

Package ‘jmdem’

April 27, 2018

Type Package

Title Fitting Joint Mean and Dispersion Effects Models

Version 1.0

Date 2018-04-26

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Description Joint mean and dispersion effects models fit the mean and dispersion parameters of a response variable by two separate linear models, the mean and dispersion submodels, simultaneously. It also allows the users to choose either the deviance or the Pearson residuals as the response variable of the dispersion submodel. Furthermore, the package provides the possibility to nest the submodels in one another, if one of the parameters has significant explanatory power on the other. Wu & Li (2016) <doi:10.1016/j.csda.2016.04.015>.

License GPL-2

Imports VGAM, statmod

NeedsCompilation no

Repository CRAN

Date/Publication 2018-04-27 08:40:56 UTC

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anova.jmdem	<i>Analysis of Deviance for Joint Mean and Dispersion Effect Models Fits</i>
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Description

Compute an analysis of deviance table for one or more double generalised linear model fits.

Usage

```
## S3 method for class 'jmdem'
anova(object, ..., test = NULL, type = c("1", "3"),
       print.results = TRUE)
```

Arguments

object, ...	one or several objects of class <code>jmdem</code> , typically the result of a call to <code>jmdem</code> .
test	a character string, (partially) matching one of "Rao" or "Wald". See stat.anova.jmdem .
type	a character string or integer, specifying whether a type "1" (<i>sequential</i>) analysis or a type "3" (<i>partial</i>) analysis should be conducted. It is only relevant if a single object is specified in <code>object</code> . Both numeric and character inputs are allowed. See details for type 1 and type 3 analysis.
print.results	logical, TRUE if the result table should be printed directly, FALSE if the results should be saved in an user-defined object.

Details

Specifying a single object gives a analysis of deviance table for that fit. If type 1 analysis is specified, a sequential analysis will be conducted. That is, the reductions in the residual deviance as each term of the formula is *added* in turn are given in as the rows of a table, plus the residual deviances themselves.

Type 3 analysis gives the reduction in the residual deviance of the fitted model after *removing* each term of the formula individually, that in turn are given as the rows of a table.

If more than one object is specified, the table has a row for the residual degrees of freedom and deviance for each model. For all but the first model, the change in degrees of freedom and deviance is also given. (This only makes statistical sense if the models are nested.) It is conventional to list the models from smallest to largest, but this is up to the user.

The table will optionally contain "Rao" or "Wald" test statistics (and P values) comparing the model specified in the current row and the row above (type 1) or the full model (type 3). Both "Rao" and "Wald" test statistics are asymptotically chi-square distributed. "LRT" (Likelihood ratio test) and "F" ((F test) are not included in `anova.jmdem` because the comparison of the deviances of two joint mean and dispersion effects models is questionable, if not even invalid. One important argument is that the dependent variables of two different dispersion submodels given two different mean submodels are not the identical.

Value

An object of class "anova" inheriting from class "data.frame".

If `print.results = TRUE`,

`table.x` the anova table constructed for the mean submodel.

`table.z` the anova table constructed for the dispersion submodel.

Warning

The comparison between two or more models will only be valid if they are fitted to the same dataset. This may be a problem if there are missing values and R's default of `na.action = na.omit` is used, and `anova` will detect this with an error.

Author(s)

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References

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See Also

[jmdem](#), [anova](#)

Examples

```
## Example in jmdem(...)
MyData <- simdata.jmdem.sim(mformula = y ~ x, dformula = ~ z,
                           mfamily = poisson(),
                           dfamily = Gamma(link = "log"),
                           beta.true = c(0.5, 4),
                           lambda.true = c(2.5, 3), n = 100)

fit <- jmdem(mformula = y ~ x, dformula = ~ z, data = MyData,
            mfamily = poisson, dfamily = Gamma(link = "log"),
            dev.type = "deviance", method = "CG")
```

```
## Run a partial analysis (type 3) with Wald test
anova(fit, test = "Wald", type = 3)
```

jmdem

Fitting Joint Mean and Dispersion Effects Models

Description

jmdem is used to fit joint mean and dispersion effects models, specified by giving a symbolic description of the linear predictors for the mean and dispersion and a description of the error distribution

Usage

```
jmdem(mformula, dformula, data, mfamily = gaussian, dfamily = Gamma,
      weights, subset, dev.type = c("deviance", "pearson"),
      moffset = NULL, doffset = NULL, mustart = NULL, phistart = NULL,
      betastart = NULL, lambdastart = NULL, hessian = TRUE, na.action,
      grad.func = TRUE, fit.method = "jmdem.fit",
      method = c("Nelder-Mead", "BFGS", "CG", "L-BFGS-B", "SANN", "Brent"),
      df.adj = FALSE, disp.adj = FALSE, full.loglik = FALSE,
      beta.first = TRUE, prefit = TRUE, mcontrasts = NULL,
      dcontrasts = NULL, control = list(...),
      minv.method = c("solve", "chol2inv", "ginv"), ...)
```

```
jmdem.fit(x, y, z = NULL, weights, mfamily = gaussian, dfamily = Gamma,
          mu, phi, beta, lambda, moffset = NULL, doffset = NULL,
          dev.type = c("deviance", "pearson"), hessian = TRUE,
          method = c("Nelder-Mead", "BFGS", "CG", "L-BFGS-B", "SANN", "Brent"),
          disp.adj = FALSE, df.adj = FALSE, full.loglik = FALSE,
          control = list(), mintercept = TRUE, dintercept = TRUE,
          grad.func = TRUE, lower = -Inf, upper = Inf, ...)
```

Arguments

mformula	an object of class "formula" (or one that can be coerced to that class): a symbolic description of the <i>mean</i> submodel to be fitted. The details of model specification are given under 'Details'.
dformula	a symbolic description of the <i>dispersion</i> submodel to be fitted. The details are also given under 'Details'.
data	an optional data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model. If not found in data, the variables are taken from environment(formula), typically the environment from which jmdem is called.
mfamily	a description of the error distribution and link function to be used in the <i>mean</i> submodel. This can be a character string naming a family function, a family function or the result of a call to a family function. (See family for details of family functions.)

dfamily	a description of the error distribution and link function to be used in the <i>dispersion</i> submodel. (Also see family for details of family functions.)
weights	an optional vector of 'prior weights' to be used in the fitting process. Should be NULL or a numeric vector.
subset	an optional vector specifying a subset of observations to be used in the fitting process.
dev.type	a specification of the type of residuals to be used as the response of the <i>dispersion</i> submodel. The ML estimates of the jmdem are the optima of either the quasi-likelihood function for <i>deviance residuals</i> , or the pseudo-likelihood function for <i>Pearson</i> residuals.
moffset	an a priori known component to be included in the linear predictor of the <i>mean</i> submodel during fitting. This should be NULL or a numeric vector of length equal to the number of cases. One or more offset terms can be included in the formula instead or as well, and if more than one is specified their sum is used. See model.offset .
doffset	an a priori known component to be included in the linear predictor of the <i>dispersion</i> submodel during fitting. See model.offset .
mustart, mu	a vector of starting values of individual means.
phistart, phi	a vector of starting values of individual dispersion.
betastart, beta	a vector of starting values for the regression parameters of the <i>mean</i> submodel.
lambdastart, lambda	a vector of starting values for the regression parameters of the <i>dispersion</i> submodel.
hessian	the method used to compute the information matrix. Hessian matrix will be calculated for "TRUE", Fisher matrix for "FALSE".
na.action	a function which indicates what should happen when the data contain NAs. The default is set by the na.action setting of options , and is na.fail if that is unset. The 'factory-fresh' default is na.omit . Another possible value is NULL, no action. Value na.exclude can be useful.
grad.func	the gradient function will be included in the optimisation for the "BFGS", "CG" and "L-BFGS-B" methods for "TRUE". If it is NULL, a finite-difference approximation will be used. For the "SANN" method it specifies a function to generate a new candidate point. If it is NULL a default Gaussian Markov kernel is used.
fit.method	the method to be used in fitting the model. The default method "jmdem.fit" uses the general-purpose optimisation (optim): the alternative "model.frame" returns the model frame and does no fitting. User-supplied fitting functions can be supplied either as a function or a character string naming a function, with a function which takes the same arguments as jmdem.fit . If specified as a character string it is looked up from within the <i>stats</i> namespace.
method	the method to be used for the optimisation. See optim for details.

<code>df.adj</code>	an adjustment factor for the degrees of freedom $(n-p)/n$, where n is the number of observations and p is the number of parameters to be estimated in <code>jmdem</code> , will be multiplied to the likelihood function before the optimisation for "TRUE".
<code>disp.adj</code>	an adjustment factor for the dispersion weight will be multiplied to the estimated dispersion parameter during the optimisation for "TRUE". For details, please see McCullagh and Nelder (1989, Ch. 10, P. 362).
<code>full.loglik</code>	the full likelihood function instead of the quasi- or pseudo-likelihood function will be used for the optimisation for TRUE.
<code>beta.first</code>	the mean effects will be estimated (assuming constant sample dispersion) at the initial stage for TRUE. For FALSE, the dispersion effects will be estimated first (assuming constantly zero mean for the whole sample).
<code>prefit</code>	a specification whether <code>jmdem</code> uses <code>glm</code> to prefit the starting values of the mean and dispersion parameters. For FALSE, the initial parameter values of all the regressors are set to zero and the sample mean and sample dispersion will be used as the starting values of the corresponding submodel intercepts instead. If the submodels have no intercept, all parameters will also be set to zero. The sample mean and sample dispersion will then be used as <code>mustart</code> and <code>phistart</code> in the internal computation (they will not be officially recorded in <code>mustart</code> and <code>phistart</code> in the output object). Default value is TRUE.
<code>mcontrasts</code>	an optional list for the mean effect contrasts. See the <code>contrasts.arg</code> of <code>model.matrix.default</code> .
<code>dcontrasts</code>	an optional list for the dispersion effect contrasts. See the <code>contrasts.arg</code> of <code>model.matrix.default</code> .
<code>control</code>	a list of parameters for controlling the fitting process. For <code>jmdem.fit</code> this is passed to <code>jmdem.control</code> .
<code>minv.method</code>	the method used to invert matrices during the estimation process. "solve" gives the solutions of a system of equations, "chol2inv" gives the inverse from Choleski or QR decomposition and "ginv" gives the generalized inverse of a matrix. If none of the methods is specified or if they are specified in a vector such as <code>c("solve", "chol2inv", "ginv")</code> , the matrices will be inverted by the methods in the sequence as given in the vector until it is found.
<code>x, y, z</code>	<code>x</code> is a <i>mean</i> submodel's design matrix of dimension $n * p$, <code>z</code> is a <i>dispersion</i> submodel's design matrix of dimension $n * k$, and <code>y</code> is a vector of observations of length n . If <code>z</code> is NULL, the <i>dispersion</i> submodel only contains an intercept.
<code>minterscept</code>	a specification whether the intercept term is included in the <i>mean</i> submodel.
<code>dinterscept</code>	a specification whether the intercept term is included in the <i>dispersion</i> submodel.
<code>lower, upper</code>	bounds on the variables for the "L-BFGS-B" optimisation method.
<code>...</code>	For <code>control</code> : arguments to be used to form the default control argument if it is not supplied directly. For <code>jmdem</code> and <code>jmdem.fit</code> : further arguments passed to or from other methods.

Details

A typical predictor has the form `response ~ terms` where `response` is the (numeric) response vector and `terms` is a series of terms which specifies a linear predictor for response.

A terms specification of the form `first + second` indicates all the terms in `first` together with all the terms in `second` with any duplicates removed. A specification of the form `first:second` indicates the set of terms obtained by taking the interactions of all terms in `first` with all terms in `second`. The specification `first * second` indicates the cross of `first` and `second`. This is the same as `first + second + first:second`.

The terms in the formula will be re-ordered so that main effects come first, followed by the interactions, all second-order, all third-order and so on: to avoid this pass a terms object as the formula.

An additional term `response ~ terms + eta` can be added to `dformula` if the *mean* submodel is nested in the *dispersion* submodel in the form such that

$$g(E(y_i)) = \mathbf{x}_i\boldsymbol{\beta} = \eta_i, h(\phi) = \mathbf{z}_i\boldsymbol{\lambda} + \eta_i\gamma.$$

In the contrary, if the *dispersion* submodel is nested in the *mean* submodel such that

$$g(E(y_i)) = \mathbf{x}_i\boldsymbol{\beta} + \delta_i\kappa, h(\phi_i) = \mathbf{z}_i\boldsymbol{\lambda} = \delta_i,$$

`mformula` can be specified as `response ~ terms + delta`.

Non-NULL weights can be used to indicate that different observations have different dispersions (with the values in `weights` being inversely proportional to the dispersions); or equivalently, when the elements of `weights` are positive integers w_i , that each response y_i is the mean of w_i unit-weight observations. For a binomial GLM prior weights are used to give the number of trials when the response is the proportion of successes: they would rarely be used for a Poisson GLM.

If more than one of `etastart` and `mustart` is specified, the first in the list will be used. It is often advisable to supply starting values for a quasi family, and also for families with unusual links such as `gaussian("log")`.

`glm.fit` is the workhorse function: it is not normally called directly but can be more efficient where the response vector, design matrix and family have already been calculated.

Value

<code>coefficients</code>	a named vector of estimated coefficients of both the mean and <i>dispersion</i> submodel
<code>beta</code>	estimated coefficients of the <i>mean</i> submodel
<code>lambda</code>	estimated coefficients of the <i>dispersion</i> submodel
<code>residuals</code>	the <i>working</i> residuals, that is the residuals in the final iteration of the <code>optim</code> fit. Depending on the type of deviance specified by <code>dev.type</code> , <code>residuals</code> corresponds to <code>deviance.residuals</code> or <code>pearson.residuals</code> . Since cases with zero weights are omitted, their working residuals are NA.
<code>deviance.residuals</code>	the <i>deviance</i> residuals resulting from the final iteration of the <code>optim</code> fit.
<code>pearson.residuals</code>	the <i>pearson</i> residuals resulting from the final iteration of the <code>optim</code> fit.
<code>fitted.values</code>	the fitted mean values, obtained by transforming the linear predictors by the inverse of the link function.
<code>dispersion</code>	the fitted individual dispersion values, obtained by transforming the linear predictors of the <i>dispersion</i> submodel by the corresponding inverse of the link function.

mean.rank	the numeric rank of the fitted <i>mean</i> submodel.
dispersion.rank	the numeric rank of the fitted <i>dispersion</i> submodel.
rank	the total numeric rank of the fitted model. mean.rank and dispersion.rank are the corresponding ranks of the fitted <i>mean</i> and <i>dispersion</i> submodels.
mean.family	the family object used for the <i>mean</i> submodel.
dispersion.family	the family object used for the <i>dispersion</i> submodel.
mean.linear.predictors	the linear fit on link scale of the <i>mean</i> submodel.
dispersion.linear.predictors	the linear fit on link scale of the <i>dispersion</i> submodel.
deviance	the residual sum of squares of the complete fitted model.
individual.loglik	individual value of the log-likelihood function given the estimated mean and dispersion.
aic	the <i>Akaike Information Criterion</i> , minus twice the maximised log-likelihood plus twice the number of parameters.
iter	number of iterations needed for the fit.
weights	the working weights, that is the weights in the final iteration of the <code>optim</code> fit.
prior.weights	the weights initially supplied, a vector of 1s if none were.
info.matrix	the information matrix given the estimated model coefficients. The diagonal elements of its inverse are the standard errors of the model parameters.
df.residual	the residual degrees of freedom of the complete fitted model.
y	the y vector used.
x	the <i>mean</i> submodel design matrix.
z	the <i>dispersion</i> submodel design matrix.
log.llh	the maximised log-likelihood of the entire sample.
converged	logical. Was the <code>optim</code> algorithm judged to have converged?
gradient	logical. Was the gradient function included in the <code>optim</code> algorithm?
deviance.type	the type of residual deviance specified, it is either "deviance" or "pearson".
information.type	the type of information matrix specified, it is either "Hessian" or "Fisher".
dispersion.adjustment	logical. Was the dispersion parameter adjusted by an adjustment factor during the optimisation?
df.adjustment	logical. Was the likelihood function adjusted by the degrees of freedom adjustment factor?
optim.method	the name of the method used in <code>optim</code> .
control	the value of the control argument used.
data	the evaluated dataset specified in the <code>data</code> argument.

mean.model	the model frame of the <i>mean</i> submodel.
dispersion.model	the model frame of the <i>dispersion</i> submodel.
call	the matched call.
mean.formula	the formula of the <i>mean</i> submodel supplied.
dispersion.formula	the formula of the <i>dispersion</i> submodel supplied.
fit.method	the name of the fit function used, currently always "jmdem.fit".
mean.offset	the offset vector used in the <i>mean</i> submodel.
dispersion.offset	the offset vector used in the <i>dispersion</i> submodel.
dispersion.deviance	the deviance sum of squares of the <i>dispersion</i> submodel.
dispersion.df.residual	the residual degrees of freedom of the <i>dispersion</i> submodel.
null.deviance	the residual sum of squares of the complete null model.
df.null	the residual degrees of freedom for the complete null model.
dispersion.null.deviance	the residual sum of squares of the dispersion null submodel.
dispersion.df.null	the residual degrees of freedom for the dispersion null submodel.
beta.null	the estimated coefficients of the mean null submodel.
lambda.null	the estimated coefficients of the dispersion null submodel.
dispersion.null	the estimated dispersion of the complete null model.
residuals.null	the residuals of the complete null model.
mustart	the vector of starting values for individual means used.
phistart	the vector of starting values for individual dispersion used.
betastart	the vector of starting values for the <i>mean</i> submodel parameters used.
lambdastart	the vector of starting values for the <i>dispersion</i> submodel parameters used.
mean.terms	the terms object used for the <i>mean</i> submodel.
dispersion.terms	the terms object used for the <i>dispersion</i> submodel.
xlevels	a record of the levels of the factors used in fitting the <i>mean</i> submodel.
zlevels	a record of the levels of the factors used in fitting the <i>dispersion</i> submodel.
mean.contrasts	the contrasts used for the <i>mean</i> submodel.
dispersion.contrasts	the contrasts used for the <i>dispersion</i> submodel.
na.action	information returned by model.frame on the special handling of NAs.
init.mean.fit	the initial values of the <i>mean</i> submodel coefficients, linear predictors and fitted values.

`init.dispersion.fit`
the initial values of the *dispersion* submodel coefficients, linear predictors and fitted values.

`matrix.inverse.method`
information returned on the method used for inverting matrices during optimisation.

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See Also

[anova.jmdem](#), [summary.jmdem](#), etc. for `jmdem` methods, and the generic functions [effects](#), [fitted.values](#), and [residuals](#).

Examples

```
## Fit poisson counts by unnested mean and dispersion submodels.
## Use log-links for both submodels. Set dispersion fitting based
## on deviance residuals. Use conjugate gradient (CG) as
## optimisation method.
MyData <- simdata.jmdem.sim(mformula = y ~ x, dformula = ~ z,
                           mfamily = poisson(),
                           dfamily = Gamma(link = "log"),
                           beta.true = c(0.5, 4),
                           lambda.true = c(2.5, 3), n = 100)

fit <- jmdem(mformula = y ~ x, dformula = ~ z, data = MyData,
            mfamily = poisson, dfamily = Gamma(link = "log"),
            dev.type = "deviance", method = "CG")

## Fit Gaussian responses by nesting dispersion submodel in the mean
## submodel. Use default link for both submodels. Set dispersion fitting
## based on pearson residuals. Use quasi-Newton (BFGS) as optimisation
## method. Adjust degrees of freedom for the likelihood function.
MyData <- simdata.jmdem.sim(mformula = y ~ x + delta, dformula = ~ z,
                           mfamily = gaussian(),
                           dfamily = Gamma(link = "log"),
                           beta.true = c(0.5, 4, 1),
                           lambda.true = c(2.5, 3), n = 100)

fit <- jmdem(mformula = y ~ x + delta, dformula = ~ z, data = MyData,
            mfamily = gaussian, dfamily = Gamma, dev.type = "pearson",
            method = "BFGS", df.adj = TRUE)
```

jmdem.control

Auxiliary for Controlling JMDEM Fitting

Description

Auxiliary function for `jmdem` fitting. Typically only used internally by `jmdem.fit`, but may be used to construct a control argument to either function.

Usage

```
jmdem.control(maxit = 100, epsilon = 1e-8, prefit.trace = FALSE,
             fit.trace = FALSE, null.approx = 1e-8, trace = 0,
             fnscale = -1, parscale = 1, ndeps = 0.001,
             abstol = -Inf, reltol = sqrt(.Machine$double.eps),
             alpha = 1, beta = 0.5, gamma = 2, REPORT = 10,
             type = 1, lmm = 5, factr = 1e+07, pgtol = 0,
             temp = 10, tmax = 10)
```

Arguments

maxit	integer giving the maximal number of optimisation iterations.
epsilon	positive convergence tolerance ϵ ; the iterations converge when $ dev - dev_{old} / (dev + 0.1) < \epsilon$.
prefit.trace	logical indicating if output should be produced for each iteration in the prefit process.
fit.trace	logical indicating if output should be produced for each iteration in the jmdem.fit process.
null.approx	approximation of zeros to avoid estimation abortion in the case of $\log(0)$ or $1/0$. The following control arguments are used by <code>optim</code> . Please refer to <code>optim</code> for details
trace	non-negative integer. If positive, tracing information on the progress of the optimisation is produced. Higher values may produce more tracing information: for method "L-BFGS-B" there are six levels of tracing.
fnscale	An overall scaling to be applied to the value of <code>fn</code> and <code>gr</code> during optimisation. If negative, turns the problem into a maximisation problem. Optimisation is performed on <code>fn(par)/fnscale</code> .
parscale	A vector of scaling values for the parameters. Optimisation is performed on <code>par/parscale</code> and these should be comparable in the sense that a unit change in any element produces about a unit change in the scaled value. Not used (nor needed) for <code>method = "Brent"</code> .
ndeps	A vector of step sizes for the finite-difference approximation to the gradient, on <code>par/parscale</code> scale. Defaults to $1e-3$.
abstol	The absolute convergence tolerance. Only useful for non-negative functions, as a tolerance for reaching zero.
reltol	Relative convergence tolerance. The algorithm stops if it is unable to reduce the value by a factor of <code>reltol * (abs(val) + reltol)</code> at a step. Defaults to <code>sqrt(.Machine\$double.eps)</code> , typically about $1e-8$.
alpha, beta, gamma	Scaling parameters for the "Nelder-Mead" method. <code>alpha</code> is the reflection factor (default 1.0), <code>beta</code> the contraction factor (0.5) and <code>gamma</code> the expansion factor (2.0).
REPORT	The frequency of reports for the "BFGS", "L-BFGS-B" and "SANN" methods if <code>control\$trace</code> is positive. Defaults to every 10 iterations for "BFGS" and "L-BFGS-B", or every 100 temperatures for "SANN".
type	for the conjugate-gradients ("CG") method. Takes value 1 for the Fletcher-Reeves update, 2 for Polak-Ribiere and 3 for Beale-Sorenson.
lmm	is an integer giving the number of BFGS updates retained in the "L-BFGS-B" method, It defaults to 5.
factr	controls the convergence of the "L-BFGS-B" method. Convergence occurs when the reduction in the objective is within this factor of the machine tolerance. Default is $1e7$, that is a tolerance of about $1e-8$.

pgtol	helps control the convergence of the "L-BFGS-B" method. It is a tolerance on the projected gradient in the current search direction. This defaults to zero, when the check is suppressed.
tmax	controls the "SANN" method. It is the starting temperature for the cooling schedule. Defaults to 10.
temp	is the number of function evaluations at each temperature for the "SANN" method. Defaults to 10.

Details

The control argument of `jmdem` is by default passed to the control argument of `jmdem.fit`, which uses its elements as arguments to `jmdem.control`: the latter provides defaults and sanity checking.

When `trace` is true, calls to `cat` produce the output for each iteration. Hence, `options(digits = *)` can be used to increase the precision, see the example.

Value

A list with components named as the arguments.

Author(s)

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See Also

[jmdem.fit](#), the fitting procedure used by `jmdem`.

Examples

```
## Example in jmdem(...). Limit maximum iteration number to 20 and
## trace the deviance development in the fitting process
MyData <- simdata.jmdem.sim(mformula = y ~ x, dformula = ~ s,
                           mfamily = poisson(),
                           dfamily = Gamma(link = "log"),
                           beta.true = c(0.5, 4),
                           lambda.true = c(2.5, 3), n = 100)

fit <- jmdem(mformula = y ~ x, dformula = ~ s, data = MyData,
            mfamily = poisson, dfamily = Gamma(link = "log"),
            dev.type = "deviance", method = "CG",
            control = list(maxit = 20, fit.trace = TRUE))

## Change to a small convergence tolerance and trace the optimisation
## process in optim
jmdem.control(list(epsilon = 1e-14, trace = 1))
```

jmdem.sim

Simulate joint mean and dispersion effects models fits

Description

Simulate iterative `jmdem` fits on user-defined model settings

Usage

```
jmdem.sim(mformula = "y ~ 1 + x", dformula = "~ 1 + z", data = NULL,
          beta.true, lambda.true, mfamily = gaussian,
          dfamily = Gamma, dev.type = c("deviance", "pearson"),
          x.str = list(type = "numeric", random.func = "runif", param = list()),
          z.str = list(type = "numeric", random.func = "runif", param = list()),
          n = NULL, simnum = NULL, trace = FALSE, asymp.test = FALSE,
          weights = NULL, moffset = NULL, doffset = NULL,
          mustart = NULL, phistart = NULL, betastart = NULL,
          lambdastart = NULL, hessian = TRUE, na.action,
          grad.func = TRUE, fit.method = "jmdem.fit",
          method = c("Nelder-Mead", "BFGS", "CG", "L-BFGS-B", "SANN", "Brent"),
          df.adj = FALSE, disp.adj = FALSE, full.loglik = FALSE,
          mcontrasts = NULL, dcontrasts = NULL, beta.first = TRUE,
          prefit = TRUE, control = list(...),
          minv.method = c("solve", "chol2inv", "ginv"), ...)
```

```
simdata.jmdem.sim(mformula = "y ~ 1 + x", dformula = "~ 1 + z", beta.true, lambda.true,
```

```
x.str = list(type = "numeric", random.func = "runif", param = list()),
z.str = list(type = "numeric", random.func = "runif", param = list()),
mfamily = gaussian, dfamily = Gamma, weights = NULL, n, simnum = 1,
      moffset = NULL, doffset = NULL)
```

```
getdata.jmdem.sim(object)
```

Arguments

mformula	the user-defined true mean submodel, expressed in form of an object of class "formula". The number of regressors and their interactions can be specified here, but not their true parameter values.
dformula	the user-defined true dispersion submodel. See mformula.
data	an optional data frame or list of several data frames. If no data are provided, jmdem.sim will generate its own data for simulation by simdata.jmdem.sim.
beta.true	a vector of the true parameter values of the mean submodel. The number of elements in beta.true must be identical with the number of parameters to be estimated in mformula, including the intercept if there exists one in the model.
lambda.true	a vector of the true parameter values of the dispersion submodel. The number of elements in lambda.true must be identical with the number of parameters to be estimated in dformula, including the intercept if there exists one in the model.
mfamily	a description of the error distribution and link function to be used in the <i>mean</i> submodel. This can be a character string naming a family function, a family function or the result of a call to a family function. (See family for details of family functions.)
dfamily	a description of the error distribution and link function to be used in the <i>dispersion</i> submodel. (Also see family for details of family functions.)
dev.type	a specification of the type of residuals to be used as the response of the <i>dispersion</i> submodel. The ML estimates of the jmdem are the optima of either the quasi-likelihood function for <i>deviance residuals</i> , or the pseudo-likelihood function for <i>Pearson residuals</i> .
x.str	a list of user-specified structure for the generation of the mean submodel design matrix, including the type (numeric, character, logical etc.), an r function (random.func) to generate the values of the regressors and the corresponding parameters (param) to be passed on to (random.func). Note that all parameters that belong to the same random.func must be put in a list(...). See details.
z.str	a list of user-specified structure for the generation of the dispersion submodel design matrix, including the type (numeric, character, logical etc.), an r function (random.func) to generate the values of the regressors and the corresponding parameters (param) to be passed on to (random.func). Note that all parameters that belong to the same random.func must be put in a list(...). See details.
n	a numeric value specifying the sample size in each simulation.
simnum	a numeric value specifying the number of simulations.
trace	a specification whether the estimated coefficients should be printed to screen after each simulation.

asympt.test	a specification whether the Rao's score and Wald tests should be conducted for each simulation.
...	for control: arguments to be used to form the default control argument if it is not supplied directly. For <code>jmdem.sim</code> : further arguments passed to or from other methods. The following arguments are used for JMDEM fitting. See <code>jmdem</code> for details.
weights	an optional vector of 'prior weights' to be used in the fitting process. Should be NULL or -a numeric vector.
moffset	an a priori known component to be included in the linear predictor of the <i>mean</i> submodel during fitting. This should be NULL or a numeric vector of length equal to the number of cases. One or more offset terms can be included in the formula instead or as well, and if more than one is specified their sum is used. See <code>model.offset</code> .
doffset	an a priori known component to be included in the linear predictor of the <i>dispersion</i> submodel during fitting. See <code>model.offset</code> .
mustart	a vector of starting values of individual means.
phistart	a vector of starting values of individual dispersion.
betastart	a vector of starting values for the regression parameters of the <i>mean</i> submodel.
lambdastart	a vector of starting values for the regression parameters of the <i>dispersion</i> submodel.
hessian	the method used to compute the information matrix. Hessian matrix will be calculated for "TRUE", Fisher matrix for "FALSE".
na.action	a function which indicates what should happen when the data contain NAs. The default is set by the <code>na.action</code> setting of <code>options</code> , and is <code>na.fail</code> if that is unset. The 'factory-fresh' default is <code>na.omit</code> . Another possible value is NULL, no action. Value <code>na.exclude</code> can be useful.
grad.func	the gradient function will be included in the optimisation for the "BFGS", "CG" and "L-BFGS-B" methods for "TRUE". If it is NULL, a finite-difference approximation will be used. For the "SANN" method it specifies a function to generate a new candidate point. If it is NULL a default Gaussian Markov kernel is used.
fit.method	the method to be used in fitting the model. The default method " <code>jmdem.fit</code> " uses the general-purpose optimisation (<code>optim</code>): the alternative " <code>model.frame</code> " returns the model frame and does no fitting. User-supplied fitting functions can be supplied either as a function or a character string naming a function, with a function which takes the same arguments as <code>jmdem.fit</code> . If specified as a character string it is looked up from within the <code>stats</code> namespace.
method	the method to be used for the optimisation. See <code>optim</code> for details.
df.adj	an adjustment factor for the degrees of freedom $(n-p)/n$, where n is the number of observations and p is the number of parameters to be estimated in <code>jmdem</code> , will be multiplied to the likelihood function before the optimisation for "TRUE".
disp.adj	an adjustment factor for the dispersion weight will be multiplied to the estimated dispersion parameter during the optimisation for "TRUE". For details, please see McCullagh and Nelder (1989, Ch. 10, P. 362).

<code>full.loglik</code>	the full likelihood function instead of the quasi- or pseudo-likelihood function will be used for the optimisation for TRUE.
<code>mcontrasts</code>	an optional list for the mean effect contrasts. See the <code>contrasts.arg</code> of <code>model.matrix.default</code> .
<code>dcontrasts</code>	an optional list for the dispersion effect contrasts. See the <code>contrasts.arg</code> of <code>model.matrix.default</code> .
<code>beta.first</code>	the mean effects will be estimated (assuming constant sample dispersion) at the initial stage for TRUE. For FALSE, the dispersion effects will be estimated first (assuming constantly zero mean for the whole sample).
<code>prefit</code>	a specification whether <code>jmdem</code> uses <code>glm</code> to prefit the starting values of the mean and dispersion parameters. For FALSE, the initial parameter values of all the regressors are set to zero and the sample mean and sample dispersion will be used as the starting values of the corresponding submodel intercepts instead. If the submodels have no intercept, all parameters will also be set to zero. The sample mean and sample dispersion will then be used as <code>mustart</code> and <code>phistart</code> in the internal computation (they will not be officially recorded in <code>mustart</code> and <code>phistart</code> in the output object). Default value is TRUE.
<code>control</code>	a list of parameters for controlling the fitting process. For <code>jmdem.fit</code> this is passed to <code>jmdem.control</code> .
<code>minv.method</code>	the method used to invert matrices during the estimation process. "solve" gives the solutions of a system of equations, "chol2inv" gives the inverse from Choleski or QR decomposition and "ginv" gives the generalised inverse of a matrix. If none of the methods is specified or if they are specified in a vector such as <code>c("solve", "chol2inv", "ginv")</code> , the matrices will be inverted by the methods in the sequence as given in the vector until it is found.
<code>object</code>	one or several objects of class <code>jmdem.sim</code> , typically the result of a call to <code>jmdem.sim</code> .

Details

`jmdem.sim` simulates the fitting of datasets in which the regressors of the mean and dispersion submodels are generated according to the specification given in `x.str` and `z.str`. The response variable will be then generated according to the distribution specified in `mfamily` with linear predictor of the mean given by `mformula` and the linear predictor of the dispersion given by `dformula`.

The specifications in `x.str` and `z.str` are rather flexible if more than one independent variables are included in any of the submodels. For instance, if one of the two independent variables of the mean submodel is numeric generated from the normal distribution of mean 0 and standard deviation 1, and the other one is a 4-level factor 0, 1, 2, 3 generated from the uniform distribution, then they can be specified in a vector using `c(...)`, such as: `x.str = list(type = c("numeric", "factor"), random.func = c("rnorm", "rnorm"))`.

Note that the higher the number of simulations specified in `simnum`, the more stabilised are the aggregated simulation results. The larger the sample size in each simulation, the less fluctuated are the estimated results among the simulations.

Users gain `simdata.jmdem.sim` higher control on the simulation by generating a number of datasets upon their own settings first, and not running `jmdem.sim` at the same time. By taking these steps, users also have the flexibility to edit the datasets according their own individual requirements, before calling them in `jmdem.sim`.

Users can also extract the datasets used in `jmdem.sim` by `getdata.jmdem.sim`. This function is useful if the datasets are generated in `jmdem.sim` where users do not have access prior to the simulations.

`getdata.jmdem.sim` and `simdata.jmdem.sim` can also be useful if the users would like to conduct various simulations with different `jmdem` settings on the same data.

Value

An object of class `jmdem.sim` contains of a list of `jmdem` fits with full model information. That means, each element of the `jmdem.sim` object contains the same attributes as a `jmdem` object. See *values* of `jmdem` for details.

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See Also

[jmdem](#), [summary.jmdem.sim](#)

Examples

```
## Run 10 JMDEM simulations with samples of size 50. The response
## variable is Gaussian with mean beta_0 + beta_1 * x and variance
## log(sigma^2) = lambda_0 + lambda_1 * z. The observations of
## the predictor x should be random numbers generated from the normal
## distribution with mean 0 and standard deviation 2. The observations
## of z are factors with three levels between 0 and 2, generated from
## the uniform distribution. The true values of the mean submodel's
## intercept and slope are 1.5 and 4, as well as 2.5, 3 and -0.2 for
## the dispersion submodel's intercept and slope.
sim <- jmdem.sim(mformula = y ~ x, dformula = ~ z, beta.first = TRUE,
               mfamily = gaussian, dfamily = Gamma(link = "log"),
               x.str = list(type = "numeric", random.func = "rnorm",
                             param = list(mean = 0, sd = 2)),
               z.str = list(type = "factor", random.func = "runif",
                             param = list(min = 0, max = 2)),
               beta.true = c(1.5, 4), lambda.true = c(2.5, 3, -0.2),
               grad.func = TRUE, method = "BFGS", n = 50,
               simnum = 10)
```

Description

These functions are all [methods](#) for class `jmdem` or `summary.jmdem` objects.

Usage

```
## S3 method for class 'jmdem'
formula(x, submodel = c("both", "mean", "dispersion"), ...)

## S3 method for class 'jmdem'
family(object, submodel = c("both", "mean", "dispersion"), ...)

## S3 method for class 'jmdem'
residuals(object, type = c("deviance", "pearson", "working",
                           "response", "partial"), ...)
```

Arguments

<code>x</code> , <code>object</code>	the function <code>family</code> accesses the family objects which are stored within objects created by <code>jmdem</code> .
<code>submodel</code>	character. The family of the specified submodel. For both, the families of the mean and dispersion submodels will be return in a list of 2 elements.
<code>type</code>	character. For residuals, the type of residuals which should be returned. The alternatives are: "deviance" (default), "pearson", "working", "response", and "partial".
<code>...</code>	further arguments passed to methods.

Details

`family` is a generic function with methods for class "jmdem". See [family](#) for details.

Here `formula` is referred to the case that it is called on a fitted `jmdem` model object. The default first, depending on the specified `submodel` argument, looks for a "mean.formula" and/or "dispersion.formula" component of the `jmdem` object (and evaluates it), then a "mean.terms" and/or "dispersion.terms" component, then a `mformula` and/or `dformula` parameter of the call (and evaluates its value) and finally a "formula" attribute.

The references define the types of residuals: Davison & Snell is a good reference for the usages of each.

The partial residuals are a matrix of working residuals, with each column formed by omitting a term from the model.

How residuals treats cases with missing values in the original fit is determined by the `na.action` argument of that fit. If `na.action = na.omit` omitted cases will not appear in the residuals, whereas if `na.action = na.exclude` they will appear, with residual value NA. See also [naresid](#).

For fits done with `y = FALSE` the response values are computed from other components.

Author(s)

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See Also

[jmdem](#), [anova.jmdem](#), [coef](#), [deviance](#), [df.residual](#), [effects](#), [fitted](#), [weighted.residuals](#), [residuals](#), [residuals.jmdem](#), [summary.jmdem](#), [weights](#).

Examples

```
## The jmdem(...) example
MyData <- simdata.jmdem.sim(mformula = y ~ x, dformula = ~ z,
                           mfamily = poisson(),
                           dfamily = Gamma(link = "log"),
                           beta.true = c(0.5, 4),
                           lambda.true = c(2.5, 3), n = 100)

fit <- jmdem(mformula = y ~ x, dformula = ~ z, data = MyData,
            mfamily = poisson, dfamily = Gamma(link = "log"),
            dev.type = "deviance", method = "CG")

coef(fit)
plot(resid(fit), fitted(fit))
abline(h = 0, lty = 2, col = "gray")
```

model.matrix.jmdem *Construct Design Matrices*

Description

model.matrix creates a design (or model) matrix, e.g., by expanding factors to a set of dummy variables (depending on the contrasts) and expanding interactions similarly.

Usage

```
## S3 method for class 'jmdem'
model.matrix(object, submodel = c("both", "mean", "dispersion"), ...)
```

Arguments

object	the function family accesses the family objects which are stored within objects created by jmdem.
submodel	character. The family of the specified submodel. For both, the families of the mean and dispersion submodels will be return in a list of 2 elements.
...	further arguments passed to or from other methods.

Details

model.matrix creates a design matrix from the description given in terms(object), using the data in data which must supply variables with the same names as would be created by a call to model.frame(object) or, more precisely, by evaluating attr(terms(object), "variables").

Value

The design matrix for a regression-like model with the specified formula and data.

There is an attribute "assign", an integer vector with an entry for each column in the matrix giving the term in the formula which gave rise to the column. Value 0 corresponds to the intercept (if any), and positive values to terms in the order given by the term.labels attribute of the terms structure corresponding to object.

If there are any factors in terms in the model, there is an attribute "contrasts", a named list with an entry for each factor. This specifies the contrasts that would be used in terms in which the factor is coded by contrasts (in some terms dummy coding may be used), either as a character vector naming a function or as a numeric matrix.

Author(s)

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References

Chambers, J. M. (1992). *Data for models*. Chapter 3 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

See Also

[model.frame](#), [model.extract](#), [terms](#)

Examples

```
## Example in jmdem(...)
MyData <- simdata.jmdem.sim(mformula = y ~ x, dformula = ~ z,
                           mfamily = poisson(),
                           dfamily = Gamma(link = "log"),
                           beta.true = c(0.5, 4),
                           lambda.true = c(2.5, 3), n = 100)

fit <- jmdem(mformula = y ~ x, dformula = ~ z, data = MyData,
            mfamily = poisson, dfamily = Gamma(link = "log"),
```

```

dev.type = "deviance", method = "CG")

## Extract the design matrix of the mean submodel
model.matrix(fit, submodel = "mean")

```

predict.jmDEM

Predict Method for JMDEM Fits

Description

Obtains predictions and optionally estimates standard errors of those predictions from a fitted joint mean and dispersion effect model object.

Usage

```

## S3 method for class 'jmDEM'
predict(object, newdata = NULL, type = c("link", "response"),
        se.fit = FALSE, na.action = na.pass, ...)

```

Arguments

object	a fitted object of class inheriting from "jmDEM".
newdata	optionally, a data frame in which to look for variables with which to predict. If omitted, the fitted linear predictors are used.
type	the type of prediction required. The default is on the scale of the linear predictors; the alternative "response" is on the scale of the response variable. Thus for a default binomial model the default predictions are of log-odds (probabilities on logit scale) and type = "response" gives the predicted probabilities.
se.fit	logical switch indicating if standard errors are required.
na.action	function determining what should be done with missing values in newdata. The default is to predict NA.
...	further arguments passed to or from other methods.

Details

If newdata is omitted the predictions are based on the data used for the fit. In that case how cases with missing values in the original fit is determined by the na.action argument of that fit. If na.action = na.omit omitted cases will not appear in the residuals, whereas if na.action = na.exclude they will appear (in predictions and standard errors), with residual value NA. See also [napredict](#).

Value

If se.fit = FALSE, a vector or matrix of predictions.

If se.fit = TRUE, a list with components

fit	Predictions, as for se.fit = FALSE.
se.fit	Estimated standard errors.

Note

Variables are first looked for in newdata and then searched for in the usual way (which will include the environment of the formula used in the fit). A warning will be given if the variables found are not of the same length as those in newdata if it was supplied.

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See Also

[jmdem](#)

Examples

```
## Example in jmdem(...)
MyData <- simdata.jmdem.sim(mformula = y ~ x, dformula = ~ z,
                           mfamily = poisson(),
                           dfamily = Gamma(link = "log"),
                           beta.true = c(0.5, 4),
                           lambda.true = c(2.5, 3), n = 100)

fit <- jmdem(mformula = y ~ x, dformula = ~ z, data = MyData,
            mfamily = poisson, dfamily = Gamma(link = "log"),
            dev.type = "deviance", method = "CG")

## Predict on the scale of the response variable with standard errors.
predict(fit, type = "response", se.fit = TRUE)

## Predict based on a new observation on the scale of the linear
## predictors with standard errors.
predict(fit, newdata = data.frame(x = -1.5, z = 100), se.fit = TRUE)
```

score.jmdem, wald.jmdem

Asymptotic tests for fits of joint mean and dispersion effects models

Description

Computes a score (Rao) or Wald chi-squared test statistics for comparing two jmdem models.

Usage

```
score.jmdem(object, ...)
```

```
wald.jmdem(object, ...)
```

Arguments

object a model or list of two or more models fitted by jmdem to be tested. Pairwise tests will be conducted.

... a list of two or more fitted models to be tested.

Details

Given a vector of model coefficients of length p , $\Theta = (\theta_1, \dots, \theta_q, \theta_{q+1}, \dots, \theta_p)^T$, the score and Wald tests are usually used to test the null hypothesis against an alternative

$$H_0 : \theta_{q+1} = \dots = \theta_p = 0 \text{ vs. } H_0 \text{ not true}$$

Thus, they are asymptotic tests on the explanatory power of one or more regressors. And the result of the score and Wald tests only makes sense if the models involved are nested, i.e. all coefficients of a "smaller" (null, restricted) model are included in a "bigger" (alternative, unrestricted) model.

The main difference between the score and Wald tests is that the score test only requires the knowledge of the fitted coefficients of the "small" model. The Wald test, on the other hand, only need the estimates of the "bigger" model. Nevertheless, these tests are asymptotically equivalent, i.e. for large samples, the test statistics of these tests on the same set of models should be very close.

The key assumption is that the coefficient estimates asymptotically follow a (multivariate) normal distribution with mean and variance equal to the model parameters and their variance-covariance matrix.

score.jmdem and wald.jmdem extract the fitted coefficients and their variance-covariance matrix from the model objects, and evaluate the test statistics subsequently. So it is not necessary to specify the coefficients and variance-covariance matrix in the function arguments.

score.jmdem and wald.jmdem only return the test statistics. They are asymptotically chi-square distributed with $p - q$ degrees of freedom.

Value

score.jmdem and wald.jmdem return a column matrix containing the test statistics of the pairwise comparisons of all models given by the user in object and ...

Note

The score test is sometimes also called the Rao's score test or Lagrange multiplier (LM) test in different literatures.

Normally, asymptotic tests include likelihood ratio (LR), Rao's score and Wald tests. The likelihood ratio test is omitted here because the comparison of the deviances of two joint mean and dispersion effects models is questionable, if not even invalid. One important argument is that the dependent variables of two different dispersion submodels given two different mean submodels are not the identical.

Author(s)

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See Also

[anova.jmdem](#), [anova](#), [jmdem](#)

Examples

```
## Example in jmdem(...)
MyData <- simdata.jmdem.sim(mformula = y ~ x + delta, dformula = ~ z,
                           mfamily = gaussian(),
                           dfamily = Gamma(link = "log"),
                           beta.true = c(0.5, 4, 1),
                           lambda.true = c(2.5, 3), n = 100)

fit <- jmdem(mformula = y ~ x + delta, dformula = ~ z, data = MyData,
            mfamily = gaussian, dfamily = Gamma, dev.type = "pearson",
            method = "BFGS", df.adj = TRUE)

fit.1 <- update(fit, mformula = . ~ . - delta)

fit.2 <- update(fit.1, mformula = . ~ . - x)

## conduct a Wald tests
wald.jmdem(fit, fit.1, fit.2)

## should deliver the same results as above
wald.jmdem(object = list(fit, fit.1, fit.2))

## conduct the score test and compute the p-value directly.
raotest <- score.jmdem(fit, fit.2)
pchisq(raotest, df = abs(df.residual(fit) - df.residual(fit.2)),
       lower.tail = FALSE)
```

Description

This is a utility function, used in `jmdem` method for `anova(..., test != NULL)` and should not be used by the average user.

Usage

```
stat.anova.jmdem(table, test = c("Rao", "Wald"))
```

Arguments

table numeric matrix as results from `anova.jmdem(..., test = NULL, print.results = FALSE)` saved as the attributes `table.x` or `table.z`.

test a character string, partially matching one of "Rao" or "Wald".

Value

A matrix which is the original table, augmented by a column of test statistics, depending on the test argument.

Author(s)

Ka Yui Karl Wu (kykarlwu@gmail.com)

References

Hastie, T. J. and Pregibon, D. (1992). *Generalized linear models*. Chapter 6 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

See Also

[anova.jmdem](#)

Examples

```
## Example in jmdem(...)
MyData <- simdata.jmdem.sim(mformula = y ~ x, dformula = ~ z,
                           mfamily = poisson(),
                           dfamily = Gamma(link = "log"),
                           beta.true = c(0.5, 4),
                           lambda.true = c(2.5, 3), n = 100)

fit <- jmdem(mformula = y ~ x, dformula = ~ z, data = MyData,
            mfamily = poisson, dfamily = Gamma(link = "log"),
            dev.type = "deviance", method = "CG")

stat.anova.jmdem(anova(fit, test = "Rao", print.results = FALSE)$table.x)
```

Description

These functions are all [methods](#) for class `jmdem` or `summary.jmdem` objects.

Usage

```
## S3 method for class 'jmdem'
summary(object, correlation = FALSE, symbolic.cor = FALSE, ...)

## S3 method for class 'summary.jmdem'
print(x, digits = max(3L, getOption("digits") - 3L),
      scientific = FALSE, symbolic.cor = x$symbolic.cor,
      signif.stars = getOption("show.signif.stars"), ...)
```

Arguments

<code>object</code>	an object of class "jmdem", usually, a result of a call to jmdem .
<code>x</code>	an object of class "summary.jmdem", usually, a result of a call to <code>summary.jmdem</code> .
<code>correlation</code>	logical; if TRUE, the correlation matrix of the estimated parameters is returned and printed.
<code>digits</code>	the number of significant digits to use when printing.
<code>scientific</code>	logical; if TRUE, scientific notation is used when printing.
<code>symbolic.cor</code>	logical. If TRUE, print the correlations in a symbolic form (see symnum) rather than as numbers.
<code>signif.stars</code>	logical. If TRUE, 'significance stars' are printed for each coefficient.
<code>...</code>	further arguments passed to or from other methods.

Details

`print.summary.jmdem` tries to be smart about formatting the coefficients, standard errors, etc. and additionally gives 'significance stars' if `signif.stars` is TRUE. The `coefficients`, `mean.coefficients` and `dispersion.coefficients` components of the result give the estimated coefficients and their estimated standard errors, together with their ratio. This third column is labelled t-ratio and a fourth column gives the two-tailed p-value corresponding to the t-ratio based on a Student t distribution.

Aliased coefficients are omitted in the returned object but restored by the `print` method.

Correlations are printed to the same decimal places specified in `digits` (or symbolically): to see the actual correlations print `summary(object)$correlation` directly.

For more details, see [summary.glm](#).

Value

call	the component from object.
mean.family	the component from object.
dispersion.family	the component from object.
deviance	the component from object.
mean.terms	the component from object.
dispersion.terms	the component from object.
aic	the component from object.
mean.contrasts	the component from object.
dispersion.contrasts	the component from object.
df.residual	the component from object.
null.deviance	the component from object.
df.null	the component from object.
information.type	the component from object.
iter	the component from object.
mean.na.action	the component from object.
dispersion.na.action	the component from object.
deviance.resid	the deviance residuals.
pearson.resid	the pearson residuals.
resid	the working residuals depends on the setting of deviance.type.
coefficients	the matrix of coefficients, standard errors, z-values and p-values. Aliased coefficients are omitted.
mean.coefficients	the matrix of coefficients, standard errors, z-values and p-values of the mean submodel.
dispersion.coefficients	the matrix of coefficients, standard errors, z-values and p-values of the dispersion submodel.
deviance.type	the type of residual deviance specified, it is either "deviance" or "pearson".
aliased	named logical vector showing if the original coefficients are aliased.
df	a 3-vector of the rank of the model and the number of residual degrees of freedom, plus number of coefficients (including aliased ones).
covariance	the estimated covariance matrix of the estimated coefficients.
digits	the number of significant digits to use when printing.
scientific	logical value of using scientific notation when printing.
covmat.method	named method used to invert the covariance matrix.
correlation	(only if correlation is true.) The estimated correlations of the estimated coefficients.
symbolic.cor	(only if correlation is true.) The value of the argument symbolic.cor.

Author(s)

Ka Yui Karl Wu (kykar1wu@gmail.com)

See Also

[jmdem](#), [summary](#)

Examples

```
## Example in jmdem(...)
MyData <- simdata.jmdem.sim(mformula = y ~ x, dformula = ~ z,
                           mfamily = poisson(),
                           dfamily = Gamma(link = "log"),
                           beta.true = c(0.5, 4),
                           lambda.true = c(2.5, 3), n = 100)

fit <- jmdem(mformula = y ~ x, dformula = ~ z, data = MyData,
            mfamily = poisson, dfamily = Gamma(link = "log"),
            dev.type = "deviance", method = "CG")

## Summarise fit with correlation matrix
summary(fit, correlation = TRUE, digits = 4)
```

summary.jmdem.sim

Summarising JMDEM Simulations

Description

These functions are all [methods](#) for class `jmdem.sim` or `summary.jmdem.sim` objects.

Usage

```
## S3 method for class 'jmdem.sim'
summary(object, digits = max(3L, getOption("digits") - 3L),
        scientific = FALSE, pvalue = 0.05,
        minv.method = c("solve", "chol2inv", "ginv"),
        other.call = FALSE, details = FALSE, ...)

## S3 method for class 'summary.jmdem.sim'
print(x, digits = max(3L, getOption("digits") - 3L), scientific = FALSE,
      pvalue = 0.05, signif.stars = getOption("show.signif.stars"),
      other.call = FALSE, details = FALSE, ...)
```

Arguments

<code>object</code>	an object of class "jmdem.sim", usually, a result of a call to jmdem.sim .
<code>x</code>	an object of class "summary.jmdem.sim", usually, a result of a call to <code>summary.jmdem.sim</code> .
<code>digits</code>	the number of significant digits to use when printing.

scientific	logical; if TRUE, scientific notation is used when printing.
pvalue	a value between 0 and 1. It is used to compute the coverage proportion of the true parameter values by the simulated fits.
minv.method	the method used to invert matrices during the estimation process. "solve" gives the solutions of a system of equations, "chol2inv" gives the inverse from Choleski or QR decomposition and "ginv" gives the generalised inverse of a matrix. If none of the methods is specified or if they are specified in a vector such as c("solve", "chol2inv", "ginv"), the matrices will be inverted by the methods in the sequence as given in the vector until it is found.
signif.stars	logical. If TRUE, 'significance stars' are printed for each coefficient.
other.call	logical. If true, the rest of simulation call (i.e. without the mean and dispersion submodel formulas, families, true values) will be shown.
details	logical. If true, coefficients, standard errors, true parameter coverage (TRUE/FALSE) and asymptotic test statistics of each simulation will be listed.
...	further arguments passed to or from other methods.

Details

The arithmetic mean of the coefficients, standard errors and coverage by the confidence intervals estimated in all simulations will be listed in a table. A detail listing of each simulation's results can be provided if required by `details = TRUE`. The summary also includes the averages of the Rao's score and Wald test statistics of all simulation fits.

`print.summary.jmdem.sim` tries to be smart about formatting the coefficients, standard errors, etc according the number of significant digits (default of user-specified) or the usage of scientific notation or not.

Value

digits	the number of significant digits to use when printing.
scientific	logical value of using scientific notation when printing.
details	logical value of printing details of each simulation.
other.call	logical value of printing other parameters of the simulation call.
pvalue	numeric value between 0 and 1 used for the computation of the true parameter coverage.
beta.true	user-defined vector containing the true parameter values of the mean submodel.
lambda.true	user-defined vector containing the true parameter values of the dispersion submodel.
simcall	the component from object.
mformula	the component from object.
dformula	the component from object.
mfamily	the component from object.
dfamily	the component from object.
coefficients	mean and dispersion submodel parameter coefficients fitted in each simulation saved in a data.frame.

stderr	standard errors of all mean and dispersion submodel parameter coefficients estimated in each simulation saved in a <code>data.frame</code> .
iterations	a vector containing the running numbers of each simulation.
confint	confidence intervals of all mean and dispersion submodel parameter coefficients estimated in each simulation saved in a <code>data.frame</code> .
coverage	the coverage of all true submodel parameters by the confidence intervals estimated in each simulation saved in a <code>data.frame</code> .
asympt.test	Rao's score and Wald test statistics of each simulation saved in a <code>data.frame</code> .
average.summary	Arithmetic means of the coefficients, standard errors, confidence interval convergence estimated in all simulations saved in a <code>data.frame</code> .
average.asympt.test	(Arithmetic means of the Rao's score and Wald test statistics estimated in all simulations saved in a <code>data.frame</code> .)

Author(s)

Ka Yui Karl Wu (kykarlwu@gmail.com)

See Also

[jmDEM.sim](#), [jmDEM](#), [summary](#)

Examples

```
## Example in jmDEM.sim(...)
sim <- jmDEM.sim(mformula = y ~ x, dformula = ~ z, beta.first = TRUE,
  mfamily = gaussian, dfamily = Gamma(link = "log"),
  x.str = list(type = "numeric", random.func = "rnorm",
    param = list(mean = 0, sd = 2)),
  z.str = list(type = "factor", random.func = "runif",
    param = list(min = 0, max = 2)),
  beta.true = c(1.5, 4), lambda.true = c(2.5, 3, -0.2),
  grad.func = TRUE, method = "BFGS", n = 50,
  simnum = 10)

## Summarise simulation
summary(sim, details = FALSE, other.call = TRUE)
```

update.jmDEM

Update and Re-fit a JMDEM Call

Description

update will update and (by default) re-fit a model. It does this by extracting the call stored in the object, updating the call and (by default) evaluating that call. Sometimes it is useful to call update with only one argument, for example if the data frame has been corrected.

Usage

```
## S3 method for class 'jmdem'
update(object, mformula, dformula, ...)
```

Arguments

object	An existing fit from a jmdem model function
mformula	Changes to the formula of the mean submodel - see update.formula for details.
dformula	Changes to the formula of the dispersion submodel - see update.formula for details.
...	Additional arguments to the call, or arguments with changed values. Use name = NULL to remove the argument name.

Author(s)

Ka Yui Karl Wu (kykarlwu@gmail.com)

References

Chambers, J. M. (1992). *Linear models*. Chapter 4 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

See Also

[update.formula](#)

Examples

```
## Example in jmdem(...): Update the dispersion fitting based on Pearson
## residuals and change from Nelder-Mead to BFGS as optimisation method.
MyData <- simdata.jmdem.sim(mformula = y ~ x, dformula = ~ z,
                           mfamily = poisson(),
                           dfamily = Gamma(link = "log"),
                           beta.true = c(0.5, 4),
                           lambda.true = c(2.5, 3), n = 100)

fit <- jmdem(mformula = y ~ x, dformula = ~ z, data = MyData,
            mfamily = poisson, dfamily = Gamma(link = "log"),
            dev.type = "deviance", method = "CG")

update(fit, dev.type = "pearson", method = "BFGS")
```


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