

# Package ‘MatrixModels’

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**Description** Modelling with sparse and dense 'Matrix' matrices, using modular prediction and response module classes.

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## R topics documented:

glm4 . . . . .	2
glpModel-class . . . . .	4
lm.fit.sparse . . . . .	5
mkRespMod . . . . .	7
Model-class . . . . .	8
model.Matrix . . . . .	9
modelMatrix-class . . . . .	10
predModule-class . . . . .	11

resid-et-al . . . . .	13
respModule-class . . . . .	13
reweightPred . . . . .	15
solveCoef . . . . .	15
updateMu . . . . .	16
updateWts . . . . .	17

<b>Index</b>	<b>18</b>
--------------	-----------

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glm4	<i>Fitting Generalized Linear Models (using S4)</i>
------	---

---

### Description

glm4, very similarly as standard R's `glm()` is used to fit generalized linear models, specified by giving a symbolic description of the linear predictor and a description of the error distribution.

It is more general, as it fits linear, generalized linear, non-linear and generalized nonlinear models.

### Usage

```
glm4(formula, family, data, weights, subset, na.action,
      start = NULL, etastart, mustart, offset,
      sparse = FALSE, drop.unused.levels = FALSE, doFit = TRUE,
      control = list(...),
      model = TRUE, x = FALSE, y = TRUE, contrasts = NULL, ...)
```

### Arguments

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

start, etastart, mustart	starting values for the parameters in the linear predictor, the predictor itself and for the vector of means.
offset	this can be used to specify an <i>a priori</i> known component to be included in the linear predictor during fitting. This should be NULL or a numeric vector of length equal to the number of cases. One or more <code>offset</code> 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> .
sparse	logical indicating if the model matrix should be sparse or not.
drop.unused.levels	used only when <code>sparse</code> is TRUE: Should factors have unused levels dropped? (This used to be true, <i>implicitly</i> in the first versions up to July 2010; the default has been changed for compatibility with R's standard (dense) <code>model.matrix()</code> ).
doFit	logical indicating if the model should be fitted (or just returned unfitted).
control	a list with options on fitting; currently passed unchanged to (hidden) function <code>IRLS()</code> .
model, x, y	currently ignored; here for back compatibility with <code>glm</code> .
contrasts	currently ignored
...	potentially arguments passed on to fitter functions; not used currently.

## Value

an object of class `glpModel`.

## See Also

`glm()` the standard R function;  
`lm.fit.sparse()` a sparse least squares fitter.

The resulting class `glpModel` documentation.

## Examples

```
### All the following is very experimental -- and probably will change: -----

data(CO2, package="datasets")
## dense linear model
str(glm4(uptake ~ 0 + Type*Treatment, data=CO2, doFit = FALSE), 4)
## sparse linear model
str(glm4(uptake ~ 0 + Type*Treatment, data=CO2, doFit = FALSE,
        sparse = TRUE), 4)

## From example(glm): -----

## Dobson (1990) Page 93: Randomized Controlled Trial :
str(trial <- data.frame(counts=c(18,17,15,20,10,20,25,13,12),
                       outcome=gl(3,1,9,labels=LETTERS[1:3]),
                       treatment=gl(3,3,labels=letters[1:3])))
glm.D93 <- glm(counts ~ outcome + treatment, family=poisson, data=trial)
```

```

summary(glm.D93)
c.glm <- unname(coef(glm.D93))
glmM <- glm4(counts ~ outcome + treatment, family = poisson, data=trial)
glmM2 <- update(glmM, quick = FALSE) # slightly more accurate
glmM3 <- update(glmM, quick = FALSE, finalUpdate = TRUE)
      # finalUpdate has no effect on 'coef'
stopifnot( identical(glmM2@pred@coef, glmM3@pred@coef),
            all.equal(glmM @pred@coef, c.glm, tolerance=1e-7),
            all.equal(glmM2@pred@coef, c.glm, tolerance=1e-12))

## Watch the iterations --- and use no intercept --> more sparse X
## 1) dense generalized linear model
glmM <- glm4(counts ~ 0+outcome + treatment, poisson, trial,
             verbose = TRUE)
## 2) sparse generalized linear model
glmS <- glm4(counts ~ 0+outcome + treatment, poisson, trial,
             verbose = TRUE, sparse = TRUE)
str(glmS, max.lev = 4)
stopifnot( all.equal(glmM@pred@coef, glmS@pred@coef),
            all.equal(glmM@pred@Vtr, glmS@pred@Vtr) )

## A Gamma example, from McCullagh & Nelder (1989, pp. 300-2)
clotting <- data.frame(u = c(5,10,15,20,30,40,60,80,100),
                     lot1 = c(118,58,42,35,27,25,21,19,18),
                     lot2 = c(69,35,26,21,18,16,13,12,12))
str(gmN <- glm4(lot1 ~ log(u), data=clotting, family=Gamma, verbose=TRUE))
glm. <- glm(lot1 ~ log(u), data=clotting, family=Gamma)
stopifnot( all.equal(gmN@pred@coef, unname(coef(glm.)), tolerance=1e-7) )

```

---

glpModel-class

*Class "glpModel" of General Linear Prediction Models*


---

## Description

The class "glpModel" conceptually contains a very large class of "*General Linear Prediction Models*".

Its resp slot (of class "*respModule*") may model linear, non-linear, generalized linear and non-linear generalized response models.

## Objects from the Class

Objects can be created by calls of the form `new("glpModel", ...)`, but typically rather are returned by our modeling functions, e.g., the (experimental, hence currently hidden) `glm4()`.

## Slots

resp: a "*respModule*" object.

pred: a "*predModule*" object.

**Extends**

Class "[Model](#)", directly.

**Methods**

**coef** signature(object = "glpModel"): extract the coefficient vector  $\beta$  from the object.

**fitted** signature(object = "glpModel"): fitted values; there may be several types, corresponding to the residuals, see there (below).

**residuals** signature(object = "glpModel"): residuals, depending on the type of the model, there are several types of residuals and correspondingly residuals, see [residuals.glm](#) from the **stats** package.

**See Also**

[glm4\(\)](#) returns fitted glpModel objects.

The constituents of this class are [respModule](#) and [predModule](#), both of which have several sub classes.

**Examples**

```
showClass("glpModel")
## Use  example(glm4)  or see  help(glm4)  for many more examples.
```

---

lm.fit.sparse

*Fitter Function for Sparse Linear Models*


---

**Description**

A basic computing engine for sparse linear least squares regression.

Note that the exact interface (arguments, return value) currently is **experimental**, and is bound to change. Use at your own risk!

**Usage**

```
lm.fit.sparse(x, y, w = NULL, offset = NULL,
              method = c("qr", "cholesky"),
              tol = 1e-7, singular.ok = TRUE, order = NULL,
              transpose = FALSE)
```

**Arguments**

x	<i>sparse</i> design matrix of dimension $n * p$ , i.e., an R object of a <a href="#">class</a> extending <a href="#">dsparseMatrix</a> ; typically the result of <a href="#">sparse.model.matrix</a> .
y	vector of observations of length $n$ , or a matrix with $n$ rows.
w	vector of weights (length $n$ ) to be used in the fitting process. Weighted least squares is used with weights $w$ , i.e., $\text{sum}(w * e^2)$ is minimized. <b>Not yet implemented !</b>
offset	numeric of length $n$ ). This can be used to specify an <i>a priori</i> known component to be included in the linear predictor during fitting.
method	a character string specifying the (factorization) method. Currently, "qr" or "cholesky".
tol	[for back-compatibility only; unused:] tolerance for the qr decomposition. Default is $1e-7$ .
singular.ok	[for back-compatibility only; unused:] logical. If FALSE, a singular model is an error.
order	integer or NULL, for method == "qr", will determine how the fill-reducing ordering (aka permutation) for the "symbolic" part is determined (in <a href="#">cs_amd()</a> ), with the options 0: natural, 1: Chol, 2: LU, and 3: QR, where 3 is the default.
transpose	logical; if true, use the transposed matrix $t(x)$ instead of $x$ .

**Value**

Either a single numeric vector or a list of four numeric vectors.

**See Also**

[glm4](#) is an alternative (much) more general fitting function.

[sparse.model.matrix](#) from the **Matrix** package; the non-sparse function in standard R's package **stats**: [lm.fit\(\)](#).

**Examples**

```
dd <- expand.grid(a = as.factor(1:3),
                b = as.factor(1:4),
                c = as.factor(1:2),
                d = as.factor(1:8))
n <- nrow(dd <- dd[rep(seq_len(nrow(dd)), each = 10), ])
set.seed(17)
dM <- cbind(dd, x = round(rnorm(n), 1))
## randomly drop some
n <- nrow(dM <- dM[- sample(n, 50),])
dM <- within(dM, { A <- c(2,5,10)[a]
                  B <- c(-10,-1, 3:4)[b]
                  C <- c(-8,8)[c]
                  D <- c(10*(-5:-2), 20*c(0, 3:5))[d]
                  Y <- A + B + A*B + C + D + A*D + C*x + rnorm(n)/10
                  wts <- sample(1:10, n, replace=TRUE)
```

```

      rm(A,B,C,D)
    })
    str(dM) # 1870 x 7

X <- Matrix::sparse.model.matrix( ~ (a+b+c+d)^2 + c*x, data = dM)
dim(X) # 1870 x 69
X[1:10, 1:20]

## For now, use 'MatrixModels:::' --- TODO : export once interface is clear!

Xd <- as(X,"matrix")
system.time(fmDense <- lm.fit(Xd, y = dM[,"Y"]))
system.time( r1 <- MatrixModels:::lm.fit.sparse(X, y = dM[,"Y"]) ) # *is* faster
stopifnot(all.equal(r1, unname(fmDense$coeff), tolerance = 1e-12))
system.time(
  r2 <- MatrixModels:::lm.fit.sparse(X, y = dM[,"Y"], method = "chol" )
stopifnot(all.equal(r1, r2$coef, tolerance = 1e-12),
          all.equal(fmDense$residuals, r2$residuals, tolerance=1e-9)
)
## with weights:
system.time(fmD.w <- with(dM, lm.wfit(Xd, Y, w = wts)))
system.time(fm.w1 <- with(dM, MatrixModels:::lm.fit.sparse(X, Y, w = wts)))
system.time(fm.w2 <- with(dM, MatrixModels:::lm.fit.sparse(X, Y, w = wts,
                                                         method = "chol" ) )
stopifnot(all.equal(fm.w1, unname(fmD.w$coeff), tolerance = 1e-12),
          all.equal(fm.w2$coef, fm.w1, tolerance = 1e-12),
          all.equal(fmD.w$residuals, fm.w2$residuals, tolerance=1e-9)
)

```

---

mkRespMod

*Create a respModule object*


---

## Description

Create a [respModule](#) object, which could be from a derived class such as [glmRespMod](#) or [nlsRespMod](#).

## Usage

```
mkRespMod(fr, family = NULL, n1env = NULL, n1mod = NULL)
```

## Arguments

fr	a model frame, usually created by a call to <a href="#">model.frame</a> .
family	an optional <a href="#">glm family</a> object ( <a href="#">glmRespMod</a> objects only).
n1env	an environment for evaluation of the nonlinear model, n1mod. ( <a href="#">nlsRespMod</a> objects only).
n1mod	the nonlinear model function, as a function call ( <a href="#">nlsRespMod</a> objects only).

**Details**

The internal representation of a statistical model based on a linear predictor expression is derived from a `formula` expression and a data argument, possibly supplemented with a `family` object and/or a nonlinear model expression. The steps to obtain this representation usually involve calls to `model.frame` and to `model.matrix` or `model.Matrix`, which encapsulate important parts of this process. This function encapsulates other operations related to weights and offsets and to the model family to create a `respModule` object.

**Value**

an object of a class inheriting from `respModule`.

**See Also**

The `respModule` class description.

**Examples**

```
## see help("glpModel-class")
```

---

Model-class

*Mother Class "Model" of all S4 Models*

---

**Description**

Class "Model" is meant to be the mother class of all (S4) model classes. As some useful methods are already defined for "Model" objects, derived classes inherit those "for free".

**Objects from the Class**

A virtual Class: No objects may be created from it.

**Slots**

`call`: the `call` which generated the model.

`fitProps`: a `list`; must be named, i.e., have unique `names`, but can be empty.

When the main object is a *fitted* model, the list will typically have components such as `iter` (non-negative integer) and `convergence` (`logical` typically).

**Methods**

**formula** signature(`x = "Model"`): extract the model formula - if there is one, or `NULL`.

**update** signature(`object = "Model"`): Update the model with a new formula, new data, ..... etc. This semantically equivalent (and as R function almost identical) to the standard `update` (package `stats`).

**See Also**

the `glpModel` class in package **MatrixModels** which extends this class.

**Examples**

```
showClass("Model")
```

---

model.Matrix	<i>Construct Possibly Sparse Design or Model Matrices</i>
--------------	---

---

**Description**

`model.Matrix` creates design matrix, very much like the standard R function `model.matrix`, however returning a dense or sparse object of class `modelMatrix`.

**Usage**

```
model.Matrix(object, data = environment(object),
             contrasts.arg = NULL, xlev = NULL,
             sparse = FALSE, drop.unused.levels = FALSE, ...)
```

**Arguments**

object	an object of an appropriate class. For the default method, a model <a href="#">formula</a> or a <a href="#">terms</a> object.
data	a data frame created with <code>model.frame</code> . If another sort of object, <code>model.frame</code> is called first.
contrasts.arg	A list, whose entries are values (numeric matrices or character strings naming functions) to be used as replacement values for the <a href="#">contrasts</a> replacement function and whose names are the names of columns of data containing <a href="#">factors</a> .
xlev	to be used as argument of <code>model.frame</code> if data has no "terms" attribute.
sparse	logical indicating if the result should be sparse (of class <code>sparseModelMatrix</code> ), using <code>sparse.model.matrix()</code> (package <b>Matrix</b> ).
drop.unused.levels	used only when <code>sparse</code> is TRUE: Should factors have unused levels dropped? (This used to be true, <i>implicitly</i> in the first versions up to July 2010; the default has been changed for compatibility with R's standard (dense) <code>model.matrix()</code> ).
...	further arguments passed to or from other methods.

**Details**

`model.Matrix()` is a simple wrapper either (`sparse = FALSE`) around the traditional `model.matrix()` returning a `"ddenseModelMatrix"`, or (`sparse = TRUE`) around `sparse.model.matrix()`, returning a `"dsparseModelMatrix"` object.

`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")`.

For more details, see `model.matrix`.

**Value**

an object inheriting from class `modelMatrix`, by default, `ddenseModelMatrix`.

**See Also**

`model.matrix`, `sparse.model.matrix`.

**Examples**

```
data(CO2, package="datasets")
class(sm <- model.Matrix(~ 0+Type*Treatment, data=CO2, sparse=TRUE))
class(dm <- model.Matrix(~ 0+Type*Treatment, data=CO2, sparse=FALSE))
stopifnot(dim(sm) == c(84,4), dim(sm) == dim(dm), all(sm == dm))
```

---

modelMatrix-class	<i>Class "modelMatrix" and SubClasses</i>
-------------------	---

---

**Description**

The class `"modelMatrix"` and notably its subclass `"dsparseModelMatrix"` are used to encode additional information, analogously to what the standard R function `model.matrix()` returns.

**Objects from the Classes**

Only `"dsparseModelMatrix"` and `"ddenseModelMatrix"` are “actual” (aka non-virtual) classes. For these, objects can be created by calls of the form `new("dsparseModelMatrix", x, assign, contrast)`, where `x` is a `dgCMatrix` classed object.

**Slots**

The `"modelMatrix"` mother class contains `Matrix` plus two extra slots,

**assign:** "integer" vector of length `ncol(.)`, coding the variables which make up the matrix columns, see `model.matrix`.

**contrasts:** a named `list` of `contrasts`, as in `model.matrix()`.

**Dim:** integer vector of length two with the matrix dimensions.

**Dimnames:** list of length two, the `dimnames(.)` of the matrix.

whereas the (current only) actual classes "d\*ModelMatrix", have at least an additional (numeric slot "x". E.g., "dsparseModelMatrix" has the additional slots

**i,p:** row number and "pointer" integer vectors, see class "dgCMatrix".

**x:** "numeric" vector of non-zero entries.

**factors:** a (possibly empty) [list](#) of factorizations.

### Extends

"dsparseModelMatrix" extends class "dgCMatrix" directly,

"ddenseModelMatrix" extends class "dgeMatrix" directly.

### Methods

**show** signature(object = "modelMatrix"): [show\(.\)](#) the matrix, but also the assign and contrasts slots.

**print** signature(x = "modelMatrix"): as [show\(\)](#), however (via ...) allowing to pass further arguments for printing the matrix.

### Author(s)

Martin Maechler

### See Also

[sparse.model.matrix](#) will return a "dsparseModelMatrix" object. [model.Matrix](#) which is a simple wrapper around the traditional [model.matrix](#) and returns a "ddenseModelMatrix" object.

### Examples

```
showClass("modelMatrix")
showClass("dsparseModelMatrix")

## see  example(model.Matrix)
```

---

predModule-class

*Class "predModule" and SubClasses*

---

### Description

The class "predModule" and notably its subclasses "dPredModule" and "sPredModule" encapsulate information about linear predictors in statistical models. They incorporate a [modelMatrix](#), the corresponding coefficients and a representation of a triangular factor from the, possibly weighted or otherwise modified, model matrix.

### Objects from the Classes

Objects are typically created by coercion from objects of class [ddenseModelMatrix](#) or [dsparseModelMatrix](#).

**Slots**

The virtual class "predModule" and its two subclasses all have slots

X: a `modelMatrix`.

coef: "numeric" coefficient vector of length `ncol(.) := p`.

Vtr: "numeric" vector of length  $p$ , to contain  $V'r$  ("**V** transposed **r**").

fac: a representation of a triangular factor, the Cholesky decomposition of  $V'V$ .

The actual classes "dPredModule" and "sPredModule" specify specific (sub) classes for the two non-trivial slots,

X: a "`ddenseModelMatrix`" or "`dsparseModelMatrix`", respectively.

fac: For the "dPredModule" class this factor is a `Cholesky` object. For the "sPredModule" class it is of class `CHMfactor`.

**Methods**

`coerce` signature(from = "ddenseModelMatrix", to = "predModule"): Creates a "dPredModule" object.

`coerce` signature(from = "dsparseModelMatrix", to = "predModule"): Creates an "sPredModule" object.

**Author(s)**

Douglas Bates

**See Also**

`model.Matrix()` which returns a "`ddenseModelMatrix`" or "`dsparseModelMatrix`" object, depending if its `sparse` argument is `false` or `true`. In both cases, the resulting "`modelMatrix`" can then be coerced to a sparse or dense "`predModule`".

**Examples**

```
showClass("dPredModule")
showClass("sPredModule")

## see  example(model.Matrix)
```

resid-et-al

*Aliases for Model Extractors***Description**

Aliases for model extractors; it is an old S and R tradition to have aliases for these three model extractor functions:

`resid()` equivalent to `residuals()`.

`fitted.values()` equivalent to `fitted()`.

`coefficients()` equivalent to `coef()`.

We provide S4 generics and methods for these.

**Methods**

**resid** signature(object = "ANY"): return the residuals; this is a rarely used *alias* for `residuals()`.

**fitted.values** signature(object = "ANY"): return the fitted values; this is a rarely used *alias* for `fitted()`.

**coefficients** signature(object = "ANY"): return the coefficients of a model; this is a rarely used *alias* for `coef()`.

**See Also**

[residuals](#); [Methods](#) for general information about formal (S4) methods.

respModule-class

*"respModule" and derived classes***Description**

The "respModule" class is the virtual base class of response modules for `glpModel` model objects. Classes that inherit from "respModule" include `glmRespMod`, for generalized linear models, `nlsRespMod`, for nonlinear models and `nglmRespMod` for generalized nonlinear models.

**Objects from the Class**

Objects from these classes are usually created with `mkRespMod` as part of an `glpModel` object returned by model-fitting functions such as the hidden function `glm4`.

**Slots**

- mu:** Fitted mean response.
- offset:** offset in the linear predictor – always present even if it is a vector of zeros. In an [nlsRespMod](#) object the length of the offset can be a multiple of the length of the response.
- sqrtXwt:** the matrix of weights for the model matrices, derived from the `sqrttrwt` slot.
- sqrttrwt:** Numeric vector of the square roots of the weights for the residuals. For `respModule` and [nlsRespMod](#) objects these are constant. For [glmRespMod](#) and [nglmRespMod](#) objects these are updated at each iteration of the iteratively reweighted least squares algorithm.
- weights:** Prior weights – always present even when it is a vector of ones.
- y:** Numeric response vector.
- family:** a glm family, see [family](#) for details - `glmRespMod` objects only.
- eta:** numeric vector, the linear predictor that is transformed to the conditional mean via the link function - `glmRespMod` objects only.
- n:** a numeric vector used for calculation of the aic family function (it is really only used with the binomial family but we need to include it everywhere) - `glmRespMod` objects only.
- n1env:** an environment in which to evaluate the nonlinear model function - `nlsRespMod` objects only.
- n1mod:** an unevaluated call to the nonlinear model function - `nlsRespMod` objects only.
- pnames:** a character vector of parameter names - `nlsRespMod` objects only.

**Methods**

- fitted** `signature(object = "respModule")`: fitted values; there may be several types, corresponding to the residuals, see there (below).
- residuals** `signature(object = "respModule")`: residuals, depending on the type of the model, there are several types of residuals and correspondingly residuals, see [residuals.glm](#) from the `stats` package. Because many of these types of residuals are identical except for objects that inherit from `"glmRespMod"`, a separate method is defined for this subclass.

**See Also**

[mkRespMod](#)

**Examples**

```
showClass("respModule")
showClass("glmRespMod")
showClass("nlsRespMod")
```

---

reweightPred	<i>Reweight Prediction Module Structure Internals</i>
--------------	---

---

**Description**

Update any internal structures associated with sqrtXwt and the weighted residuals. The "V" matrix is evaluated from X using the sqrtXwt matrix and a Vtr vector is calculated.

**Usage**

```
reweightPred(predM, sqrtXwt, wtres, ...)
```

**Arguments**

predM	a predictor module
sqrtXwt	the sqrtXwt matrix
wtres	the vector of weighted residuals
...	potentially further arguments used in methods; not used currently.

**Value**

updated predM

**Methods**

```
signature(predM = "dPredModule", sqrtXwt = "matrix", wtres = "numeric") ..
signature(predM = "sPredModule", sqrtXwt = "matrix", wtres = "numeric") ..
```

**Examples**

```
## TODO
```

---

solveCoef	<i>Solve for the Coefficients or Coefficient Increment</i>
-----------	--

---

**Description**

The squared length of the intermediate solution is attached as an attribute of the returned value.

**Usage**

```
solveCoef(predM, ...)
```

**Arguments**

predM            prediction module, i.e. from class [predModule](#).  
 ...              potentially further arguments used in methods; not used currently.

**Value**

coefficient vector or increment of coef.-vector.

**Methods**

signature(predM = "dPredModule") ..  
 signature(predM = "sPredModule") ..

**Examples**

```
## TODO
```

---

updateMu	<i>Update 'mu', the Fitted Mean Response</i>
----------	--

---

**Description**

Updates the mean vector  $\mu$  given the linear predictor  $\gamma$ . Evaluate the residuals and the weighted sum of squared residuals.

**Usage**

```
updateMu(respM, gamma, ...)
```

**Arguments**

respM            a response module, see the [respModule](#) class.  
 gamma            the value of the linear predictor before adding the offset  
 ...              potentially further arguments used in methods; not used currently.

**Details**

Note that the offset is added to the linear predictor before calculating mu.

The sqrtXwt matrix can be updated but the sqrtRwt should not be in that the weighted sum of squared residuals should be calculated relative to fixed weights. Reweighting is done in a separate call.

**Value**

updated respM

**Methods**

```
signature(respM = "glmRespMod", gamma = "numeric") ..  
signature(respM = "nglmRespMod", gamma = "numeric") ..  
signature(respM = "nlsRespMod", gamma = "numeric") ..  
signature(respM = "respModule", gamma = "numeric") ..
```

**See Also**

The [respModule](#) class (and specific subclasses); [glm4](#).

**Examples**

```
## TODO
```

---

updateWts

*Update the Residual and X Weights - Generic and Methods*

---

**Description**

Update the residual weights `qrtrwt` and  $X$  weights `sqrtXwt`.

**Usage**

```
updateWts(respM, ...)
```

**Arguments**

`respM` a response module, see the [respModule](#) class.  
`...` potentially further arguments used in methods; not used currently.

**Value**

updated response module.

**Methods**

```
signature(respM = "glmRespMod") ..  
signature(respM = "respModule") ..
```

**Examples**

```
## TODO
```

# Index

- \* **array**
  - lm.fit.sparse, 5
- \* **classes**
  - glpModel-class, 4
  - Model-class, 8
  - modelMatrix-class, 10
  - predModule-class, 11
  - respModule-class, 13
- \* **methods**
  - reweightPred, 15
  - solveCoef, 15
  - updateMu, 16
  - updateWts, 17
- \* **models**
  - glm4, 2
  - mkRespMod, 7
  - model.Matrix, 9
  - resid-et-al, 13
- \* **regression**
  - glm4, 2
  - lm.fit.sparse, 5
  - reweightPred, 15
  - solveCoef, 15
  - updateMu, 16
  - updateWts, 17
- as.data.frame, 2
- call, 8
- CHMfactor, 12
- Cholesky, 12
- class, 6
- coef, 13
- coef, glpModel-method (glpModel-class), 4
- coefficients, ANY-method (resid-et-al), 13
- coerce, ddenseModelMatrix, predModule-method (predModule-class), 11
- coerce, dsparseModelMatrix, predModule-method (predModule-class), 11
- contrasts, 9, 10
- ddenseModelMatrix, 10–12
- ddenseModelMatrix-class (modelMatrix-class), 10
- denseModelMatrix-class (modelMatrix-class), 10
- dgCMatrix, 10, 11
- dgeMatrix, 11
- dimnames, 10
- dPredModule-class (predModule-class), 11
- dsparseMatrix, 6
- dsparseModelMatrix, 10–12
- dsparseModelMatrix-class (modelMatrix-class), 10
- factor, 9
- family, 2, 7, 8, 14
- fitted, 13
- fitted, glpModel-method (glpModel-class), 4
- fitted, respModule-method (respModule-class), 13
- fitted.values, ANY-method (resid-et-al), 13
- formula, 2, 8, 9
- formula, Model-method (Model-class), 8
- glm, 2, 3
- glm4, 2, 5, 6, 17
- glmRespMod, 7, 13, 14
- glmRespMod-class (respModule-class), 13
- glpModel, 3, 9, 13
- glpModel-class, 4
- list, 8, 10, 11
- lm.fit, 6
- lm.fit.sparse, 3, 5
- logical, 8
- Matrix, 10

- Methods, [13](#)
- mkRespMod, [7](#), [13](#), [14](#)
- Model, [5](#)
- Model-class, [8](#)
- model.frame, [7–9](#)
- model.Matrix, [8](#), [9](#), [11](#), [12](#)
- model.matrix, [3](#), [8–11](#)
- model.offset, [3](#)
- modelMatrix, [9–12](#)
- modelMatrix-class, [10](#)
  
- na.exclude, [2](#)
- na.fail, [2](#)
- na.omit, [2](#)
- names, [8](#)
- nglmRespMod, [13](#), [14](#)
- nglmRespMod-class (respModule-class), [13](#)
- nlsRespMod, [7](#), [13](#), [14](#)
- nlsRespMod-class (respModule-class), [13](#)
- NULL, [8](#)
- numeric, [11](#)
  
- offset, [3](#)
- options, [2](#)
  
- predModule, [4](#), [5](#), [16](#)
- predModule-class, [11](#)
- print,modelMatrix-method  
(modelMatrix-class), [10](#)
  
- qr, [6](#)
  
- resid,ANY-method (resid-et-al), [13](#)
- resid-et-al, [13](#)
- residuals, [13](#)
- residuals,glmRespMod-method  
(respModule-class), [13](#)
- residuals,glpModel-method  
(glpModel-class), [4](#)
- residuals,respModule-method  
(respModule-class), [13](#)
- residuals.glm, [5](#), [14](#)
- respModule, [4](#), [5](#), [7](#), [8](#), [16](#), [17](#)
- respModule-class, [13](#)
- reweightPred, [15](#)
- reweightPred,dPredModule,matrix,numeric-method  
(reweightPred), [15](#)
- reweightPred,sPredModule,matrix,numeric-method  
(reweightPred), [15](#)
  
- reweightPred-methods (reweightPred), [15](#)
  
- show, [11](#)
- show,modelMatrix-method  
(modelMatrix-class), [10](#)
- solveCoef, [15](#)
- solveCoef,dPredModule-method  
(solveCoef), [15](#)
- solveCoef,sPredModule-method  
(solveCoef), [15](#)
- solveCoef-methods (solveCoef), [15](#)
- sparse.model.matrix, [6](#), [9–11](#)
- sparseModelMatrix, [9](#)
- sparseModelMatrix-class  
(modelMatrix-class), [10](#)
- sPredModule-class (predModule-class), [11](#)
  
- terms, [9](#)
  
- update, [8](#)
- update,Model-method (Model-class), [8](#)
- updateMu, [16](#)
- updateMu,glmRespMod,numeric-method  
(updateMu), [16](#)
- updateMu,nglmRespMod,numeric-method  
(updateMu), [16](#)
- updateMu,nlsRespMod,numeric-method  
(updateMu), [16](#)
- updateMu,respModule,numeric-method  
(updateMu), [16](#)
- updateMu-methods (updateMu), [16](#)
- updateWts, [17](#)
- updateWts,glmRespMod-method  
(updateWts), [17](#)
- updateWts,respModule-method  
(updateWts), [17](#)
- updateWts-methods (updateWts), [17](#)