations increases because of the need to do two eigenvalue decompositions of order nearly equal to the number of observations. So it is a good choice when fitting large numbers of small data sets, but not a good choice for fitting large data sets.

## Value

A list with the components:

<code>varcomp</code>	vector of length two containing the residual and block components of variance.
<code>se.varcomp</code>	standard errors for the components of variance.
<code>reml.residuals</code>	standardized residuals in the null space of the design matrix.

If `fixed.estimate=TRUE` then the components from the diagonalized weighted least squares fit are also returned.

## Author(s)

Gordon Smyth

## References

Venables, W., and Ripley, B. (2002). *Modern Applied Statistics with S-Plus*, Springer.

## See Also

[glmGam.fit](#), [lme](#), [lm](#), [lm.fit](#)

### Examples

```
# Compare with first data example from Venable and Ripley (2002),  
# Chapter 10, "Linear Models"  
library(MASS)  
data(petrol)  
out <- mixedModel2(Y~SG+VP+V10+EP, random=No, data=petrol)  
cbind(varcomp=out$varcomp,se=out$se.varcomp)
```

---

mscale

*M Scale Estimation*

---

### Description

Robust estimation of a scale parameter using Hampel's redescending psi function.

### Usage

```
mscale(u, na.rm=FALSE)
```

### Arguments

`u` numeric vector of residuals.  
`na.rm` logical. Should missing values be removed?

### Details

Estimates a scale parameter or standard deviation using an M-estimator with 50% breakdown. This means the estimator is highly robust to outliers. If the input residuals `u` are a normal sample, then `mscale(u)` should be equal to the standard deviation.

### Value

numeric constant giving the estimated scale.

### Author(s)

Gordon Smyth

### References

Yohai, V. J. (1987). High breakdown point and high efficiency robust estimates for regression. *Ann. Statist.* 15, 642-656.  
Stromberg, A. J. (1993). Computation of high breakdown nonlinear regression parameters. *J. Amer. Statist. Assoc.* 88, 237-244.  
Smyth, G. K., and Hawkins, D. M. (2000). Robust frequency estimation using elemental sets. *Journal of Computational and Graphical Statistics* 9, 196-214.

**Examples**

```
u <- rnorm(100)
sd(u)
mscale(u)
```

---

permp *Exact permutation p-values*

---

**Description**

Calculates exact p-values for permutation tests when permutations are randomly drawn with replacement.

**Usage**

```
permp(x, nperm, n1, n2, total.nperm=NULL, method="auto", twosided=TRUE)
```

**Arguments**

x	number of permutations that yielded test statistics at least as extreme as the observed data. May be a vector or an array of values.
nperm	total number of permutations performed.
n1	sample size of group 1. Not required if total.nperm is supplied.
n2	sample size of group 2. Not required if total.nperm is supplied.
total.nperm	total number of permutations allowable from the design of the experiment.
method	character string indicating computation method. Possible values are "exact", "approximate" or "auto".
twosided	logical, is the test two-sided and symmetric between the two groups?

**Details**

This function can be used for calculating exact p-values for permutation tests where permutations are sampled with replacement, using theory and methods developed by Phipson and Smyth (2010). The input values are the total number of permutations done (nperm) and the number of these that were considered at least as extreme as the observed data (x).

total.nperm is the total number of distinct values of the test statistic that are possible. This is generally equal to the number of possible permutations, unless a two-sided test is conducted with equal sample sizes, in which case total.nperm is half the number of permutations, because the test statistic must then be symmetric in the two groups. Usually total.nperm is computed automatically from n1 and n2, but can also be supplied directly by the user.

When method="exact", the p-values are computed to full machine precision by summing a series terms. When method="approximate", an approximation is used that is faster and uses less memory. If method="auto", the exact calculation is used when total.nperm is less than or equal to 10,000 and the approximation is used otherwise.

**Value**

vector or array of p-values, of same dimensions as x

**Author(s)**

Belinda Phipson and Gordon Smyth

**References**

Phipson B, and Smyth GK (2010). Permutation p-values should never be zero: calculating exact p-values when permutations are randomly drawn. *Statistical Applications in Genetics and Molecular Biology*, Volume 9, Issue 1, Article 39. <http://www.statsci.org/smyth/pubs/PermPValuesPreprint.pdf>

**Examples**

```
x <- 0:5
# Both calls give same results
permp(x=x, nperm=99, n1=6, n2=6)
permp(x=x, nperm=99, total.nperm=462)
```

---

plot.limdil

*Plot or print an object of class limdil*

---

**Description**

Plot or print the results of a limiting dilution analysis.

**Usage**

```
## S3 method for class 'limdil'
print(x, ...)
## S3 method for class 'limdil'
plot(x, col.group=NULL, cex=1, lwd=1, legend.pos="bottomleft", ...)
```

**Arguments**

x	object of class limdil.
col.group	vector of colors for the groups of the same length as levels(x\$group).
cex	relative symbol size
lwd	relative line width
legend.pos	positioning on plot of legend when there are multiple groups
...	other arguments to be passed to plot or print. Note that pch and lty are reserved arguments for the plot method.

**Details**

The print method formats results similarly to a regression or anova summary in R.

The plot method produces a plot of a limiting dilution experiment similar to that in Bonnefoix et al (2001). The basic design of the plot was made popular by Lefkovits and Waldmann (1979).

The plot shows frequencies and confidence intervals for the multiple groups. A novel feature is that assays with 100% successes are included in the plot and are represented by down-pointing triangles.

**Author(s)**

Yifang Hu and Gordon Smyth

**References**

Bonnefoix, T, Bonnefoix, P, Callanan, M, Verdiel, P, and Sotto, JJ (2001). Graphical representation of a generalized linear model-based statistical test estimating the fit of the single-hit poisson model to limiting dilution assays. *The Journal of Immunology* 167, 5725-5730.

Lefkovits, I, and Waldmann, H (1979). *Limiting dilution analysis of cells in the immune system*. Cambridge University Press, Cambridge.

**See Also**

[limdil](#) describes the limdil class.

---

power.fisher.test      *Power of Fisher's Exact Test for Comparing Proportions*

---

**Description**

Calculate by simulation the power of Fisher's exact test for comparing two proportions given two margin counts.

**Usage**

```
power.fisher.test(p1, p2, n1, n2, alpha=0.05, nsim=100, alternative="two.sided")
```

**Arguments**

p1	first proportion to be compared.
p2	second proportion to be compared.
n1	first sample size.
n2	second sample size.
alpha	significance level.
nsim	number of data sets to simulate.
alternative	indicates the alternative hypothesis and must be one of "two.sided", "greater" or "less".

**Details**

Computes the power of Fisher's exact test for testing the null hypothesis that  $p_1$  equals  $p_2$  against the alternative that they are not equal.

**Value**

Estimated power of the test.

**Author(s)**

Gordon Smyth

**See Also**

[fisher.test](#), [power.t.test](#)

**Examples**

```
power.fisher.test(0.5,0.9,20,20) # 70% chance of detecting difference
```

---

qresiduals

*Randomized Quantile Residuals*

---

**Description**

Compute randomized quantile residuals for generalized linear models.

**Usage**

```
qresiduals(glm.obj,dispersion=NULL)
qresid(glm.obj,dispersion=NULL)
qres.binom(glm.obj)
qres.pois(glm.obj)
qres.nbinom(glm.obj)
qres.gamma(glm.obj,dispersion=NULL)
qres.invgauss(glm.obj,dispersion=NULL)
qres.tweedie(glm.obj,dispersion=NULL)
qres.default(glm.obj,dispersion=NULL)
```

**Arguments**

glm.obj	Object of class glm. The generalized linear model family is assumed to be binomial for qres.binom, poisson for qres.pois, negative binomial for qres.nbinom, Gamma for qres.gamma, inverse Gaussian for qres.invgauss or tweedie for qres.tweedie.
dispersion	a positive real number. Specifies the value of the dispersion parameter for a Gamma or inverse Gaussian generalized linear model if known. If NULL, the dispersion will be estimated by its Pearson estimator.



## Details

Quantile residuals are based on the idea of inverting the estimated distribution function for each observation to obtain exactly standard normal residuals. In the case of discrete distributions, such as the binomial and Poisson, some randomization is introduced to produce continuous normal residuals. Quantile residuals are the residuals of choice for generalized linear models in large dispersion situations when the deviance and Pearson residuals can be grossly non-normal. Quantile residuals are the only useful residuals for binomial or Poisson data when the response takes on only a small number of distinct values.

## Value

Numeric vector of standard normal quantile residuals.

## Author(s)

Gordon Smyth

## References

Dunn, K. P., and Smyth, G. K. (1996). Randomized quantile residuals. *Journal of Computational and Graphical Statistics* **5**, 1-10. <http://www.statsci.org/smyth/pubs/residual.html>

Dunn, PK, and Smyth, GK (2018). *Generalized linear models with examples in R*. Springer, New York, NY. <https://doi.org/10.1007/978-1-4419-0118-7>

## See Also

[residuals.glm](#)

## Examples

```
# Poisson example: quantile residuals show no granularity
y <- rpois(20,lambda=4)
x <- 1:20
fit <- glm(y~x, family=poisson)
qr <- qresiduals(fit)
qqnorm(qr)
abline(0,1)

# Gamma example:
# Quantile residuals are nearly normal while usual resids are not
y <- rchisq(20, df=1)
fit <- glm(y~1, family=Gamma)
qr <- qresiduals(fit, dispersion=2)
qqnorm(qr)
abline(0,1)

# Negative binomial example:
if(require("MASS")) {
fit <- glm(Days~Age,family=negative.binomial(2),data=quine)
summary(qresiduals(fit))
}
```

```
fit <- glm.nb(Days~Age,link=log,data = quine)
summary(qresiduals(fit))
}
```

remlscore

*REML for Heteroscedastic Regression***Description**

Fits a heteroscedastic regression model using residual maximum likelihood (REML).

**Usage**

```
remlscore(y, X, Z, trace=FALSE, tol=1e-5, maxit=40)
```

**Arguments**

y	numeric vector of responses
X	design matrix for predicting the mean
Z	design matrix for predicting the variance
trace	Logical variable. If true then output diagnostic information at each iteration.
tol	Convergence tolerance
maxit	Maximum number of iterations allowed

**Details**

Write  $\mu_i = E(y_i)$  for the expectation of the  $i$ th response and  $s_i = (y_i)$ . We assume the heteroscedastic regression model

$$\mu_i = \mathbf{x}_i^T \boldsymbol{\beta}$$

$$\log(\sigma_i^2) = \mathbf{z}_i^T \boldsymbol{\gamma},$$

where  $\mathbf{x}_i$  and  $\mathbf{z}_i$  are vectors of covariates, and  $\boldsymbol{\beta}$  and  $\boldsymbol{\gamma}$  are vectors of regression coefficients affecting the mean and variance respectively.

Parameters are estimated by maximizing the REML likelihood using REML scoring as described in Smyth (2002).

**Value**

List with the following components:

beta	vector of regression coefficients for predicting the mean
se.beta	vector of standard errors for beta
gamma	vector of regression coefficients for predicting the variance
se.gam	vector of standard errors for gamma
mu	estimated means

phi	estimated variances
deviance	minus twice the REML log-likelihood
h	numeric vector of leverages
cov.beta	estimated covariance matrix for beta
cov.gam	estimated covariate matrix for gamma
iter	number of iterations used

**Author(s)**

Gordon Smyth

**References**

Smyth, G. K. (2002). An efficient algorithm for REML in heteroscedastic regression. *Journal of Computational and Graphical Statistics* **11**, 836-847.

**Examples**

```
data(welding)
attach(welding)
y <- Strength
# Reproduce results from Table 1 of Smyth (2002)
X <- cbind(1,(Drying+1)/2,(Material+1)/2)
colnames(X) <- c("1","B","C")
Z <- cbind(1,(Material+1)/2,(Method+1)/2,(Preheating+1)/2)
colnames(Z) <- c("1","C","H","I")
out <- remlscore(y,X,Z)
cbind(Estimate=out$gamma,SE=out$se.gam)
```

remlscoregamma

*Approximate REML for gamma regression with structured dispersion***Description**

Estimates structured dispersion effects using approximate REML with gamma responses.

**Usage**

```
remlscoregamma(y,X,Z,mLink="log",dLink="log",trace=FALSE,tol=1e-5,maxit=40)
```

**Arguments**

y	numeric vector of responses
X	design matrix for predicting the mean
Z	design matrix for predicting the variance
mLink	character string or numeric value specifying link for mean model

dlink	character string or numeric value specifying link for dispersion model
trace	Logical variable. If true then output diagnostic information at each iteration.
tol	Convergence tolerance
maxit	Maximum number of iterations allowed

### Details

Write  $\mu_i = E(y_i)$  for the expectation of the  $i$ th response and  $s_i = (y_i)$ . We assume the heteroscedastic regression model

$$\mu_i = \mathbf{x}_i^T \boldsymbol{\beta}$$

$$\log(\sigma_i^2) = \mathbf{z}_i^T \boldsymbol{\gamma},$$

where  $\mathbf{x}_i$  and  $\mathbf{z}_i$  are vectors of covariates, and  $\boldsymbol{\beta}$  and  $\boldsymbol{\gamma}$  are vectors of regression coefficients affecting the mean and variance respectively.

Parameters are estimated by maximizing the REML likelihood using REML scoring as described in Smyth and Verbyla (2001). See also Smyth and Verbyla (1999a,b).

### Value

List with the following components:

beta	Vector of regression coefficients for predicting the mean
se.beta	<Standard errors for beta
gamma	Vector of regression coefficients for predicting the variance
se.gam	Standard errors for gamma
mu	Estimated means
phi	Estimated dispersions
deviance	Minus twice the REML log-likelihood
h	Leverages

### References

Smyth, G. K., and Verbyla, A. P. (1999a). Adjusted likelihood methods for modelling dispersion in generalized linear models. *Environmetrics* 10, 695-709. <http://www.statsci.org/smyth/pubs/ties98tr.html>

Smyth, G. K., and Verbyla, A. P. (1999b). Double generalized linear models: approximate REML and diagnostics. In *Statistical Modelling: Proceedings of the 14th International Workshop on Statistical Modelling*, Graz, Austria, July 19-23, 1999, H. Friedl, A. Berghold, G. Kauermann (eds.), Technical University, Graz, Austria, pages 66-80. <http://www.statsci.org/smyth/pubs/iwsm99-Preprint.pdf>

Smyth, GK, and Verbyla, AP (2009). Leverage adjustments for dispersion modelling in generalized nonlinear models. *Australian and New Zealand Journal of Statistics* 51, 433-448.

## Examples

```
data(welding)
attach(welding)
y <- Strength
X <- cbind(1,(Drying+1)/2,(Material+1)/2)
colnames(X) <- c("1","B","C")
Z <- cbind(1,(Material+1)/2,(Method+1)/2,(Preheating+1)/2)
colnames(Z) <- c("1","C","H","I")
out <- remlscoregamma(y,X,Z)
```

---

sage.test

*Exact Binomial Tests For Comparing Two SAGE Libraries (Obsolete)*

---

## Description

Computes p-values for differential abundance for each tag between two digital libraries, conditioning on the total count for each tag. The counts in each group as a proportion of the whole are assumed to follow a binomial distribution.

## Usage

```
sage.test(x, y, n1=sum(x), n2=sum(y))
```

## Arguments

x	integer vector giving counts in first library. Non-integer values are rounded to the nearest integer.
y	integer vector giving counts in second library. Non-integer values are rounded to the nearest integer.
n1	total number of tags in first library. Non-integer values are rounded to the nearest integer.
n2	total number of tags in second library. Non-integer values are rounded to the nearest integer.

## Details

This function was originally written for comparing SAGE libraries (a method for counting the frequency of sequence tags in samples of RNA). It can however be used for comparing any two digital libraries from RNA-Seq, ChIP-Seq or other technologies with respect to technical variation.

An exact two-sided binomial test is computed for each tag. This test is closely related to Fisher's exact test for 2x2 contingency tables but, unlike Fisher's test, it conditions on the total number of counts for each tag. The null hypothesis is that the expected counts are in the same proportions as the library sizes, i.e., that the binomial probability for the first library is  $n1/(n1+n2)$ .

The two-sided rejection region is chosen analogously to Fisher's test. Specifically, the rejection region consists of those values with smallest probabilities under the null hypothesis.

When the counts are reasonably large, the binomial test, Fisher's test and Pearson's chisquare all give the same results. When the counts are smaller, the binomial test is usually to be preferred in this context.

This function is a later version of the earlier `sage.test` function in the `sagenhaft` Bioconductor package. This function has been made obsolete by `binomTest` in the `edgeR` package.

### Value

Numeric vector of p-values.

### Note

This function is kept in the `statmod` package so as not to break code that depends on it but it has been replaced by `binomTest` in the `edgeR` Bioconductor package and is no longer updated. It may be removed in a later release of this package.

### Author(s)

Gordon Smyth

### References

[http://en.wikipedia.org/wiki/Binomial\\_test](http://en.wikipedia.org/wiki/Binomial_test)

[http://en.wikipedia.org/wiki/Fisher's\\_exact\\_test](http://en.wikipedia.org/wiki/Fisher's_exact_test)

[http://en.wikipedia.org/wiki/Serial\\_analysis\\_of\\_gene\\_expression](http://en.wikipedia.org/wiki/Serial_analysis_of_gene_expression)

<http://en.wikipedia.org/wiki/RNA-Seq>

### See Also

The `binomTest` function in the `edgeR` package on Bioconductor is a newer and better version of this function, see <https://bioconductor.org/packages/edgeR>.

`binom.test` in the `stats` package performs univariate binomial tests.

### Examples

```
sage.test(c(0,5,10),c(0,30,50),n1=10000,n2=15000)
# Univariate equivalents:
binom.test(5,5+30,p=10000/(10000+15000))$p.value
binom.test(10,10+50,p=10000/(10000+15000))$p.value
```

tweedie

*Tweedie Generalized Linear Models***Description**

Produces a generalized linear model family object with any power variance function and any power link. Includes the Gaussian, Poisson, gamma and inverse-Gaussian families as special cases.

**Usage**

```
tweedie(var.power=0, link.power=1-var.power)
```

**Arguments**

`var.power` index of power variance function  
`link.power` index of power link function. `link.power=0` produces a log-link. Defaults to the canonical link, which is `1-var.power`.

**Details**

This function provides access to a range of generalized linear model response distributions which are not otherwise provided by R, or any other package for that matter. It is also useful for accessing distribution/link combinations which are disallowed by the R `glm` function.

Let  $\mu_i = E(y_i)$  be the expectation of the  $i$ th response. We assume that

$$\mu_i^q = x_i^T b, \text{var}(y_i) = \phi \mu_i^p$$

where  $x_i$  is a vector of covariates and  $b$  is a vector of regression coefficients, for some  $\phi$ ,  $p$  and  $q$ . This family is specified by `var.power = p` and `link.power = q`. A value of zero for  $q$  is interpreted as  $\log(\mu_i) = x_i^T b$ .

The variance power  $p$  characterizes the distribution of the responses  $y$ . The following are some special cases:

<b>p</b>	<b>Response distribution</b>
0	Normal
1	Poisson
(1, 2)	Compound Poisson, non-negative with mass at zero
2	Gamma
3	Inverse-Gaussian
> 2	Stable, with support on the positive reals

The name Tweedie has been associated with this family by Joergensen (1987) in honour of M. C. K. Tweedie.

**Value**

A family object, which is a list of functions and expressions used by `glm` and `gam` in their iteratively reweighted least-squares algorithms. See `family` and `glm` in the R base help for details.

**Author(s)**

Gordon Smyth

**References**

Tweedie, M. C. K. (1984). An index which distinguishes between some important exponential families. In *Statistics: Applications and New Directions*. Proceedings of the Indian Statistical Institute Golden Jubilee International Conference. (Eds. J. K. Ghosh and J. Roy), pp. 579-604. Calcutta: Indian Statistical Institute.

Joergensen, B. (1987). Exponential dispersion models. *J. R. Statist. Soc. B* **49**, 127-162.

Smyth, G. K. (1996). Regression modelling of quantity data with exact zeroes. Proceedings of the Second Australia-Japan Workshop on Stochastic Models in Engineering, Technology and Management. Technology Management Centre, University of Queensland, pp. 572-580.

Joergensen, B. (1997). *Theory of Dispersion Models*, Chapman and Hall, London.

Smyth, G. K., and Verbyla, A. P., (1999). Adjusted likelihood methods for modelling dispersion in generalized linear models. *Environmetrics* **10**, 695-709.

**See Also**

[glm](#), [family](#), [dtweedie](#)

**Examples**

```
y <- rgamma(20, shape=5)
x <- 1:20
# Fit a poisson generalized linear model with identity link
glm(y~x, family=tweedie(var.power=1, link.power=1))

# Fit an inverse-Gaussian glm with log-link
glm(y~x, family=tweedie(var.power=3, link.power=0))
```

---

welding

*Data: Tensile Strength of Welds*


---

**Description**

This is a highly fractionated two-level factorial design employed as a screening design in an off-line welding experiment performed by the National Railway Corporation of Japan. There were 16 runs and 9 experimental factors. The response variable is the observed tensile strength of the weld, one of several quality characteristics measured. All other variables are at plus and minus levels.



**Usage**

```
data(welding)
```

**Format**

A data frame containing the following variables. All the explanatory variables are numeric with two levels, -1 and 1.

<b>Variable</b>	<b>Description</b>
Rods	Kind of welding rods
Drying	Period of drying
Material	Welded material
Thickness	Thickness
Angle	Angle
Opening	Opening
Current	Current
Method	Welding method
Preheating	Preheating
Strength	Tensile strength of the weld in kg/mm. The response variable.

**Source**

<http://www.statsci.org/data/general/welding.html>

**References**

Smyth, G. K., Huele, F., and Verbyla, A. P. (2001). Exact and approximate REML for heteroscedastic regression. *Statistical Modelling* **1**, 161-175.

Smyth, G. K. (2002). An efficient algorithm for REML in heteroscedastic regression. *Journal of Computational and Graphical Statistics* **11**, 1-12.

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