

# Package ‘MuMIn’

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**Description** Model selection and model averaging based on information criteria (AICc and alike).

**License** GPL-2

**Depends** R (>= 3.0.0)

**Imports** stats

**Suggests**

stats4, nlme, mgcv (>= 1.7.5), lme4 (>= 0.999375-16), gamm4, MASS, nnet, survival, geepack

**Enhances** aod, coxme, glmmML, MCMCglmm, pscl, spdep, unmarked, ordinal, gee, splm, logistf, caper, betareg, aods3, cplm

**LazyLoad** yes

**LazyData** yes

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MuMIn-package	<i>Multi-model inference</i>
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## Description

The package **MuMIn** contains functions to streamline information-theoretic model selection and carry out model averaging based on the information criteria.

## Details

The collection of functions includes:

[dredge](#) performs automated model selection with subsets of the supplied ‘global’ model, and optional choices of other model properties (such as different link functions). The set of models may be generated either with ‘all possible’ combinations, or tailored according to the conditions specified.

[pdredge](#) does the same, but can parallelize model fitting process using a cluster.

[model.sel](#) creates a model selection table from hand-picked models.

[model.avg](#) calculates model averaged parameters, with standard errors and confidence intervals.

[AICc](#) calculates second-order Akaike information criterion.

For a complete list of functions, use `library(help = "MuMIn")`.

By default,  $AIC_c$  is used to rank the models and to obtain model selection probabilities, though any other information criteria can be utilised. At least the following ones are currently implemented in R: [AIC](#) and [BIC](#) in package **stats**, and [QAIC](#), [QAICc](#), [ICOMP](#), [CAICF](#), and [Mallows’ Cp](#) in **MuMIn**. There is also [DIC](#) extractor for MCMC models, and [QIC](#) for GEE.

Most of R’s common modelling functions are supported, for a full inventory see [list of supported models](#).

## Author(s)

Kamil Bartoń

## References

Burnham, K. P. and Anderson, D. R (2002) *Model selection and multimodel inference: a practical information-theoretic approach*. 2nd ed. New York, Springer-Verlag.

## See Also

[AIC](#), [step](#) or [stepAIC](#) for stepwise model selection by AIC.

## Examples

```
options(na.action = "na.fail") # change the default "na.omit" to prevent models
                                # from being fitted to different datasets in
                                # case of missing values.

fm1 <- lm(y ~ ., data = Cement)
ms1 <- dredge(fm1)

# Visualize the model selection table:

par(mar = c(3,5,6,4))
plot(ms1, labAsExpr = TRUE)

model.avg(ms1, subset = delta < 4)

confset.95p <- get.models(ms1, cumsum(weight) <= .95)
avgmod.95p <- model.avg(confset.95p)
summary(avgmod.95p)
confint(avgmod.95p)
```

---

AICc

*Second-order Akaike Information Criterion*


---

## Description

Calculate second-order Akaike information criterion for one or several fitted model objects (AIC<sub>c</sub>, AIC for small samples).

## Usage

```
AICc(object, ..., k = 2, REML = NULL)
```

## Arguments

<code>object</code>	a fitted model object for which there exists a <code>logLik</code> method, or a <code>logLik</code> object.
<code>...</code>	optionally more fitted model objects.
<code>k</code>	the ‘penalty’ per parameter to be used; the default <code>k = 2</code> is the classical AIC.
<code>REML</code>	optional logical value, passed to the <code>logLik</code> method indicating whether the restricted log-likelihood or log-likelihood should be used. The default is to use the method used for model estimation.

**Value**

If just one object is provided, returns a numeric value with the corresponding  $AIC_c$ ; if more than one object are provided, returns a `data.frame` with rows corresponding to the objects and columns representing the number of parameters in the model (`df`) and  $AIC_c$ .

**Note**

$AIC_c$  should be used instead AIC when sample size is small in comparison to the number of estimated parameters (Burnham & Anderson 2002 recommend its use when  $n/K < 40$ ).

**Author(s)**

Kamil Bartoń

**References**

Burnham, K. P. and Anderson, D. R. (2002) *Model selection and multimodel inference: a practical information-theoretic approach*. 2nd ed. New York, Springer-Verlag.

Hurvich, C. M. and Tsai, C.-L. (1989) Regression and time series model selection in small samples, *Biometrika* 76: 297–307.

**See Also**

Akaike's An Information Criterion: [AIC](#)

Other implementations: [AICc](#) in package **AICcmodavg**, [AICc](#) in package **bbmle** and [aicc](#) in package **glmulti**

**Examples**

```
#Model-averaging mixed models

data(Orthodont, package = "nlme")

# Fit model by REML
fm2 <- lme(distance ~ Sex*age, data = Orthodont,
  random = ~ 1|Subject / Sex, method = "REML")

# Model selection: ranking by AICc using ML
ms2 <- dredge(fm2, trace = TRUE, rank = "AICc", REML = FALSE)

(attr(ms2, "rank.call"))

# Get the models (fitted by REML, as in the global model)
fmList <- get.models(ms2, 1:4)

# Because the models originate from dredge(..., rank = AICc, REML = FALSE),
# the default weights in model.avg are ML based:
summary(model.avg(fmList))

# same result
```

```
#model.avg(fmList, rank = "AICc", rank.args = list(REML=FALSE))
```

---

Beetle

*Flour beetle mortality data*


---

## Description

Mortality of flour beetles (*Tribolium confusum*) due to exposure to gaseous carbon disulfide CS<sub>2</sub>, from Bliss (1935).

## Usage

```
Beetle
```

## Format

Beetle is a data frame with 5 elements.

**dose** The dose of CS<sub>2</sub> in mg/L

**n.tested** Number of beetles tested

**n.killed** Number of beetles killed

**Prop** A matrix with two columns named **n.killed** and **n.survived**

**mortality** Observed mortality rate.

## Source

Bliss C. I. (1935) The calculation of the dosage-mortality curve. *Annals of Applied Biology*, 22: 134–167.

## References

Burnham, K. P. and Anderson, D. R. (2002) *Model selection and multimodel inference: a practical information-theoretic approach*. 2nd ed. New York, Springer-Verlag.

## Examples

```
# "Logistic regression example"
# from Burnham & Anderson (2002) chapter 4.11

# Fit a global model with all the considered variables
globmod <- glm(Prop ~ dose + I(dose^2) + log(dose) + I(log(dose)^2),
  data = Beetle, family = binomial)

# A logical expression defining the subset of models to use:
# * either log(dose) or dose
# * the quadratic terms can appear only together with linear terms
msubset <- expression(xor(dose,log(dose)) & (dose | !I(dose^2))
  & (log(dose) | !I(log(dose)^2)))
```

```

# Table 4.6

# Use varying argument to fit models with different link functions
# Note the use of alist rather than list in order to keep the
# family objects unevaluated
varying.link <- list(family = alist(
  logit = binomial("logit"),
  probit = binomial("probit"),
  cloglog = binomial("cloglog")
))

(ms12 <- dredge(globmod, subset = msubset, varying = varying.link,
  rank = AIC))

# Table 4.7 "models justifiable a priori"
(ms3 <- subset(ms12, has(dose, !I(dose^2))))
# The same result, but would fit the models again:
# ms3 <- update(ms12, update(globmod, . ~ dose), subset =,
#   fixed = ~dose)

mod3 <- get.models(ms3, 1:3)

# Table 4.8. Predicted mortality probability at dose 40.

# calculate confidence intervals on logit scale
logit.ci <- function(p, se, quantile = 2) {
  C. <- exp(quantile * se / (p * (1 - p)))
  p / (p + (1 - p) * c(C., 1/C.))
}

mavg3 <- model.avg(mod3, revised.var = FALSE)

pred <- sapply(mod3, predict, newdata = list(dose = 40), se.fit = TRUE,
  type = "response")

# get predictions both from component and averaged models
pred <- lapply(c(component = mod3, list(averaged = mavg3)), predict,
  newdata = list(dose = 40), type = "response", se.fit = TRUE)
# reshape predicted values
pred <- t(sapply(pred, function(x) unlist(x)[1:2]))
colnames(pred) <- c("fit", "se.fit")

# build the table
tab <- cbind(
  c(Weights(ms3), NA),
  pred,
  matrix(logit.ci(pred[, "fit"], pred[, "se.fit"],
    quantile = c(rep(1.96, 3), 2)), ncol = 2)
)
colnames(tab) <- c("Akaike weight", "Predicted(40)", "SE", "Lower CI",
  "Upper CI")
rownames(tab) <- c(as.character(ms3$family), "model averaged")
print(tab, digits = 3, na.print = "")

# Figure 4.3

```

```

newdata <- list(dose = seq(min(Beetle$dose), max(Beetle$dose), length.out = 25))

# add model-averaged prediction with CI, using the same method as above
avpred <- predict(mavg3, newdata, se.fit = TRUE, type = "response")

avci <- matrix(logit.ci(avpred$fit, avpred$se.fit, quantile = 2), ncol = 2)

matplot(newdata$dose, sapply(mod3, predict, newdata, type = "response"),
        type = "l", xlab = quote(list("Dose of" ~ CS[2],(mg/L))),
        ylab = "Mortality", col = 2:4, lty = 3, lwd = 1
)
matplot(newdata$dose, cbind(avpred$fit, avci), type = "l", add = TRUE,
        lwd = 1, lty = c(1, 2, 2), col = 1)

legend("topleft", NULL, c(as.character(ms3$family), expression(averaged
%+-% CI)), lty = c(3, 3, 3, 1), col = c(2:4, 1))

```

Cement

*Cement hardening data***Description**

Cement hardening data from Woods et al (1932).

**Usage**

Cement

**Format**

Cement is a data frame with 5 variables. *x1-x4* are four predictor variables expressed as a percentage of weight.

**X1** calcium aluminate

**X2** tricalcium silicate

**X3** tetracalcium alumino ferrite

**X4** dicalcium silicate

**y** calories of heat evolved per gram of cement after 180 days of hardening.

**Source**

Woods H., Steinour H.H., Starke H.R. (1932) Effect of composition of Portland cement on heat evolved during hardening. *Industrial & Engineering Chemistry* 24, 1207-1214.

**References**

Burnham, K. P. and Anderson, D. R (2002) *Model selection and multimodel inference: a practical information-theoretic approach*. 2nd ed. New York, Springer-Verlag.

dredge

*Automated model selection***Description**

Generate a set of models with combinations (subsets) of the terms in the global model, with optional rules for model inclusion.

**Usage**

```
dredge(global.model, beta = FALSE, evaluate = TRUE, rank = "AICc",
       fixed = NULL, m.max = NA, m.min = 0, subset, marg.ex = NULL,
       trace = FALSE, varying, extra, ct.args = NULL, ...)

## S3 method for class model.selection
print(x, abbrev.names = TRUE, warnings = getOption("warn") != -1L, ...)
```

**Arguments**

<code>global.model</code>	a fitted ‘global’ model object. See ‘Details’ for a list of supported types.
<code>beta</code>	logical, should standardized coefficients be returned?
<code>evaluate</code>	whether to evaluate and rank the models. If FALSE, a list of model calls is returned.
<code>rank</code>	optional custom rank function (information criterion) to be used instead AICc, e.g. AIC, QAIC or BIC. See ‘Details’.
<code>fixed</code>	optional, either a single sided formula or a character vector giving names of terms to be included in all models. See ‘Subsetting’.
<code>m.max, m.min</code>	optionally, the maximum and minimum number of terms in a single model (excluding the intercept), <code>m.max</code> defaults to the number of terms in <code>global.model</code> . See ‘Subsetting’.
<code>subset</code>	logical expression describing models to keep in the resulting set. See ‘Subsetting’.
<code>marg.ex</code>	a character vector specifying names of variables for which NOT to check for marginality restrictions when generating model formulas. If this argument is set to TRUE, all combinations of terms are used (i.e. no checking). If NA or missing, the exceptions will be found based on the terms of <code>global.model</code> . See ‘Details’.
<code>trace</code>	if TRUE, all calls to the fitting function (i.e. updated <code>global.model</code> calls) are printed before actual fitting takes place.
<code>varying</code>	optionally, a named list describing the additional arguments to vary between the generated models. Item names correspond to the arguments, and each item provides a list of choices (i.e. <code>list(arg1 = list(choice1, choice2, ...), ...)</code> ). Complex elements in the choice list (such as family objects) should be either named (uniquely) or quoted (unevaluated, e.g. using <a href="#">alist</a> , see <a href="#">quote</a> ), otherwise it may produce rather unpleasant effects. See example in <a href="#">Beetle</a> .
<code>extra</code>	optional additional statistics to include in the result, provided as functions, function names or a list of such (best if named or quoted). Similarly as in <code>rank</code> argument, each function must accept fitted model object as an argument and



	return a (value coercible to a) numeric vector. These can be e.g. additional information criteria or goodness-of-fit statistics. The character strings “ $R^2$ ” and “ $\text{adj}R^2$ ” are treated in a special way, and will add a likelihood-ratio based $R^2$ and modified- $R^2$ respectively to the result (this is more efficient than using <code>r.squaredLR</code> directly).
<code>x</code>	a <code>model.selection</code> object, returned by <code>dredge</code> .
<code>abbrev.names</code>	should printed variable names be abbreviated? (useful with many variables).
<code>warnings</code>	if TRUE, errors and warnings issued during the model fitting are printed below the table (currently, only with <code>pdredge</code> ). To permanently remove the warnings, set the object’s attribute “warnings” to NULL.
<code>ct.args</code>	optional list of arguments to be passed to <code>coefTable</code> (e.g. dispersion parameter for <code>glm</code> affecting standard errors used in subsequent <code>model averaging</code> ).
<code>...</code>	optional arguments for the rank function. Any can be an expression (of <code>model call</code> ), in which case any <code>x</code> within it will be substituted with a current model.

## Details

Models are fitted through repeated evaluation of modified calls to the `global.model` (in a similar fashion as with `update`). This approach, while robust in that it can be applied to a variety of different model object types is not very efficient and may be time-intensive.

Note that the number of combinations grows exponentially with number of predictor variables ( $2^N$ , less when interactions are present, see below).

The fitted model objects are not stored in the result. To get (a subset of) the models, use `get.models` on the object returned by `dredge`.

For a list of model types that can be used as a `global.model` see [list of supported models](#). Modelling functions not storing `call` in their result should be evaluated *via* the wrapper function created by `updateable`.

**Information criterion:** rank is found by a call to `match.fun` and may be specified as a function or a symbol or a character string specifying a function to be searched for from the environment of the call to `dredge`. The function rank must accept model object as its first argument and always return a scalar.

**Interactions:** By default marginality constraints are respected, so “all possible combinations” do not include models containing interactions without their respective main effects and all lower order terms. This behaviour can be altered by `marg.ex` argument, which can be used to allow for simple nested designs. For example, with global model of form `a / (x + z)`, one would use `marg.ex = "a"` and `fixed = "a"`. If `global.model` uses such a formula and `marg.ex` is missing or NA, it will be adjusted automatically.

**Subsetting:** There are three ways to constrain the resulting set of models: setting limits to the number of terms in a model with `m.max` and `m.min`, binding term(s) to all models with `fixed`, and more complex rules can be applied using argument `subset`. To be included in the selection table, the model formulation must satisfy all these conditions.

`subset` can take either a form of an *expression* or a *matrix*. The latter should be a lower triangular matrix with logical values, where columns and rows correspond to `global.model` terms. Value `subset["a", "b"] == FALSE` will exclude any model containing both terms *a* and *b*.

In the form of expression, the argument `subset` acts in a similar fashion to that in the function `subset` for `data.frames`: model terms can be referred to by name as variables in the expression, with the difference being that they are always logical (i.e. TRUE if a term exists in the model).

There is also `.(x)` and `.(+x)` notation that indicate respectively any or all model terms including a *variable* `x`. This concerns only interactions containing a particular main effect `x` (e.g. `x:z`, `v:x:z`), and *not* a variable in a complex expression, such as `x` in `I(x^2)`, so it is only useful with marginality exceptions (`marg.ex` argument).

The expression can contain any of the `global.model` terms (`getAllTerms(global.model)` lists them), as well as names of the `varying` argument items. Names of `global.model` terms take precedence when identical to names of `varying`, so to avoid ambiguity `varying` variables in subset expression should be enclosed in `V()` (e.g. `subset = V(family) == "Gamma"` assuming that `varying` is something like `list(family = c(..., "Gamma"))`).

If item names in `varying` are missing, the items themselves are coerced to names. Call and symbol elements are represented as character values (via `deparse`), and everything except numeric, logical, character and `NULL` values is replaced by item numbers (e.g. `varying = list(family = list(..., Gamma))` should be referred to as `subset = V(family) == 2`). This can quickly become confusing, therefore it is recommended to use named lists. `demo(dredge.varying)` provides examples.

The subset expression can also contain variable ``*nvar*`` (backtick-quoted), equal to number of terms in the model (**not** the number of estimated parameters).

To make inclusion of a model term conditional on presence of another model term, the function `dc` (“**d**ependency **c**hain”) can be used in the subset expression. `dc` takes any number of term names as arguments, and allows a term to be included only if all preceding ones are also present (e.g. `subset = dc(a, b, c)` allows for models of form `a`, `a+b` and `a+b+c` but not `b`, `c`, `b+c` or `a+c`).

subset expression can have a form of an unevaluated call, expression object, or a one sided formula. See ‘Examples’.

Compound model terms (such as interactions, ‘as-is’ expressions within `I()` or smooths in `gam`) should be treated as non-syntactic names and enclosed in backticks (e.g. `subset = `a:b` && `s(x, k = 2)` || `I(log(x))`), see Quotes). Mind the spacing, names must match exactly the term names as given by getAllTerms.`

*subset expression syntax summary:*

`a & b` indicates that model terms `a` and `b` must be present (see [Logical Operators](#))

`V(x)` indicates a `varying` variable `x`

`.(x)` indicates that at least one term containing variable `x` must be present

`.(+x)` indicates that all the terms containing variable `x` must be present

`dc(a, b, c, ...)` ‘dependency chain’: `b` is allowed only if `a` is present, and `c` only if both `a` and `b` are present, etc.

``*nvar*`` number of variables

To simply keep certain terms in all models, use of argument `fixed` is much more efficient. The fixed formula is interpreted in the same manner as model formula and so the terms need not to be quoted.

**Missing values:** Use of `na.action = "na.omit"` (R’s default) or `"na.exclude"` in `global.model` must be avoided, as it results with sub-models fitted to different data sets, if there are missing values. Error is thrown if it is detected.

It is a common mistake to give `na.action` as an argument in the call to `dredge` (typically resulting in an error from the `rank` function to which the argument is passed through ‘...’), while the correct way is either to pass `na.action` in the call to the `global.model` or to set it as a [global option](#).

**Methods:** There are [subset](#) and [plot](#) methods, the latter creates a graphical representation of model weights and variable relative importance. Coefficients can be extracted with `coef` or [coefTable](#).

**Value**

dredge returns an object of class `model.selection`, being a `data.frame` with models' coefficients (or presence/NA for factors), *df* - number of parameters, log-likelihood, the information criterion value,  $\Delta_{IC}$  and 'Akaike weights'. Models are ordered by the value of the information criterion specified by rank (lowest on top).

The attribute "calls" is a list containing the model calls used (arranged in the same order as the models). A model call can be retrieved with `getCall(*, i)` where *i* is a vector of model index or name (if given as character string).

Other attributes: "global" - the `global.model` object, "rank" - the rank function used, "call" - the matched call, and "warnings" - list of errors and warnings given by the modelling function during the fitting, with model number appended to each.

**Note**

Users should keep in mind the hazards that a "thoughtless approach" of evaluating all possible models poses. Although this procedure is in certain cases useful and justified, it may result in selecting a spurious "best" model, due to the model selection bias.

*"Let the computer find out" is a poor strategy and usually reflects the fact that the researcher did not bother to think clearly about the problem of interest and its scientific setting* (Burnham and Anderson, 2002).

**Author(s)**

Kamil Barton

**See Also**

[pdredge](#) is a parallelized version of this function (uses a cluster).

[get.models](#), [model.avg](#), [model.sel](#) for manual model selection tables.

Possible alternatives: [glmulti](#) in package **glmulti** and [bestglm](#) (**bestglm**). [regsubsets](#) in package **leaps** also performs all-subsets regression.

*Lasso* variable selection provided by various packages, e.g. **glmnet**, **lars** or **glmLasso**.

**Examples**

```
# Example from Burnham and Anderson (2002), page 100:

options(na.action = "na.fail") # prevent fitting models to different datasets

fm1 <- lm(y ~ ., data = Cement)
dd <- dredge(fm1)
subset(dd, delta < 4)

# Visualize the model selection table:

par(mar = c(3,5,6,4))
plot(dd, labAsExpr = TRUE)

# Model average models with delta AICc < 4
model.avg(dd, subset = delta < 4)
```

```

#or as a 95% confidence set:
model.avg(dd, subset = cumsum(weight) <= .95) # get averaged coefficients

#Best model
summary(get.models(dd, 1)[[1]])

## Not run:
# Examples of using subset:
# keep only models containing X3
dredge(fm1, subset = ~ X3) # subset as a formula
dredge(fm1, subset = expression(X3)) # subset as expression object
# the same, but more effective:
dredge(fm1, fixed = "X3")
# exclude models containing both X1 and X2 at the same time
dredge(fm1, subset = !(X1 && X2))
# Fit only models containing either X3 or X4 (but not both);
# include X3 only if X2 is present, and X2 only if X1 is present.
dredge(fm1, subset = dc(X1, X2, X3) && xor(X3, X4))
# the same as above, but without using "dc"
dredge(fm1, subset = (X1 | !X2) && (X2 | !X3) && xor(X3, X4))

# Include only models with up to 2 terms (and intercept)
dredge(fm1, m.max = 2)

## End(Not run)

# Add R^2 and F-statistics, use the extra argument
dredge(fm1, m.max = 1, extra = c("R^2", F = function(x)
  summary(x)$fstatistic[[1]]))

# with summary statistics:
dredge(fm1, m.max = 1, extra = list(
  "R^2", "*" = function(x) {
    s <- summary(x)
    c(Rsq = s$r.squared, adjRsq = s$adj.r.squared,
      F = s$fstatistic[[1]])
  })
)

# Add other information criteria (but rank with AICc):

dredge(fm1, m.max = 1, extra = alist(AIC, BIC, ICOMP, Cp))

```

## Description

`simplify.formula` rewrites a formula using shorthand notation. Currently only the factor crossing operator `*` is applied, so that expanded expression such as `a+b+a:b` becomes `a*b`. `expand.formula` does the opposite, additionally expanding other expressions, i.e. all nesting (`/`), grouping and `^`.

**Usage**

```
simplify.formula(x)
expand.formula(x)
```

**Arguments**

`x` a formula or an object from which it can be extracted (such as a fitted model object).

**Author(s)**

Kamil Bartoń

**See Also**

[formula](#)  
[delete.response](#), [drop.terms](#), and [reformulate](#)

**Examples**

```
simplify.formula(y ~ a + b + a:b + (c + b)^2)
simplify.formula(y ~ a + b + a:b + 0)

expand.formula(~ a * b)
```

---

get.models

*Evaluate models from selection table*


---

**Description**

Generate a list of fitted model objects from a `model.selection` table, optionally using parallel computation in a cluster.

**Usage**

```
get.models(object, subset, cluster = NA, ...)
```

**Arguments**

`object` object returned by [dredge](#).  
`subset` subset of models, an expression evaluated within the model selection table (see ‘Details’).  
`cluster` optionally, a cluster object. If it is a valid cluster, models are evaluated using parallel computation.  
`...` additional arguments to update the models. For example, in `lme` one may want to use `method = "REML"` while using `"ML"` for model selection.

**Details**

The argument `subset` must be explicitly provided. This is to assure that a potentially long list of models is not fitted unintentionally. To evaluate all models, set `subset` to `NA` or `TRUE`.

If `subset` is a character vector, it is interpreted as names of rows to be selected.

**Value**

`list` of fitted model objects.

**Note**

`pget.models` is still available, but is deprecated.

**Author(s)**

Kamil Bartoń

**See Also**

`dredge` and `pdredge`, `model.avg`  
`makeCluster` in packages **parrallel** and **snow**

**Examples**

```
# Mixed models:

fm2 <- lme(distance ~ age + Sex, data = Orthodont,
  random = ~ 1 | Subject, method = "ML")
ms2 <- dredge(fm2)

# Get top-most models, but fitted by REML:
(confset.d4 <- get.models(ms2, subset = delta < 4, method = "REML"))

## Not run:
# Get the top model:
get.models(ms2, subset = 1)[[1]]

## End(Not run)
```

---

importance

*Relative variable importance*

---

**Description**

Sum of ‘Akaike weights’ over all models including the explanatory variable.

**Usage**

```
importance(x)
```

**Arguments**

`x` either a list of fitted model objects, or a "model.selection" or "averaging" object.

**Value**

a numeric vector of relative importance values, named as the predictor variables.

**Author(s)**

Kamil Bartoń

**See Also**

[Weights](#)

[dredge](#), [model.avg](#), [mod.sel](#)

**Examples**

```
# Generate some models
fm1 <- lm(y ~ ., data = Cement)
ms1 <- dredge(fm1)

# Importance can be calculated/extracted from various objects:
importance(ms1)
## Not run:
importance(subset(mod.sel(ms1), delta <= 4))
importance(model.avg(ms1, subset = delta <= 4))
importance(subset(ms1, delta <= 4))
importance(get.models(ms1, delta <= 4))

## End(Not run)

# Re-evaluate the importances according to BIC
# note that re-ranking involves fitting the models again

# nobs is not used here for backwards compatibility
lognobs <- log(length(resid(fm1)))

importance(subset(mod.sel(ms1, rank = AIC, rank.args = list(k = lognobs)),
  cumsum(weight) <= .95))

# This gives a different result than previous command, because subset is
# applied to the original selection table that is ranked with AICc
importance(model.avg(ms1, rank = AIC, rank.args = list(k = lognobs),
  subset = cumsum(weight) <= .95))
```

---

Information criteria    *Various information criteria*


---

**Description**

Calculate Mallows'  $C_p$  and Bozdogan's ICOMP and CAIFC information criteria.

Extract or calculate Deviance Information Criterion from MCMCglmm and mer object.

**Usage**

```
Cp(object, ..., dispersion = NULL)
ICOMP(object, ..., REML = NULL)
CAICF(object, ..., REML = NULL)
DIC(object, ...)
```

**Arguments**

object	a fitted model object (in case of ICOMP and CAICF, logLik and vcov methods must exist for the object). For DIC, an object of class MCMCglmm or mer.
...	optionally more fitted model objects.
dispersion	the dispersion parameter. If NULL, it is inferred from object.
REML	optional logical value, passed to the logLik method indicating whether the restricted log-likelihood or log-likelihood should be used. The default is to use the method used for model estimation.

**Details**

Mallows'  $C_p$  statistic is the residual deviance plus twice the estimate of  $\sigma^2$  times the residual degrees of freedom. It is closely related to AIC (and a multiple of it if the dispersion is known).

ICOMP (I for informational and COMP for complexity) penalizes the covariance complexity of the model, rather than the number of parameters directly.

CAICF (C is for 'consistent' and F denotes the use of the Fisher information matrix) includes with penalty the natural logarithm of the determinant of the estimated Fisher information matrix.

**Value**

If just one object is provided, the functions return a numeric value with the corresponding IC; otherwise a data.frame with rows corresponding to the objects is returned.

**References**

- Mallows, C. L. (1973) Some comments on  $C_p$ . *Technometrics* 15: 661–675.
- Bozdogan, H. and Haughton, D.M.A. (1998) Information complexity criteria for regression models. *Comp. Stat. & Data Analysis* 28: 51-76.
- Anderson, D. R. and Burnham, K. P. (1999) Understanding information criteria for selection among capture-recapture or ring recovery models. *Bird Study* 46: 14–21.
- Spiegelhalter, D.J., Best, N.G., Carlin, B.R., van der Linde, A. (2002) Bayesian measures of model complexity and fit. *Journal of the Royal Statistical Society Series B-Statistical Methodology* 64: 583–616.



**See Also**

[AIC](#) and [BIC](#) in **stats**, [AICc](#). [QIC](#) for GEE model selection. [extractDIC](#) in package **arm**, on which the (non-visible) method `extractDIC.mer` used by `DIC` is based.

---

`merge.model.selection` *Combine model selection tables*

---

**Description**

Combine two model selection tables.

**Usage**

```
## S3 method for class model.selection
merge(x, y, suffixes = c(".x", ".y"), ...)
```

**Arguments**

<code>x, y</code>	model.selection objects to be combined.
<code>suffixes</code>	a character vector with two elements that are appended respectively to row names of the combined tables.
<code>...</code>	ignored.

**Value**

A model.selection object containing models from both model selection tables.

**Note**

Both  $\Delta_{IC}$  values and *Akaike weights* are recalculated in the resulting tables.

Models in the combined model selection tables must be comparable, i.e. fitted to the same data, however only very basic checking is done to verify that. The models must also be ranked by the same information criterion.

Unlike the `merge` method for `data.frame`, this method appends second table to the first (similarly to `rbind`).

**Author(s)**

Kamil Bartoń

**See Also**

[dredge](#), [model.sel](#), [merge](#), [rbind](#).

**Examples**

```
## Not run:
require(mgcv)

ms1 <- dredge(glm(Prop ~ dose + I(dose^2) + log(dose) + I(log(dose)^2),
  data = Beetle, family = binomial, na.action = na.fail))

fm2 <- gam(Prop ~ s(dose, k = 3), data = Beetle, family = binomial)

merge(ms1, model.sel(fm2))

## End(Not run)
```

---

Model utilities

---

*Model utility functions*


---

**Description**

These functions extract or calculate various values from provided fitted model objects(s). They are mainly meant for internal use, but may be also useful for end-users.

`beta.weights` computes standardized coefficients (beta weights) for a model;

`coeffs` extracts model coefficients;

`getAllTerms` extracts independent variable names from a model object;

`coefTable` extracts a table of coefficients, standard errors and associated degrees of freedom when possible;

`model.names` generates shorthand (alpha)numeric names for one or several fitted models.

**Usage**

```
beta.weights(model)
```

```
coeffs(model)
```

```
getAllTerms(x, ...)
```

```
## S3 method for class terms
```

```
getAllTerms(x, offset = TRUE, intercept = FALSE, ...)
```

```
coefTable(model, ...)
```

```
## S3 method for class lme
```

```
coefTable(model, adjustSigma, ...)
```

```
## S3 method for class gee
```

```
coefTable(model, ..., type = c("naive", "robust"))
```

```
model.names(object, ..., labels = NULL, use.letters = FALSE)
```

**Arguments**

<code>model</code>	a fitted model object.
<code>object</code>	a fitted model object or a list of such objects.
<code>x</code>	a fitted model object or a formula.
<code>offset</code>	should 'offset' terms be included?
<code>intercept</code>	should terms names include the intercept?
<code>labels</code>	optionally, a character vector with names of all the terms, e.g. from a global model. <code>model.names</code> enumerates the model terms in order of their appearance in the list and in the models. So, changing the order of the models would lead to different names. The argument 'labels' can be used to prevent this happening.
<code>...</code>	for <code>model.names</code> , more fitted model objects. For <code>coefTable</code> arguments that are passed to appropriate <code>vcov</code> or <code>summary</code> method (e.g. dispersion parameter for <code>glm</code> may be used here). In other functions often not used.
<code>use.letters</code>	logical, whether letters should be used instead of numeric codes.
<code>type</code>	for GEE models, the type of covariance estimator to calculate returned standard errors on. Either "naive" or "robust" ('sandwich').
<code>adjustSigma</code>	See <a href="#">summary.lme</a> .

**Details**

The functions `coeffs`, `getAllTerms` and `coefTable` provide interface between the model object and `model.avg` (and `dredge`). Custom methods can be written to provide support for additional classes of models.

**Note**

`coeffs`'s value is in most cases identical to that returned by [coef](#), the only difference being it returns fixed effects' coefficients for mixed models, and the value is always a named numeric vector.

Use of `tTable` is deprecated in favour of `coefTable`.

**Author(s)**

Kamil Bartoń

---

`model.avg`

*Model averaging*

---

**Description**

Model averaging based on an information criterion.

## Usage

```
model.avg(object, ..., revised.var = TRUE)

## Default S3 method:
model.avg(object, ..., beta = FALSE, rank = NULL, rank.args = NULL,
          revised.var = TRUE, dispersion = NULL, ct.args = NULL)

## S3 method for class model.selection
model.avg(object, subset, fit = FALSE, ..., revised.var = TRUE)
```

## Arguments

object	a fitted model object or a list of such objects, or a <code>model.selection</code> object. See ‘Details’.
...	for default method, more fitted model objects. Otherwise, arguments that are passed to the default method.
beta	logical, should standardized coefficients be returned?
rank	optionally, a custom rank function (information criterion) to use instead of AICc, e.g. BIC or QAIC, may be omitted if object is a model list returned by <code>get.models</code> or a <code>model.selection</code> object. See ‘Details’.
rank.args	optional list of arguments for the rank function. If one is an expression, an x within it is substituted with a current model.
revised.var	logical, indicating whether to use revised formula for standard errors. See <a href="#">par.avg</a> .
dispersion	the dispersion parameter for the family used. See <a href="#">summary.glm</a> . This is used currently only with <code>glm</code> , is silently ignored otherwise.
ct.args	optional list of arguments to be passed to <a href="#">coefTable</a> (besides dispersion).
subset	see <a href="#">subset</a> method for <code>model.selection</code> object.
fit	if TRUE, the component models are fitted using <code>get.models</code> . See ‘Details’.

## Details

`model.avg` may be used either with a list of models, or directly with a `model.selection` object (e.g. returned by `dredge`). In the latter case, the models from the model selection table are not evaluated unless the argument `fit` is set to TRUE or some additional arguments are present (such as `rank` or `dispersion`). This results in much faster calculation, but has certain drawbacks, because the fitted component model objects are not stored, and some methods (e.g. `predict`, `fitted`, `model.matrix` or `vcov`) would not be available with the returned object. Otherwise, `get.models` is called prior to averaging, and ... are passed to it.

For a list of model types that are accepted see [list of supported models](#).

`rank` is found by a call to [match.fun](#) and typically is specified as a function or a symbol (e.g. a back-quoted name) or a character string specifying a function to be searched for from the environment of the call to `lapply`. `rank` must be a function able to accept `model` as a first argument and must always return a scalar.

Several standard methods for fitted model objects exist for class averaging, including [summary](#), [predict](#), [coef](#), [confint](#), [formula](#), and [vcov](#).

coef, vcov, confint and coefTable accept argument full that if set to TRUE, the full model-averaged coefficients are returned, rather than subset-averaged ones (when full = FALSE, being the default).

logLik returns a list of [logLik](#) objects for the component models.

## Value

An object of class averaging is a list with components:

summary	a data.frame with log-likelihood, $IC$ , $\Delta_{IC}$ and 'Akaike weights' for the component models.
coef.shrinkage	a vector of full model-averaged coefficients, see 'Note'.
coefArray	an array of component models' coefficients, their standard errors, and degrees of freedom.
term.codes	names of the terms with numerical codes used in the summary.
avg.model	the model averaged parameters. A data.frame containing averaged coefficients, unconditional standard error, adjusted SE (if <i>dfs</i> are available) and z-values (coefficient and SE) and significance (assuming a normal error distribution).
importance	relative importance of the predictor variables (including interactions), calculated as a sum of the <i>Akaike weights</i> over all of the models in which the parameter of interest appears.
term.names	character vector giving names of all terms in the model.
x, formula	the model matrix and formula corresponding to the one that would be used in a single model. formula contains only the averaged coefficients.
call	the matched call.

In addition, the object has following attributes:

modelList	a list of component model objects.
beta	logical, were standardized coefficients used?
revised.var	if TRUE, the standard errors were calculated with the revised formula (See <a href="#">par.avg</a> ).

## Note

The 'subset' (or 'conditional') average only averages over the models where the parameter appears. An alternative, the 'full' average assumes that a variable is included in every model, but in some models the corresponding coefficient (and its respective variance) is set to zero. Unlike the 'subset average', it does not have a tendency of biasing the value away from zero. The 'full' average is a type of shrinkage estimator and for variables with a weak relationship to the response they are smaller than 'subset' estimators.

Averaging models with different contrasts for the same factor would yield nonsense results, currently no checking for contrast consistency is done.

From version 1.0.1, print method provides only a concise output (similarly as for `lm`). To print a full summary of the results use `summary` function. Confidence intervals can be obtained with [confint](#).

## Author(s)

Kamil Bartoń

## References

Burnham, K. P. and Anderson, D. R. (2002) *Model selection and multimodel inference: a practical information-theoretic approach*. 2nd ed. New York, Springer-Verlag.

Lukacs, P. M., Burnham K. P. and Anderson, D. R. (2009) *Model selection bias and Freedman's paradox*. Annals of the Institute of Statistical Mathematics 62(1): 117–125.

## See Also

See [par.avg](#) for more details of model averaged parameter calculation.

[dredge](#), [get.models](#)

[AICc](#) has examples of averaging models fitted by REML.

[modavg](#) in package **AICcmodavg**, and [coef.glmulti](#) in package **glmulti** also perform model averaging.

## Examples

```
# Example from Burnham and Anderson (2002), page 100:
fm1 <- lm(y ~ ., data = Cement, na.action = na.fail)
(ms1 <- dredge(fm1))

#models with delta.aicc < 4
summary(model.avg(ms1, subset = delta < 4))

#or as a 95% confidence set:
avgmod.95p <- model.avg(ms1, cumsum(weight) <= .95)
confint(avgmod.95p)

## Not run:
# The same result, but re-fitting the models via get.models
confset.95p <- get.models(ms1, cumsum(weight) <= .95)
model.avg(confset.95p)

# Force re-fitting the component models
model.avg(ms1, cumsum(weight) <= .95, fit = TRUE)
# Models are also fitted if additional arguments are given
model.avg(ms1, cumsum(weight) <= .95, rank = "AIC")

## End(Not run)

## Not run:
# using BIC (Schwarzs Bayesian criterion) to rank the models
BIC <- function(x) AIC(x, k = log(length(residuals(x))))
model.avg(confset.95p, rank = BIC)
# the same result, using AIC directly, with argument k
# x in a quoted rank argument is substituted with a model object
# (in this case it does not make much sense as the number of observations is
# common to all models)
model.avg(confset.95p, rank = AIC, rank.args = alist(k = log(length(residuals(x)))))

## End(Not run)
```

---

model.sel	<i>model selection table</i>
-----------	------------------------------

---

## Description

Build a model selection table.

## Usage

```
model.sel(object, ...)
```

```
## S3 method for class model.selection
model.sel(object, rank = NULL, rank.args = NULL, ..., beta = FALSE, extra)
## Default S3 method:
model.sel(object, ..., rank = NULL, rank.args = NULL, beta = FALSE, extra)
```

## Arguments

object	a fitted model object, a list of such objects, or a "model.selection" object.
...	more fitted model objects.
rank	optional, custom rank function (information criterion) to use instead of AICc, e.g. QAIC or BIC, may be omitted if object is a model list returned by <code>get.models</code> .
rank.args	optional list of arguments for the rank function. If one is an expression, an x within it is substituted with a current model.
beta	logical, should standardized coefficients be returned?
extra	optional additional statistics to include in the result, provided as functions, function names or a list of such (best if named or quoted). See <a href="#">dredge</a> for details.

## Value

An object of class "model.selection" with columns containing useful information about each model: the coefficients, df, log-likelihood, the value of the information criterion used,  $\Delta_{IC}$  and 'Akaike weight'. If any arguments differ between the modelling function calls, the result will include additional columns showing them (except for formulas and some other arguments).

## Author(s)

Kamil Bartoń

## See Also

[dredge](#), [AICc](#), [list of supported models](#).

Possible alternatives: [Ictab](#) (in package **bbmle**), or [aictab](#) (**AICcmodavg**).

## Examples

```
Cement$X1 <- cut(Cement$X1, 3)
Cement$X2 <- cut(Cement$X2, 2)

fm1 <- glm(formula = y ~ X1 + X2 * X3, data = Cement)
fm2 <- update(fm1, . ~ . - X1 - X2)
fm3 <- update(fm1, . ~ . - X2 - X3)

## ranked with AICc by default
(msAICc <- model.sel(fm1, fm2, fm3))

## ranked with BIC
model.sel(fm1, fm2, fm3, rank = AIC, rank.args = alist(k = log(nobs(x))))
# or
# model.sel(msAICc, rank = AIC, rank.args = alist(k = log(nobs(x))))
# or
# update(msAICc, rank = AIC, rank.args = alist(k = log(nobs(x))))
```

---

MuMIn-models

*List of supported models*


---

## Description

List of model classes accepted by `model.avg`, `model.sel`, and `dredge`.

## Details

Fitted model objects that can be used with model selection and model averaging functions include those produced by:

- `lm`, `glm` (package **stats**);
- `rlm`, `glm.nb` and `polr` (**MASS**);
- `multinom` (**nnet**);
- `lme`, `gls` (**nlme**);
- `lmer`, `glmer` (**lme4**);
- `cpglm`, `cpplmm` (**cpplm**);
- `gam`, `gamm*` (**mgcv**);
- `gamm4*` (**gamm4**);
- `glmmML` (**glmmML**);
- `glmmadmb` (**glmmADMB** from R-Forge);
- `asreml` (non-free commercial package **asreml**; allows only for REML comparisons);
- `hurdle`, `zeroinfl` (**pscl**);
- `negbin`, `betabin` (class "glimML"), package **aod**);
- `aodml`, `aodql` (**aods3**);
- `betareg` (**betareg**);



- `brglm` (**brglm**);
- `*sarlm` models, `spautolm` (**spdep**);
- `spml*` (if fitted by ML, **splm**);
- `coxph`, `survreg` (**survival**);
- `coxme`, `lmekin` (**coxme**);
- `rq` (**quantreg**);
- `clm` and `clmm` (**ordinal**);
- `logistf` (**logistf**);
- `crunch*`, `pgls` (**caper**);
- `maxlike` (**maxlike**);
- functions from package **unmarked** (within the class "unmarkedFit");
- `mark` and related functions (class `mark` from package **RMark**). Currently dredge can only manipulate formula element of the argument `model.parameters`, keeping its other elements intact.

Generalized Estimation Equation model implementations: `geeglm` from package **geepack**, `gee` from **gee**, and `yags` from **yags** (from R-Forge) can be used with `QIC` as the selection criterion.

`MCMCglmm*` models (package **MCMCglmm**) with e.g. `DIC` as the rank function are accepted by `model.sel` and `dredge`.

Other classes are also likely to be supported, in particular if they inherit from one of the above classes. In general, the models averaged with `model.avg` may belong to different types (e.g. `glm` and `gam`), provided they use the same data and response, and if it is valid to do so. This applies also to constructing model selection tables with `model.sel`.

### Note

\* In order to use `gamm`, `gamm4`, `spml` (> 1.0.0), `crunch` or `MCMCglmm` with `dredge`, an **updateable** wrapper for these functions should be created.

### See Also

`model.avg`, `model.sel` and `dredge`.

---

`par.avg`

*Parameter averaging*

---

### Description

Average a single model coefficient based on provided weights. It is mostly intended for internal use.

### Usage

```
par.avg(x, se, weight, df = NULL, level = 1 - alpha, alpha = 0.05,
        revised.var = TRUE, adjusted = TRUE)
```

## Arguments

x	vector of parameters.
se	vector of standard errors.
weight	vector of weights.
df	optional vector of degrees of freedom.
alpha, level	significance level for calculating confidence intervals.
revised.var	logical, should the revised formula for standard errors be used? See ‘Details’.
adjusted	logical, should the inflated standard errors be calculated? See ‘Details’.

## Details

Unconditional standard errors are square root of the variance estimator, calculated either according to the original equation in Burnham and Anderson (2002, equation 4.7), or a newer, revised formula from Burnham and Anderson (2004, equation 4) (if `revised.var = TRUE`, this is the default). If `adjusted = TRUE` (the default) and degrees of freedom are given, the adjusted standard error estimator and confidence intervals with improved coverage are returned (see Burnham and Anderson 2002, section 4.3.3).

## Value

`par.avg` returns a vector with named elements:

Coefficient	model coefficients,
SE	unconditional standard error,
Adjusted SE	adjusted standard error,
Lower CI, Upper CI	unconditional confidence intervals.

## Author(s)

Kamil Bartoń

## References

- Burnham, K. P. and Anderson, D. R. (2002) *Model selection and multimodel inference: a practical information-theoretic approach*. 2nd ed.
- Burnham, K. P. and Anderson, D. R. (2004) *Multimodel inference - understanding AIC and BIC in model selection*. *Sociological Methods & Research* 33(2): 261-304.

## See Also

[model.avg](#) for model averaging.

---

pdredge

*Automated model selection using parallel computation*

---

## Description

Parallelized version of dredge.

## Usage

```
pdredge(global.model, cluster = NA, beta = FALSE, evaluate = TRUE, rank = "AICc",
        fixed = NULL, m.max = NA, m.min = 0, subset, marg.ex = NULL, trace = FALSE,
        varying, extra, ct.args = NULL, check = FALSE, ...)
```

## Arguments

global.model	beta, evaluate, rank
	see <a href="#">dredge</a> .
fixed, m.max, m.min, subset, marg.ex, varying, extra, ct.args, ...	
	see <a href="#">dredge</a> .
trace	displays the generated calls, but may not work as expected since the models are evaluated in batches rather than one by one.
cluster	either a valid cluster object, or NA for a single threaded execution.
check	either integer or logical value controlling how much checking for existence and correctness of dependencies is done on the cluster nodes. See 'Details'.

## Details

All the dependencies for fitting the `global.model`, including the data and any objects the modelling function will use must be exported into the cluster worker nodes (e.g. *via* `clusterExport`). The required packages must be also loaded therein (e.g. *via* `clusterEvalQ(..., library(package))`), before the cluster is used by `pdredge`.

If `check` is TRUE or positive, `pdredge` tries to check whether all the variables and functions used in the call to `global.model` are present in the cluster nodes' `.GlobalEnv` before proceeding further. This causes false errors if some arguments of the model call (other than `subset`) would be evaluated in data environment. In that case using `check = FALSE` (the default) is desirable.

If `check` is TRUE or greater than one, `pdredge` will compare the `global.model` updated at the cluster nodes with the one given as argument.

## Value

See [dredge](#).

## Author(s)

Kamil Bartoń

## See Also

`makeCluster` and other cluster related functions in packages **parallel** or **snow**.

## Examples

```
# One of these packages is required:
## Not run: require(parallel) || require(snow)

# From example(Beetle)

Beetle100 <- Beetle[sample(nrow(Beetle), 100, replace = TRUE),]

fm1 <- glm(Prop ~ dose + I(dose^2) + log(dose) + I(log(dose)^2),
  data = Beetle100, family = binomial)

msubset <- expression(xor(dose, log(dose)) & (dose | !I(dose^2))
  & (log(dose) | !I(log(dose)^2)))
varying.link <- list(family = alist(logit = binomial("logit"),
  probit = binomial("probit"), cloglog = binomial("cloglog") ))

# Set up the cluster
clusterType <- if(length(find.package("snow", quiet = TRUE))) "SOCK" else "PSOCK"
clust <- try(makeCluster(getOption("cl.cores", 2), type = clusterType))

clusterExport(clust, "Beetle100")

# noticeable gain only when data has about 3000 rows (Windows 2-core machine)
print(system.time(dredge(fm1, subset = msubset, varying = varying.link)))
print(system.time(pdredge(fm1, cluster = FALSE, subset = msubset,
  varying = varying.link)))
print(system.time(pdd <- pdredge(fm1, cluster = clust, subset = msubset,
  varying = varying.link)))

print(pdd)

## Not run:
# Time consuming example with unmarked model, based on example(pcount).
# Having enough patience you can run this with demo(pdredge.pcount).
library(unmarked)
data(mallard)
mallardUMF <- unmarkedFramePCount(mallard.y, siteCovs = mallard.site,
  obsCovs = mallard.obs)
(ufm.mallard <- pcount(~ ivel + date + I(date^2) ~ length + elev + forest,
  mallardUMF, K = 30))
clusterEvalQ(clust, library(unmarked))
clusterExport(clust, "mallardUMF")

# stats4 is needed for AIC to work with unmarkedFit objects but is not
# loaded automatically with unmarked.
require(stats4)
invisible(clusterCall(clust, "library", "stats4", character.only = TRUE))

#system.time(print(pdd1 <- pdredge(ufm.mallard,
#  subset = p(date) | !p(I(date^2)), rank = AIC)))

system.time(print(pdd2 <- pdredge(ufm.mallard, clust,
  subset = p(date) | !p(I(date^2)), rank = AIC, extra = "adjR^2")))
```

```

# best models and null model
subset(pdd2, delta < 2 | df == min(df))

# Compare with the model selection table from unmarked
# the statistics should be identical:
models <- get.models(pdd2, delta < 2 | df == min(df), cluster = clust)

modSel(fitList(fits = structure(models, names = model.names(models,
  labels = getAllTerms(ufm.mallard)))), nullmod = "(Null)")

## End(Not run)

stopCluster(clust)

```

---

plot.model.selection    *Visualize model selection table*

---

## Description

Produces a graphical representation of model weights and relative variable importance.

## Usage

```

## S3 method for class model.selection
plot(x, ylab = NULL, xlab = NULL,
     labels = attr(x, "terms"), labAsExpr = FALSE,
     col = c("SlateGray", "SlateGray2"), col2 = "white", border = par("col"),
     par.lab = NULL, par.vlab = NULL,
     axes = TRUE, ann = TRUE, ...)

```

## Arguments

x	a "model.selection" object.
xlab, ylab	labels for the x and y axis.
labels	optional, a character vector or an expression containing model term labels (to appear on top side of the plot). Its length must be equal to number of model terms in the table. Defaults to model term names.
labAsExpr	a logical indicating whether the character labels should be interpreted ( <a href="#">parsed</a> ) as R expressions.
col, col2	vector of colors for columns (if more than one col is given, columns will be filled with alternating colors). If col2 is specified cells will be filled with gradient from col to col2. Set col2 to NA for no gradient.
border	border color for cells and axes.
par.lab, par.vlab	optional lists or parameters for term labels (top axis) and model names (right axis), respectively.
axes, ann	logical values indicating whether the axis and annotation should appear on the plot.
...	further <a href="#">graphical parameters</a> to be set for the plot (see <a href="#">par</a> ).

**Author(s)**

Kamil Barton

**See Also**[plot.default](#), [par](#)For examples, see ‘[MuMIn-package](#)’

---

predict.averaging	<i>Predict method for the averaged model</i>
-------------------	--

---

**Description**

Model-averaged predictions with optional standard errors.

**Usage**

```
## S3 method for class averaging
predict(object, newdata = NULL, se.fit = FALSE,
        interval = NULL, type = NA, backtransform = FALSE, full = TRUE, ...)
```

**Arguments**

object	an object returned by <code>model.avg</code> .
newdata	optional <code>data.frame</code> in which to look for variables with which to predict. If omitted, the fitted values are used.
se.fit	logical, indicates if standard errors should be returned. This has any effect only if the predict methods for each of the component models support it.
interval	currently not used.
type	the type of predictions to return (see documentation for <code>predict</code> appropriate for the class of used component models). If omitted, the default type is used. See ‘Details’.
backtransform	if TRUE, the averaged predictions are back-transformed from link scale to response scale. This makes sense provided that all component models use the same family, and the prediction from each of the component models is calculated on the link scale (as specified by <code>type</code> . For <code>glm</code> , use <code>type = "link"</code> ). See ‘Details’.
full	if TRUE, the full model averaged coefficients are used (only if <code>se.fit = FALSE</code> and the component objects are a result of <code>lm</code> ).
...	arguments to be passed to respective predict method (e.g. <code>level</code> for <a href="#">lme</a> model).

## Details

predicting is possible only with averaging objects with "modellist" attribute, i.e. those created *via* `model.avg` from a model list, or from `model.selection` object with argument `fit = TRUE` (note this will recreate the model objects which may be time consuming, see [model.avg](#)).

If all the component models are ordinary linear models, the prediction can be made either with the full averaged coefficients (the argument `full = TRUE` this is the default) or subset-averaged coefficients. Otherwise the prediction is obtained by calling `predict` on each component model and weighted averaging the results, which corresponds to the assumption that all predictors are present in all models, but those not estimated are equal zero. See 'Note' in [model.avg](#). Predictions from component models with standard errors are passed to `par.avg` and averaged in the same way as the coefficients.

Predictions on the response scale from generalized models can be calculated by averaging predictions of each model on the link scale, followed by inverse transformation (this is achieved with `type = "link"` and `backtransform = TRUE`). This is only possible if all component models use the same family and link function. Alternatively, predictions from each model on response scale may be averaged (with `type = "response"` and `backtransform = FALSE`). Note that this leads to results differing from those calculated with the former method. See also [predict.glm](#).

## Value

If `se.fit = FALSE`, a vector of predictions, otherwise a list with components: `fit` containing the predictions, and `se.fit` with the estimated standard errors.

## Note

This method relies on availability of the `predict` methods for the component model classes (except when all component models are of class `lm`).

The package **MuMIn** includes `predict` methods for `lme`, `gls` and `lmer` (**lme4**), all of which can calculate standard errors of the predictions (with `se.fit = TRUE`). The former two enhance the original `predict` methods from package **nlme**, and with `se.fit = FALSE` they return identical result. **MuMIn**'s versions are always used in averaged model predictions (so it is possible to predict with standard errors), but from within global environment they will be found only if **MuMIn** is before **nlme** on the [search list](#) (or directly extracted from namespace as `MuMIn::predict.lme`).

`predict` method for `mer` models currently can only calculate values on the outermost level (equivalent to `level = 0` in [predict.lme](#)).

## Author(s)

Kamil Bartoň

## See Also

[model.avg](#), and [par.avg](#) for details of model-averaged parameter calculation.  
[predict.lme](#), [predict.gls](#)

## Examples

```
# Example from Burnham and Anderson (2002), page 100:
fm1 <- lm(y ~ X1 + X2 + X3 + X4, data = Cement)
```

```

ms1 <- dredge(fm1)
confset.95p <- get.models(ms1, subset = cumsum(weight) <= .95)
avgm <- model.avg(confset.95p)

nseq <- function(x, len = length(x)) seq(min(x, na.rm = TRUE),
    max(x, na.rm=TRUE), length = len)

# New predictors: X1 along the range of original data, other
# variables held constant at their means
newdata <- as.data.frame(lapply(lapply(Cement[1:4], mean), rep, 25))
newdata$X1 <- nseq(Cement$X1, nrow(newdata))

n <- length(confset.95p)

# Predictions from each of the models in a set, and with averaged coefficients
pred <- data.frame(
  model = sapply(confset.95p, predict, newdata = newdata),
  averaged.subset = predict(avgm, newdata, full = FALSE),
  averaged.full = predict(avgm, newdata, full = TRUE)
)

opal <- palette(c(topo.colors(n), "black", "red", "orange"))
matplot(newdata$X1, pred, type = "l",
  lwd = c(rep(2,n),3,3), lty = 1,
  xlab = "X1", ylab = "y", col=1:7)

# For comparison, prediction obtained by averaging predictions of the component
# models
pred.se <- predict(avgm, newdata, se.fit = TRUE)
y <- pred.se$fit
ci <- pred.se$se.fit * 2
matplot(newdata$X1, cbind(y, y - ci, y + ci), add = TRUE, type="l",
  lty = 2, col = n + 3, lwd = 3)

legend("topleft",
  legend=c(lapply(confset.95p, formula),
    paste(c("subset", "full"), "averaged"), "averaged predictions + CI"),
  lty = 1, lwd = c(rep(2,n),3,3,3), cex = .75, col=1:8)

palette(opal)

```

---

QAIC

---

*Quasi AIC or AICc*


---

## Description

Calculate a modification of Akaike's Information Criterion for overdispersed count data (or its version corrected for small sample, "quasi-AIC<sub>c</sub>"), for one or several fitted model objects.



**Usage**

```
QAIC(object, ..., chat, k = 2)
QAICc(object, ..., chat, k = 2)
```

**Arguments**

<code>object</code>	a fitted model object.
<code>...</code>	optionally, more fitted model objects.
<code>chat</code>	$\hat{c}$ , the variance inflation factor.
<code>k</code>	the ‘penalty’ per parameter.

**Value**

If only one object is provided, returns a numeric value with the corresponding QAIC or QAIC<sub>c</sub>; otherwise returns a data.frame with rows corresponding to the objects.

**Note**

$\hat{c}$  is the dispersion parameter estimated from the global model, and can be calculated by dividing model’s deviance by the number of residual degrees of freedom.

In calculation of QAIC, the number of model parameters is increased by 1 to account for estimating the overdispersion parameter. Without overdispersion,  $\hat{c} = 1$  and QAIC is equal to AIC.

Note that `glm` does not compute maximum-likelihood estimates in models within the *quasi*- family. In case it is justified, and with a proper caution, a workaround could be used by ‘borrowing’ the `aic` element from the corresponding ‘non-quasi’ family (see ‘Example’).

**Author(s)**

Kamil Bartoń

**See Also**

[AICc](#), [quasi](#) family used for models with over-dispersion

**Examples**

```
# Based on "example(predict.glm)", with one number changed to create
# overdispersion
budworm <- data.frame(
  ldose = rep(0:5, 2), sex = factor(rep(c("M", "F"), c(6, 6))),
  numdead = c(10, 4, 9, 12, 18, 20, 0, 2, 6, 10, 12, 16))
budworm$SF = cbind(numdead = budworm$numdead,
  numalive = 20 - budworm$numdead)

budworm.lg <- glm(SF ~ sex*ldose, data = budworm, family = binomial)
(chat <- deviance(budworm.lg) / df.residual(budworm.lg))

dredge(budworm.lg, rank = "QAIC", chat = chat)
dredge(budworm.lg, rank = "AIC")

## Not run:
# A hacked constructor for quasibinomial family object, that allows for
# ML estimation
```

```

x.quasibinomial <- function(...) {
  res <- quasibinomial(...)
  res$aic <- binomial(...)$aic
  res
}
QAIC(update(budworm.lg, family = x.quasibinomial), chat = chat)

## End(Not run)

```

QIC

*QIC and quasi-Likelihood for GEE***Description**

Calculate quasi-likelihood under the independence model criterion (QIC) for Generalized Estimating Equations.

**Usage**

```

QIC(object, ..., typeR = FALSE)
QICu(object, ..., typeR = FALSE)
quasiLik(object, ...)

```

**Arguments**

<code>object</code>	a fitted model object of class <code>gee</code> , <code>geepack</code> or <code>yags</code> .
<code>...</code>	for <code>QIC</code> and <code>QIC<sub>u</sub></code> , optionally more fitted model objects.
<code>typeR</code>	logical, whether to calculate <code>QIC(R)</code> . <code>QIC(R)</code> is based on quasi-likelihood of a working correlation $R$ model. Defaults to <code>FALSE</code> , and <code>QIC(I)</code> based on independence model is returned.

**Value**

If just one object is provided, returns a numeric value with the corresponding QIC; if more than one object are provided, returns a `data.frame` with rows corresponding to the objects and one column representing QIC or `QICu`.

**Note**

This implementation is based partly on (revised) code from packages **yags** (R-Forge) and **ape**. The functions are still in experimental stage and should be used with caution.

**Author(s)**

Kamil Bartoń

**References**

Pan W. (2001) Akaike's Information Criterion in Generalized Estimating Equations. *Biometrics* 57: 120-125

Hardin J. W., Hilbe, J. M. (2003) *Generalized Estimating Equations*. Chapman & Hall/CRC

**See Also**

Methods exist for [gee](#) (package **gee**), [geeglm](#) (**geepack**), and [yags](#) (**yags** on R-Forge). [yags](#) and [compar.gee](#) from package **ape** both provide QIC values.

**Examples**

```
data(ohio)

fm1 <- geeglm(resp ~ age * smoke, id = id, data = ohio,
  family = binomial, corstr = "exchangeable", scale.fix = TRUE)
fm2 <- update(fm1, corstr = "ar1")
fm3 <- update(fm1, corstr = "unstructured")

model.sel(fm1, fm2, fm3, rank = QIC)

## Not run:
# same result:
dredge(fm1, m.min = 3, rank = QIC, varying = list(
  corstr = list("exchangeable", "unstructured", "ar1")
))

## End(Not run)
```

---

r.squaredGLMM

*Pseudo-R-squared for Generalized Mixed-Effect models*


---

**Description**

Calculate a conditional and marginal coefficient of determination for Generalized mixed-effect models ( $R^2_{GLMM}$ ).

**Usage**

```
r.squaredGLMM(x)
```

**Arguments**

x                      a fitted linear model object.

**Details**

For mixed-effects models,  $R^2$  can be categorized into two types. **Marginal**  $R^2_{GLMM}$  represents the variance explained by fixed factors, and is defined as:

$$R^2_{GLMM(m)} = \frac{\sigma_f^2}{\sigma_f^2 + \sum_{l=1}^u \sigma_l^2 + \sigma_e^2 + \sigma_d^2}$$

**Conditional**  $R^2_{GLMM}$  is interpreted as variance explained by both fixed and random factors (i.e. the entire model), and is calculated according to the equation:

$$R_{GLMM(c)}^2 = \frac{\sigma_f^2 + \sum_{l=1}^u \sigma_l^2}{\sigma_f^2 + \sum_{l=1}^u \sigma_l^2 + \sigma_e^2 + \sigma_d^2}$$

where  $\sigma_f^2$  is the variance of the fixed effect components, and  $\sum \sigma_l^2$  is the sum of all  $u$  variance components (group, individual, etc.),  $\sigma_l^2$  is the variance due to additive dispersion and  $\sigma_d^2$  is the distribution-specific variance.

### Value

r.squaredGLMM returns a numeric vector with two values for marginal and conditional  $R_{GLMM}^2$ .

### Note

$R_{GLMM}^2$  can be calculated also for fixed-effect models. In the simplest case of OLS it reduces to  $\text{var}(\text{fitted}) / (\text{var}(\text{fitted}) + \text{deviance} / 2)$ . Unlike likelihood-ratio based  $R^2$  for OLS, value of this statistic differs from that of the classical  $R^2$ .

Currently methods exist for classes: mer(Mod), lme, glmmML and (g)lm.

See note in [r.squaredLR](#) help page for comment on using  $R^2$  in model selection.

**This function is still in experimental stage and should be used with caution.**

### Author(s)

This implementation is based on R code from ‘Supporting Information’ for Nakagawa & Schielzeth (2012), and its extension by Paul Johnson.

### References

Nakagawa, S, Schielzeth, H. (2012). A general and simple method for obtaining  $R^2$  from Generalized Linear Mixed-effects Models. *Methods in Ecology and Evolution*: (online) doi:10.1111/j.2041-210x.2012.00261.x

Johnson, P. (in press). Generalization of Nakagawa & Schielzeth’s  $R_{GLMM}^2$  to all random effects specifications. *Methods in Ecology and Evolution*

### See Also

[summary.lm](#), [r.squaredLR](#)

### Examples

```
data(Orthodont, package = "nlme")

fm1 <- lme(distance ~ Sex * age, ~ 1 | Subject, data = Orthodont)

r.squaredGLMM(fm1)
r.squaredLR(fm1)
r.squaredLR(fm1, null.RE = TRUE)
```

---

r.squaredLR	<i>Likelihood-ratio based pseudo-R-squared</i>
-------------	--

---

## Description

Calculate a coefficient of determination based on the likelihood-ratio test ( $R_{LR}^2$ ).

## Usage

```
r.squaredLR(x, null = NULL, null.RE = FALSE)
```

```
null.fit(x, evaluate = FALSE, RE.keep = FALSE, envir = NULL)
```

## Arguments

x	a fitted model object.
null	a fitted <i>null</i> model. If not provided, null.fit will be used to construct it. null.fit's capabilities are limited to only a few model classes, for others the <i>null</i> model has to be specified manually.
null.RE	logical, should the null model contain random factors? Only used if no <i>null</i> model is given, otherwise omitted, with a warning.
evaluate	if TRUE evaluate the fitted model object else return the call.
RE.keep	if TRUE, the random effects of the original model are included.
envir	the environment in which the <i>null</i> model is to be evaluated, defaults to the environment of the original model's formula.

## Details

This statistic is one of the several proposed pseudo- $R^2$ 's for nonlinear regression models. It is based on an improvement from *null* (intercept only) model to the fitted model, and calculated as

$$R_{LR}^2 = 1 - \exp\left(-\frac{2}{n}(\log Lik(x) - \log Lik(0))\right)$$

where  $\log Lik(x)$  and  $\log Lik(0)$  are the log-likelihoods of the fitted and the *null* model respectively. ML estimates are used for this purpose in when models have been fitted by RESTRICTED ML (by calling logLik with argument REML = FALSE). Note that the *null* model can include the random factors of the original model, in which case the statistic represents the 'variance explained' by fixed effects.

For OLS models the value is consistent with classical  $R^2$ . In some cases (e.g. in logistic regression), the maximum  $R_{LR}^2$  is less than one. The modification proposed by Nagelkerke (1991) adjusts the  $R_{LR}^2$  to achieve 1 at its maximum:  $\bar{R}^2 = R_{LR}^2 / \max(R_{LR}^2)$  where  $\max(R_{LR}^2) = 1 - \exp(\frac{2}{n} \log Lik(0))$ .

null.fit tries to guess the *null* model call, given the provided fitted model object. This would be usually a glm. The function will give an error for an unrecognized class.

## Value

r.squaredLR returns a value of  $R_{LR}^2$ , and the attribute "adj.r.squared" gives the Nagelkerke's modified statistic. Note that this is not the same as nor equivalent to the classical 'adjusted R squared'.

null.fit returns the fitted *null* model object (if evaluate = TRUE) or an unevaluated call to fit a *null* model.

**Note**

$R^2$  is a useful goodness-of-fit measure as it has the interpretation of the proportion of the variance ‘explained’, but it performs poorly in model selection, and is not suitable for use in the same way as the information criterions.

**References**

- Cox, D. R. and Snell, E. J. (1989) *The analysis of binary data*, 2nd ed. London, Chapman and Hall
- Magee, L. (1990)  $R^2$  measures based on Wald and likelihood ratio joint significance tests. *Amer. Stat.* 44: 250-253
- Nagelkerke, N. J. D. (1991) A note on a general definition of the coefficient of determination. *Biometrika* 78: 691-692

**See Also**

[summary.lm](#), [r.squaredGLMM](#)

---

subset.model.selection

*Subsetting model selection table*

---

**Description**

Return subsets of a model selection table returned by dredge or model.sel.

**Usage**

```
## S3 method for class model.selection
subset(x, subset, select, recalc.weights = TRUE,
       recalc.delta = FALSE, ...)
## S3 method for class model.selection
x[i, j, recalc.weights = TRUE, recalc.delta = FALSE, ...]
```

**Arguments**

x	a model.selection object to be subsetted.
subset, select	logical expressions indicating columns and rows to keep. See <a href="#">subset</a> .
i, j	indices specifying elements to extract.
recalc.weights	logical value specifying whether Akaike weights should be normalized across the new set of models to sum to one.
recalc.delta	logical value specifying whether $\Delta_{IC}$ should be calculated for the new set of models (not done by default).
...	further arguments passed to <a href="#">[.data.frame]</a> .

**Value**

A model.selection object containing only the selected models (rows). When columns are selected (arguments select or j are provided), a plain data.frame is returned.

**Note**

Unlike the method for `data.frame`, extracting with only one index (i.e. `x[i]`) will select rows rather than columns.

To select rows according to presence or absence of the variables (rather than their value), a pseudo-function `has` may be used, e.g. `subset(x, has(a, !b))` will select rows with *a* **and** without *b* (this is equivalent to `!is.na(a) & is.na(b)`). `has` can take any number of arguments. Importantly, the `has()` notation cannot be used in the `subset` argument for `dredge`, where the variable names should be given directly, with the same effect.

To select rows where one variable can be present conditional on the presence of other variable(s), the function `dc` (**d**ependency **c**hain) can be used. `dc` takes any number of variables as arguments, and allows a variable to be included only if all the preceding arguments are also included (e.g. `subset = dc(a, b, c)` allows for models of form *a*, *a+b* and *a+b+c* but not *b*, *c*, *b+c* or *a+c*).

**Author(s)**

Kamil Bartoń

**See Also**

[dredge](#), [subset](#) and [\[.data.frame\]](#) for subsetting and extracting from `data.frames`.

**Examples**

```
fm1 <- lm(formula = y ~ X1 + X2 + X3 + X4, data = Cement)

# generate models where each variable is included only if the previous
# are included too, e.g. X2 only if X1 is there, and X3 only if X2 and X1
dredge(fm1, subset = dc(X1, X2, X3, X4))

# which is equivalent to
# dredge(fm1, subset = (!X2 | X1) & (!X3 | X2) & (!X4 | X3))

# alternatively, generate "all possible" combinations
ms0 <- dredge(fm1)
# ...and afterwards select the subset of models
subset(ms0, dc(X1, X2, X3, X4))
# which is equivalent to
# subset(ms0, (has(!X2) | has(X1)) & (has(!X3) | has(X2)) & (has(!X4) | has(X3)))

# Different ways of finding a confidence set of models:
# delta(AIC) cutoff
subset(ms0, delta <= 4, recalc.weights = FALSE)
# cumulative sum of Akaike weights
subset(ms0, cumsum(weight) <= .95, recalc.weights = FALSE)
# relative likelihood
subset(ms0, (weight / weight[1]) > (1/8), recalc.weights = FALSE)
```

---

updateable

---

*Make a function return updateable result*


---

**Description**

Creates a function wrapper that stores a call in the values returned by its argument `FUN`.

## Usage

```
updateable(FUN)
updateable2(FUN, Class)

# updateable wrapper for mgcv::gamm and gamm4::gamm4
uGamm(formula, random = NULL, ..., lme4 = inherits(random, "formula"))
```

## Arguments

<code>FUN</code>	function to be modified, found via <a href="#">match.fun</a> .
<code>Class</code>	optional character vector naming class(es) to be set onto the result of <code>FUN</code> (not possible with formal S4 objects).
<code>formula, random, ...</code>	arguments to be passed to <code>gamm</code> or <code>gamm4</code>
<code>lme4</code>	if <code>TRUE</code> , <code>gamm4</code> is called, <code>gamm</code> otherwise.

## Details

Most model fitting functions in **R** return an object that can be updated or re-fitted via [update](#). This is thanks to the `call` stored in the object, which can be used (possibly modified) later on. It is also utilised by `dredge` to generate sub-models.

Some functions (such as `gamm` or `MCMCglmm`) do not provide their result with the `call` element. In this case `updateable` can be used on that function to add it. The resulting wrapper should be used in exactly the same way as the original function.

## Value

A function with the same arguments as `FUN`, wrapping a call to `FUN` and adding an element named `call` to its result if possible, or an attribute `"call"` (if the returned value is atomic or a formal S4 object).

## Note

`uGamm` sets also an appropriate class onto the result (`"gamm4"` and/or `"gamm"`), which is needed for some generics defined in **MuMIn** to work (note that unlike the functions created by `updateable` it has no formal arguments of the original function). As of version 1.9.2, `MuMIn::gamm` is no longer available.

**MuMIn** replaces the default method for `getCall` (defined originally in package **stats**), with a function that can extract the call also when it is an [attribute](#) (rather than an element of the object).

## Author(s)

Kamil Barton

## See Also

[update](#), [getCall](#), [getElement](#), [attributes](#)  
[gamm](#), [gamm4](#)



**Examples**

```

# Simple example with cor.test:

# From example(cor.test)
x <- c(44.4, 45.9, 41.9, 53.3, 44.7, 44.1, 50.7, 45.2, 60.1)
y <- c( 2.6,  3.1,  2.5,  5.0,  3.6,  4.0,  5.2,  2.8,  3.8)

ct1 <- cor.test(x, y, method = "kendall", alternative = "greater")

uCor.test <- updateable(cor.test)

ct2 <- uCor.test(x, y, method = "kendall", alternative = "greater")

getCall(ct1) # --> NULL
getCall(ct2)

#update(ct1, method = "pearson") --> Error
update(ct2, method = "pearson")
update(ct2, alternative = "two.sided")

## predefined wrapper for gamm:

set.seed(0)
dat <- gamSim(6, n = 100, scale = 5, dist = "normal")

fmm1 <- uGamm(y ~s(x0)+ s(x3) + s(x2), family = gaussian, data = dat,
             random = list(fac = ~1))

getCall(fmm1)
class(fmm1)

###

## Not run:
library(caper)
data(shorebird)
shorebird <- comparative.data(shorebird.tree, shorebird.data, Species)

fm1 <- crunch(Egg.Mass ~ F.Mass * M.Mass, data = shorebird)

uCrunch <- updateable(crunch)

fm2 <- uCrunch(Egg.Mass ~ F.Mass * M.Mass, data = shorebird)

getCall(fm1)
getCall(fm2)
update(fm2) # Error with fm1
dredge(fm2)

## End(Not run)

```

---

**Weights***Akaike weights*

---

**Description**

Calculate or extract normalized model likelihoods ('Akaike weights').

**Usage**

```
Weights(x)
```

**Arguments**

**x** a numeric vector of information criterion values such as AIC, or objects returned by functions like `AIC`. There are also methods for extracting Akaike weights from a `model.selection` or `averaging` objects.

**Value**

a numeric vector of normalized likelihoods.

**Author(s)**

Kamil Bartoń

**See Also**

[importance](#)

[weights](#), which extracts fitting weights from model objects.

**Examples**

```
fm1 <- glm(Prop ~ dose, data = Beetle, family = binomial)
fm2 <- update(fm1, . ~ . + I(dose^2))
fm3 <- update(fm1, . ~ log(dose))
fm4 <- update(fm3, . ~ . + I(log(dose)^2))

round(Weights(AICc(fm1, fm2, fm3, fm4)), 3)
```

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