

Package ‘glmulti’

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Title Model Selection and Multimodel Inference Made Easy

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Depends R (>= 2.13.0), rJava (>= 0.5-0), methods, leaps

Suggests MASS, aod, lme4, pscl, survival, nnet

Description Automated model selection and model-averaging. Provides a wrapper for glm and other functions, automatically generating all possible models (under constraints set by the user) with the specified response and explanatory variables, and finding the best models in terms of some Information Criterion (AIC, AICc or BIC). Can handle very large numbers of candidate models. Features a Genetic Algorithm to find the best models when an exhaustive screening of the candidates is not feasible.

License GPL (>= 2)

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| aic | <i>Computing an IC from a fitted model object</i> |
|-----|---------------------------------------------------|

Description

These functions are used by `glmulti` to compute Information Criteria from a fitted model object. They are S4 generics, currently with methods for `glm/lm` objects. You may define your own methods if needed, to support other fitting functions or to use other IC.

Usage

```
aic(object, ...)
aicc(object, ...)
bic(object, ...)
qaic(object, ...)
qaicc(object, ...)
```

Arguments

| | |
|--------|----------------------------------------------------------|
| object | A fitted model object. |
| ... | Further arguments that may be useful for future methods. |

Details

When using `qaic` or `qaicc`, you will need to provide an estimate of the inflation factor c . This is done through the global variable `glmultiqaiccvalue`. Set this variable equal to your estimated c before running `glmulti`. Otherwise it will stop with a warning.

Value

The IC value of the model.

Author(s)

Vincent Calcagno, McGill University

See Also[glmulti](#)

`aic-methods`*Methods for Function aic*

Description

Used to compute the AIC value for several classes of models.

Methods

object = "ANY" Default method for e.g. glm and lm

`aicc-methods`*Methods for Function aicc*

Description

Used to compute the AICc value for several classes of models.

Methods

object = "ANY" Default method for e.g. glm and lm

`bic-methods`*Methods for Function bic*

Description

Used to compute the BIC value for several classes of models.

Methods

object = "ANY" Default method for e.g. glm and lm

coef.glmulti

*Model averaging and multimodel inference with glmulti***Description**

These functions, applied on a `glmulti` object, produce model-averaged estimates, unconditional confidence intervals, and predictions from the models in the confidence set (or a subset of them). They are equivalents of the standard `coef` and `predict` for single models.

Usage

```
# S3 coef method for class 'glmulti'
## S3 method for class 'glmulti'
coef(object, select="all", varweighting="Buckland",
      icmethod="Lukacs", alphaIC=0.05, ...)

# S3 predict method for class 'glmulti'
## S3 method for class 'glmulti'
predict(object, select="all", newdata=NA, se.fit=FALSE,
        varweighting="Buckland", icmethod="Lukacs", alphaIC=0.05, ...)
```

Arguments

| | |
|---------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>object</code> | an object of class <code>glmulti</code> |
| <code>select</code> | A specification of which models should be used for inference. By default all models are used, see below. |
| <code>varweighting</code> | The method to be used to compute the unconditional variance. "Buckland" (the default) implements the approach presented in Buckland et al. 1997. "Johnson" implements a slightly different approach recommended in Johnson & Omland 2004 and proposed at page 235 in Burnham & Anderson 2002. The latter results in slightly bigger estimates of the unconditional variance of model coefficients. |
| <code>icmethod</code> | Method to construct confidence intervals. One of "Standard", "Burnham" or "Lukacs". The three methods differ in their use (or not) of degrees of freedom. |
| <code>newdata</code> | New data.frame of data for which to predict values |
| <code>se.fit</code> | Whether to return unconditional variances and confidence intervals associated with predicted values |
| <code>alphaIC</code> | The alpha risk when building the confidence intervals |
| <code>...</code> | Further arguments to single-model <code>coef</code> or <code>predict</code> |

Details

`select` can be used to specify which models should be used for inference. By default all are used. If specifying an integer value x , only the x best models are used. If a numeric value is provided, if it less than one, models that sum up to $x\%$ of evidence weight are used. If it more than one, models within x IC units from the best model are used.

Value

`coef` returns a data.frame with model-averaged estimates of the different parameters in the models, as well as their unconditional variance, importance, and confidence interval according to one of three methods: "Standard" simply assumes a Normal distribution of the estimator (Buckland 1997), "Lukacs" assumes a Student distribution with degrees of freedom taken to be averaged across models (see Lukacs et al. 2010), and "Burnham" is a more sophisticated Student-based method proposed by Burnham & Anderson 2002.

`predict` returns a list of three elements: the multi-model predictions, their variability (unconditional variance and confidence interval, if `se.fit=T`), and the number of NA predicted values that were treated as zeros when averaging models.

Author(s)

Vincent Calcagno, McGill University

References

Buckland et al. 1997. Model selection: an integral part of inference. *Biometrics*. Burnham & Anderson. 2002. Model Selection and Multimodel Inference. An Information Theoretic Practical Approach. Johnson & Omland. 2004. Model selection in ecology and evolution. *TREE*. Lukacs et al. 2010. Model selection bias and Freedman's paradox. *Annals of the Institute of Statistical Mathematics*.

See Also

[glmulti](#)

consensus

Takes a consensus of several glmulti objects

Description

The function takes a list of `glmulti` objects and returns a new `glmulti` object. This object contains the best models found in all passed objects, with duplicates removed. Useful to bring back together the different parts of a parallelized exhaustive screen, or to make the consensus of several replicate genetic algorithms.

Usage

```
consensus(xs, confsetsize = NA, ...)
```

Arguments

| | |
|--------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>xs</code> | A list containing <code>glmulti</code> objects, or filenames from which <code>glmulti</code> objects can be read on the disk (typically <code>glmulti</code> objects that have been saved using <code>write</code> with <code>file="filename object"</code>). |
| <code>confsetsize</code> | The number of best models to be included in the consensus object. If NA, all available models are included. |
| <code>...</code> | Further arguments, allowing to write custom S4 methods for this generic. |

Details

The name of the returned object is the name of the first object passed, with "consensus-" prepended. The `params` slot of the returned object is taken from the first object too. Note that if not all `glmulti` objects in `xs` do contain fitted model objects, then no model object will be included in the returned `glmulti` object.

Value

A standard object of class `glmulti`

Author(s)

Vincent Calcagno, McGill University

References

Calcagno \& de Mazancourt 2010 J. Stat. Soft. v34 i12. See <http://www.jstatsoft.org/v34/i12>

See Also

[glmulti](#)

consensus-methods

Consensus method for glmulti objects.

Description

Concatenates several `glmulti` objects and makes a consensus of them.

Methods

`xs = "list"` a list of `glmulti` objects to make a consensus of. Can include actual objects or filenames pointing to objects written on the disk (typically `glmulti` objects that have been saved using `write` with `file="filename|object"`).

`getfit`*Accessing coefficients of a fitted model object*

Description

Generic S4 function used to access the coefficients (and their standard error) from a fitted model. It is used by `coef.glmulti`.

Usage

```
getfit(object, ...)
```

Arguments

| | |
|---------------------|-----------------------------------------------------------------------------------------------|
| <code>object</code> | A fitted model object, of class <code>glm</code> , <code>lm</code> or <code>codeglm.nb</code> |
| <code>...</code> | Further arguments that may be required by some methods of this generic. |

Details

Define your own method for this generic when using `glmulti` with some custom fitting function.

Value

A `data.frame`, with as rows the coefficients that are fitted in the model, and three columns: the first with the estimated coefficients, the second with the associated standard errors, and the third with degrees of freedom.

Author(s)

Vincent Calcagno, McGill University

References

Calcagno \& de Mazancourt 2010 J. Stat. Soft. v34 i12. See <http://www.jstatsoft.org/v34/i12>

See Also

[glmulti](#)

| | |
|-----------------------------|-------------------------------------------------|
| <code>getfit-methods</code> | <i>Methods for Function <code>getfit</code></i> |
|-----------------------------|-------------------------------------------------|

Description

Used by `coef.glmulti` to access the contents of fitted model objects of different classes.

Methods

object = "ANY" Default method, for e.g. `glm` objects.

object = "coxph" Method for `coxph` objects.

object = "coxph.null" Method for `coxph.null` objects.

| | |
|----------------------|-----------------------------------------------------------------------|
| <code>glmulti</code> | <i>Automated model selection and multimodel inference with (G)LMs</i> |
|----------------------|-----------------------------------------------------------------------|

Description

`glmulti` finds what are the n best models (the confidence set of models) among all possible models (the candidate set, as specified by the user). Models are fitted with the specified fitting function (default is `glm`) and are ranked with the specified Information Criterion (default is `aicc`). The best models are found either through exhaustive screening of the candidates, or using a genetic algorithm, which allows very large candidate sets to be addressed. The output can be used for model selection, variable selection, and multimodel inference.

Usage

```
# glmulti S4 generic
glmulti(y, xr, data, exclude = c(), name = "glmulti.analysis",
intercept = TRUE, marginality = FALSE,
bunch=30, chunk = 1, chunks = 1, level = 2,
minsize = 0, maxsize = -1, minK = 0, maxK = -1,
method = "h", crit = "aic", confsetsize = 100, popsize = 100,
mutrate = 10^-3, sexrate = 0.1, imm = 0.3, plotty = TRUE,
report = TRUE, deltaM = 0.05, deltaB = 0.05, conseq = 5,
fitfunction = "glm", resumefile = "id", includeobjects=TRUE, ...)
```

Arguments

y A formula, character string, or fitted model (of class `lm` or `glm`) specifying the response variable and the terms (main effects and/or interactions) to be used in the candidate models (e.g. `height~age*sex+mass`). Alternatively, a character string naming the variable to be used as response (e.g. "height") (in which case the names of the predictors must be passed through the `xr` argument) Alternatively, a custom list of (fitted) model objects can also be passed (can be convenient for small candidate sets).

| | |
|-------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| xr | An optional character array specifying the variables (categorical or quantitative) to be used as predictors, e.g. c("age", "height", "mass") |
| exclude | Optional character vector naming terms (main effects or interactions) to be excluded from the candidate models, e.g. c("mass:height") |
| intercept | Whether to include an intercept in the candidate models or not. |
| level | If 1, only main effects (terms of order 1) are used to build the candidate set. If 2, pairwise interactions are also used (higher order interactions are currently ignored) |
| data | A data.frame containing the data. If not specified, glmulti will try to find the data in the environment of the formula, from the fitted model passed as y argument, or from the global environment. |
| name | The name of this glmulti analysis. Optional. |
| marginality | Whether to apply the marginality rule or not. If TRUE, only marginal models will be considered. |
| minsize | This sets a constraint on candidate models. Minimal number of TERMS (main effects or interactions) to be included in candidate models (negative = no constraint) |
| maxsize | This sets a constraint on candidate models. Maximal number of TERMS to be included in candidate models (negative = no constraint) |
| minK | This sets a constraint on candidate models. Minimal complexity of candidate models (negative = no constraint) |
| maxK | This sets a constraint on candidate models. Maximal complexity of candidate models (negative = no constraint) |
| method | The method to be used to explore the candidate set of models. If "h" an exhaustive screening is undertaken. If "g" the genetic algorithm is employed (recommended for large candidate sets). If "l", a very fast exhaustive branch-and-bound algorithm is used. Package leaps must then be loaded, and this can only be applied to linear models with covariates and no interactions. If "d", a simple summary of the candidate set is printed, including the number of candidate models. |
| crit | The Information Criterion to be used. This should be a function that accepts a fitted model as first argument. Default is the original Akaike IC (aic). Other provided functions are the Bayes IC (bic), the small-sample corrected AIC (aicc) and QAIC/QAICc (qaic and qaicc). |
| fitfunction | The fitting function to be used. Any function similar to glm can be used. See Examples |
| confsetsize | The number of models to be looked for, i.e. the size of the returned confidence set. |
| plotty | Whether to plot the progress of the IC profile when running. |
| report | Whether to report about the progress at run time. |
| bunch | The number of model formulas to be returned (to be fitted) at each call to the enumerator. Exhaustive screening only. |

| | |
|----------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| chunk | When using an exhaustive screening approach, it can be splitted in several parts to take advantage of multiple CPUs. chunk is an integer specifying which part the current call should perform. |
| chunks | When splitting an exhaustive screening, the total number of parts the task should be divided into. For example, with a quad-core processor, 4 may be useful. Use consensus to bring back the pieces into a single object. |
| popsiz | The population size for the genetic algorithm |
| mutrate | The per locus (i.e. per term) mutation rate for genetic algorithm, between 0 and 1 |
| sexrate | The rate of sexual reproduction for the genetic algorithm, between 0 and 1 |
| imm | The rate of immigration for the genetic algorithm, between 0 and 1 |
| deltaM | The target change in mean IC (defines the stop rules for the genetic algorithm) |
| deltaB | The target change in best IC (defines the stop rules for the genetic algorithm) |
| conseq | The target successive number of times with no improvement (i.e. target changes have been attained) (defines the stop rule for the GA). The greater it is, the more stringent the stop rule. |
| resumefile | When resuming an analysis (method="r"), the name of the files from which to resume. Default uses the same as name |
| includeobjects | Whether or not to include fitted models as objects. This makes coef and predict faster and is very convenient, but can be turned off in case fitted models are very large or are not to be used after. |
| ... | Further arguments to be passed to the fitting function. E.g. maxit=50 or family=binomial |

Details

glmulti is defined as a S4 function. It acts as a frontend that calls background compiled functions (contained in archive glmulti.jar). Running the function therefore requires a Java Running Environment, and package rJava. A thorough description of this function and package can be found in the article by Calcagno and de Mazancourt (see References). print.glmulti and summary.glmulti are S3 methods which provide a synthesis of glmulti analyses.

NOTE: When calling glmulti with a model object as y, only the formula will be extracted from the object. This means that optional arguments to the fitting function (e.g. family or maxit) will NOT be extracted. These arguments should be passed to glmulti through the

Value

An object of class glmulti is returned. It is a S4 object with several slots containing relevant data for model selection and beyond.

Several standard S3 functions are provided to help access the content of this object.

Several glmulti objects can be shrunk to one using the function consensus. This is useful to get the best of several replicates (of the genetic algorithm) or to bring together the different parts of a splitted exhaustive screening. When running a genetic algorithm, two tiny java files (serialized objects) are also written to the disk at regular intervals. They can be used to resume the calculation (method="r") if it was interrupted for any reason. This can also be used to continue a GA with modified parameters (e.g. mutation rate).

Author(s)

Vincent Calcagno, McGill University, Canada

References

Buckland (1997) Model Selection: an Integral Part of Inference. *Biometrics* 10:41
 Burnham & Anderson (2002) Model Selection and Multimodel Inference: an Information Theoretic Approach
 Calcagno & de Mazancourt 2010 *J. Stat. Soft.* v34 i12. See <http://www.jstatsoft.org/v34/i12>

See Also

[consensus](#), [aic](#), [weightable](#), [summary.glmulti](#), [coef.glmulti](#), [step](#)

Examples

```
# See the document "glmulti.pdf" included in the package.
# It explains the general approach and shows how to use
# glmulti with mixed models from the lme4 package.
# Other examples:
# A. This shows how to do the same for zero-inflated poisson models
# we load the required package
library(pscl)
# a random vector of count data
round(runif(100, 0,20)*round(runif(100)))>-> vy2
# dummy predictors
va = runif(100)
vb = runif(100)
# 1. The wrapper function
zeroinfl.glmulti=function(formula, data, inflate = "|1",...) {
  zeroinfl(as.formula(paste(deparse(formula), inflate)),data=data,...)
}
# The default getfit and aicc method will work for zeroinfl objects,
# so no need to redefine them
# we can proceed directly
glmulti(vy2~va*vb,fitfunc=zeroinfl.glmulti,inflate="|1")>->bab

# B. This shows how to include some terms in ALL the models
# As above, we just prepare a wrapper of the fitting function
glm.redefined = function(formula, data, always="", ...) {
  glm(as.formula(paste(deparse(formula), always)), data=data, ...)
}
# we then use this fitting function in glmulti
glmulti(vy2~va,level=1,fitfunc=glm.redefined,always="+vb")>-> bab
# va will be shuffled but vb is always included in the models

# this procedure allows support of arbitrarily any fitting function,
# or the use of sophisticated constraints on the model structure
```

glmulti-class

Class "glmulti">

Description

Contains the results of a glmulti analysis.

Objects from the Class

Objects will never be created directly but through calls of glmulti or by applying consensus on a list of glmulti objects.

Slots

name: Object of class "character" : the name of the analysis.

params: Object of class "list" : parameter values used when calling glmulti to produce the object.

nbmods: Object of class "integer" : the number of models that have been found by glmulti.

crits: Object of class "numeric" : the IC values of the models found, in ascending order.

K: Object of class "integer" : for each model, its complexity, from best to worst model.

formulas: Object of class "list" : for each model, its formula, from best to worst.

call: Object of class "call" : the original glmulti call that produced this object.

adi: Object of class "list" : additional arguments that had been passed to the fitting function through glmulti.

objects: Object of class "list" : The list of fitted model objects for the confidence set, if includeobjects=T.

Author(s)

Vincent Calcagno, McGill University

References

Calcagno & de Mazancourt 2010 J. Stat. Soft. v34 i12. See <http://www.jstatsoft.org/v34/i12>

See Also

[summary.glmulti](#), [consensus](#), [coef.glmulti](#)

Examples

```
showClass("glmulti")
```

Description

codeglmulti finds what are the n best models (the confidence set of models) among all possible models (the candidate set, as specified by the user). Models are fitted with the specified fitting function (default is `glm`) and are ranked with the specified Information Criterion (default is `aic`). The best models are found either through exhaustive screening of the candidates or using a genetic algorithm, which allows very large candidate sets to be addressed. The output can be used for model selection, variable selection, and multimodel inference.

Methods

y = "ANY", xr = "ANY", data = "ANY", exclude = "ANY" This will stop with a warning that an improper call has been attempted.

y = "character", xr = "character", data = "ANY", exclude = "ANY" Calling `glmulti` with the names of the response variable and of the predictors as character strings. This is the original interface used in versions earlier than 0.6-1.

y = "character", xr = "missing", data = "ANY", exclude = "missing" Calling `glmulti` with a model formula represented as a character string. E.g. `"u~c+x"`

y = "formula", xr = "missing", data = "ANY", exclude = "missing" Calling `glmulti` with a model formula containing all the terms to be included in candidate models. E.g. `u~c+x`

y = "list", xr = "ANY", data = "ANY", exclude = "ANY" Calling `glmulti` on a list of (fitted) model objects. Models will not be refitted, but the information criteria will be computed and a regular `glmulti` object is returned.

y = "glm", xr = "missing", data = "ANY", exclude = "missing" Calling `glmulti` with a `glm` object from which the formula and other parameters will be extracted.

y = "lm", xr = "missing", data = "ANY", exclude = "missing" Calling `glmulti` on a `lm` object from which the formula and other parameters will be extracted.

y = "missing", xr = "ANY", data = "ANY", exclude = "ANY" If `y` is missing the `glmulti` version currently used is printed.

Description

Used to compute the QAIC value for several classes of models. Specify the estimated c value to be used through the `"glmulti-cvalue"` option.

Methods

object = "ANY" Default method for e.g. `glm` and `lm`

 qaicc-methods

Methods for Function qaicc

Description

Used to compute the QAICc value for several classes of models. Specify the estimated c value to be used through the "glmulti-cvalue" option.

Methods

object = "ANY" Default method, for e.g. glm and lm

summary.glmulti

Handling glmulti objects

Description

These standard S3 functions can be applied on glmulti to print a short report, obtain a more detailed summary, or produce different types of graphics.

Usage

```
# S3 summary method for class 'glmulti'
## S3 method for class 'glmulti'
summary(object, ...)
```

```
# S3 print method for class 'glmulti'
## S3 method for class 'glmulti'
print(x, ...)
```

```
# S3 plot method for class 'glmulti'
## S3 method for class 'glmulti'
plot(x, type="p", ...)
```

Arguments

| | |
|--------|----------------------------------------------------------------------------|
| object | A glmulti object |
| x | An object of class glmulti |
| type | The type of graph to be produced. One of "p", "r", "s" or "w" (see below). |
| ... | Further arguments. |

Details

The name of the returned object is the name of the first object passed, with "consensus-" prepended. The params slot of the returned object is taken from the first object too.

Value

plot can be used to have a graphical representation of the results. Two types are proposed:

type="p" plots the IC profile (the IC values form the best to the worst model). A horizontal line delineates models that are less than 2 IC units away from the best model.

type="r" shows diagnostics of the fit (residuals versus predicted values, and QQ plot of residuals) for the five best models. It calls the plot functions on the fitted model objects, which should be defined (e.g. plot.lm, plot.glm). This type of plot can only be used if model objects are included in the glmulti object (i.e. if includeobjects was set to true).

type="s" plots the relative importance of model terms, i.e. the overall support for each variable across all models. A vertical line is drawn at 80

type="w" plots the normalized evidence weights of the models. A vertical line delineates models that sum up to 95

print prints a brief synthesis of the analysis (e.g. the best model found, its IC value and evidence weight...)

summary returns a list with more detailed elements:

| | |
|----------------|---------------------------------------------------------------------------------------------------------------------|
| name | the name of the analysis |
| method | The method used |
| fitting | The fitting function used |
| crit | The IC used |
| level | Whether interactions between predictors were considered or not |
| marginality | Whether the marginality rule was applied |
| confsetsize | The requested size of the confidence set |
| bestic | The lowest IC found |
| icvalues | The IC values of the models in the confidence set, from lower to greater |
| bestmodel | A list containing the formula of the best model found, or of the best models found if several had the same IC value |
| generations | The number of generations it took to converge. For genetic algorithm only. |
| elapsed | The actual (system) time it took. For genetic algorithm only. |
| includeobjects | A boolean indicating whether fitted model objects are contained in the object. |

Author(s)

Vincent Calcagno, McGill University

References

Calcagno \& de Mazancourt 2010 J. Stat. Soft. v34 i12. See <http://www.jstatsoft.org/v34/i12>

See Also[glmulti](#)

| | |
|------------|-----------------------------------|
| weightable | <i>Table of relative supports</i> |
|------------|-----------------------------------|

Description

Prepares a table with model formulas, IC values and IC relative supports

Usage

```
weightable(object, ...)
```

Arguments

| | |
|--------|--------------------------|
| object | A glmulti object |
| ... | For further improvements |

Value

A data frame with the list of formulas, IC values and IC weights

Author(s)

Jarret Byrnes and Vincent Calcagno, McGill University

See Also[glmulti](#)

| | |
|--------------------|-----------------------------------|
| weightable-methods | <i>Table of relative supports</i> |
|--------------------|-----------------------------------|

Description

Prepares a table with model formulas, IC values and IC relative supports

Methods

object="glmulti" Default call

| | |
|-------|--------------------------------|
| write | <i>Writing glmulti objects</i> |
|-------|--------------------------------|

Description

The S4 method provided for `glmulti` objects writes a `glmulti` object as a `data.frame`, or alternatively as a raw R object.

Usage

```
write(x, file = "data", ncolumns = if (is.character(x)) 1 else 5,  
      append = FALSE, sep = " ")
```

Arguments

| | |
|-----------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>x</code> | An object of class <code>glmulti</code> |
| <code>file</code> | The name of the file to write into. If missing, the name is taken to be the name of the <i>glmulti</i> object.* If "\object" is at the end of the filename, then the object is written as a raw R object using <i>saveRDS</i> . |
| <code>ncolumns</code> | Not used with <i>glmulti</i> objects |
| <code>append</code> | Whether to append the output to the file, if existing. |
| <code>sep</code> | The character to be used to separate columns. |

Details

When using "\object", the file written can be read directly from R using *readRDS*, or with *consensus*.

Value

A `data.frame`. Rows correspond to all models, sorted from best to worse.. The first columns indicate whether the different terms are found in the formula of each model (0/1). The next columns contain model complexity (K), model IC, and model formula (as a character string).

Author(s)

Vincent Calcagno, McGill University

See Also

[glmulti](#), [consensus](#)

write-methods

Methods for Function write

Description

Methods for function write

Methods

x = "glmulti" Method to write glmulti objects.

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