

# Package ‘mixor’

June 14, 2018

**Type** Package

**Title** Mixed-Effects Ordinal Regression Analysis

**Version** 1.0.4

**Date** 2018-06-13

**Author** Kellie J. Archer, Donald Hedeker, Rachel Nordgren, Robert D. Gibbons

**Maintainer** Kellie J. Archer <archer.43@osu.edu>

**Description** Provides the function 'mixor' for fitting a mixed-effects ordinal and binary response models and associated methods for printing, summarizing, extracting estimated coefficients and variance-covariance matrix, and estimating contrasts for the fitted models.

**License** GPL (>= 2)

**Depends** R (>= 2.10), survival

**BuildResaveData** best

**Biarch** yes

**NeedsCompilation** yes

**LazyLoad** true

**Repository** CRAN

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mixor-package	<i>Mixed-Effects Ordinal Regression Analysis</i>
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## Description

This package provides a function `mixor` for fitting mixed-effects ordinal and binary response models and associated methods for printing, summarizing, extracting estimated coefficients and the variance-covariance matrix, and estimating contrasts for the fitted models.

## Details

Package:	mixor
Type:	Package
Title:	Mixed-Effects Ordinal Regression Analysis
Version:	1.0.4
Date:	2018-06-13
Author:	Kellie J. Archer, Donald Hedeker, Rachel Nordgren, Robert D. Gibbons
Maintainer:	Kellie J. Archer <archer.43@osu.edu>
Description:	Provides the function 'mixor' for fitting a mixed-effects ordinal and binary response models and associated methods.
License:	GPL (>=2)
Depends:	R (>= 2.10), survival
BuildResaveData:	best
Biarch:	yes
NeedsCompilation:	yes
LazyLoad:	true

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This package provides a function `mixor` for fitting mixed-effects ordinal and binary response models and associated methods for printing, summarizing, extracting estimated coefficients and the variance-covariance matrix, and estimating contrasts for the fitted models.

### Author(s)

Kellie J. Archer, Donald Hedeker, Rachel Nordgren, Robert D. Gibbons  
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### References

Hedeker D. and Gibbons R.D. (1996) A computer program for mixed-effects ordinal regression analysis. *Computer Methods and Programs in Biomedicine* 49, 157-176.

### See Also

See also [mixor](#), and examples in [norcag](#), [irt.data](#), [concen](#), [SmokeOnset](#), [schizophrenia](#)

### Examples

```
library("mixor")
data("SmokingPrevention")
# data frame must be sorted by id variable
SmokingPrevention<-SmokingPrevention[order(SmokingPrevention$class),]
# school model
Fitted.school<-mixor(thksord~thkspre+cc+tv+cctv, data=SmokingPrevention,
```

```

      id=school, link="logit")
summary(Fitted.school)
vcov(Fitted.school)
# students in classrooms analysis
Fitted.students<-mixed(thksord~thkspre+cc+tv+cctv, data=SmokingPrevention,
  id=class, link="logit", nAGQ=11)
summary(Fitted.students)
coef(Fitted.students)
vcov(Fitted.students)
cm<-matrix(c(-1,-1,-1,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,
0,0,0,1,0,0,0,1),
ncol=3,byrow=TRUE)
Contrasts(Fitted.students, contrast.matrix=cm)

```

---

AIC.mixed

*Return AIC for a Fitted Mixed Model*


---

### Description

Returns the AIC of a fitted mixed model.

### Usage

```

## S3 method for class 'mixed'
AIC(object, ...)

```

### Arguments

object	a mixed object.
...	other arguments.

### Value

AIC of the fitted mixed model.

### Author(s)

Kellie J. Archer, Donald Hedeker, Rachel Nordgren, Robert D. Gibbons

### See Also

See Also as [mixed](#), [summary.mixed](#)

**Examples**

```
library("mixor")
data("schizophrenia")
### Random intercept
SCHIZ01.fit<-mixor(imps79o ~ TxDrug + SqrtWeek + TxSWeek, data=schizophrenia,
  id=id, link="probit")
summary(SCHIZ01.fit)
AIC(SCHIZ01.fit)
```

---

**BIC.mixor***Return BIC for a Fitted Mixor Model*

---

**Description**

Returns the BIC of a fitted mixor model.

**Usage**

```
## S3 method for class 'mixor'
BIC(object, ...)
```

**Arguments**

object	a mixor object.
...	other arguments.

**Value**

BIC of the fitted mixor model.

**Author(s)**

Kellie J. Archer, Donald Hedeker, Rachel Nordgren, Robert D. Gibbons

**See Also**

See Also as [mixor](#), [summary.mixor](#)

**Examples**

```
library("mixor")
data("schizophrenia")
### Random intercept
SCHIZ01.fit<-mixor(imps79o ~ TxDrug + SqrtWeek + TxSWeek, data=schizophrenia,
  id=id, link="probit")
summary(SCHIZ01.fit)
BIC(SCHIZ01.fit)
```

---

`coef.mixed`*Extract Model Coefficients*

---

### Description

`coef.mixed` is a generic function which extracts the model coefficients from a fitted model object fit using `mixed`

### Usage

```
## S3 method for class 'mixed'  
coef(object, ...)
```

### Arguments

<code>object</code>	a <code>mixed</code> object.
<code>...</code>	other arguments.

### Value

Coefficients extracted from the model object.

### Author(s)

Kellie J. Archer, Donald Hedeker, Rachel Nordgren, Robert D. Gibbons

### See Also

See Also as [mixed](#), [summary.mixed](#)

### Examples

```
library("mixed")  
data("schizophrenia")  
### Random intercept model  
SCHIZ01.fit<-mixed(imp79o ~ TxDrug + SqrtWeek + TxSWeek, data=schizophrenia,  
  id=id, link="probit")  
coef(SCHIZ01.fit)
```

---

 concen

*Twins Trouble Concentrating Data*


---

## Description

Monozygotic and dizygotic twins trouble concentrating data

## Usage

```
data(concen)
```

## Format

A data frame with 16 observations on the following 6 variables.

ID a numeric vector indicating the unique twin pair ID

TConcen an indicator variable representing trouble concentrating (0 = absent, 1 = present)

int a numeric vector of ones; used in the stand-alone MIXOR program to represent the intercept

Mz an indicator variable representing MZ twins (1 = MZ, 0 = DZ)

Dz an indicator variable representing DZ twins (1 = DZ, 0 = MZ)

freq a numeric vector representing the frequency of the pattern

## References

Ramakrishnan V. et al (1992) Elementary methods for the analysis of dichotomous outcomes in unselected samples of twins *Genetic Epidemiology* 9, 273-287.

## Examples

```
library("mixor")
data("concen")
# sort the data by twin pair ID
concen<-concen[order(concen$ID),]
# common ICC probit model
Common.ICC<-mixor(TConcen~Mz, data=concen, id=ID, weights=freq,
  link="probit", nAGQ=10, random.effect.mean=FALSE)
summary(Common.ICC)
# Varying ICC probit model
Varying.ICC<-mixor(TConcen~Mz+Dz, data=concen, id=ID, weights=freq,
  which.random.slope=1:2, exclude.fixed.effect=2, link="probit",
  nAGQ=20, random.effect.mean=FALSE, UNID=1)
summary(Varying.ICC)
```

**Description**

This function is used to specify and estimate contrasts of interest for a mixor object.

**Usage**

```
Contrasts(fit, contrast.matrix, digits=max(3, getOption("digits") - 2),
          signif.stars=TRUE, dig.tst = max(1, min(5, digits - 1)))
```

**Arguments**

<code>fit</code>	A mixor object.
<code>contrast.matrix</code>	A matrix of contrasts of interest. Each column in the contrast matrix should be of the same length as the coef vector of the fitted mixor object.
<code>digits</code>	minimum number of significant digits to be used for most numbers.
<code>signif.stars</code>	logical; if TRUE, P-values are additionally encoded visually as "significance stars" in order to help scanning of long coefficient tables.
<code>dig.tst</code>	minimum number of significant digits for the test statistics.

**Value**

A list containing the following components:

<code>contrast.matrix</code>	a matrix specifying the contrasts of interest.
<code>Contrasts</code>	a matrix containing the estimates, SEs, Z-values, and p-values for the contrasts of interest.

**Author(s)**

Kellie J. Archer, Donald Hedeker, Rachel Nordgren, Robert D. Gibbons

**See Also**

See Also as [mixor](#), [coef.mixor](#), [vcov.mixor](#)



**Examples**

```

library("mixor")
data("SmokingPrevention")
# data frame must be sorted by id variable
SmokingPrevention<-SmokingPrevention[order(SmokingPrevention$class),]
Fitted.students<-mixor(thksord~thkspre+cc+tv+cctv, data=SmokingPrevention,
  id=class, link="logit")
summary(Fitted.students)
coef(Fitted.students)
vcov(Fitted.students)
cm<-matrix(c(-1,-1,-1,0,0,0,0,0,
            0, 0, 0,0,0,0,0,0,
            0, 0, 0,1,0,0,0,1),ncol=3,byrow=TRUE)
Contrasts(Fitted.students, contrast.matrix=cm)

```

---

deviance.mixor	<i>Return the deviance for a Fitted Mixor Model</i>
----------------	---

---

**Description**

Returns the deviance of a fitted mixor model.

**Usage**

```

## S3 method for class 'mixor'
deviance(object, ...)

```

**Arguments**

object	a mixor object.
...	other arguments.

**Value**

Deviance of the fitted mixor model.

**Author(s)**

Kellie J. Archer, Donald Hedeker, Rachel Nordgren, Robert D. Gibbons

**See Also**

See Also as [mixor](#), [summary.mixor](#), [logLik.mixor](#)

**Examples**

```

library("mixor")
data("schizophrenia")
### Random intercept
SCHIZ01.fit<-mixor(imps79o ~ TxDrug + SqrtWeek + TxSWeek, data=schizophrenia,
  id=id, link="probit")
summary(SCHIZ01.fit)
deviance(SCHIZ01.fit)

```

---

 irt.data

---

*Armed Services Vocational Aptitude Battery*


---

**Description**

Arithmetic reasoning items from the Armed Services Vocational Aptitude Battery

**Usage**

```
data(irt.data)
```

**Format**

A data frame with 128 observations on the following 13 variables.

ID a numeric vector indicating unique pattern identifier

Resp item response (0 = incorrect; 1 = correct)

int a numeric vector of ones; used in MIXOR stand-alone program to represent the intercept

Item1 Arithmetic reasoning item 1 (0 = no; 1 = yes)

Item2 Arithmetic reasoning item 2 (0 = no; 1 = yes)

Item3 Arithmetic reasoning item 3 (0 = no; 1 = yes)

Item4 Arithmetic reasoning item 4 (0 = no; 1 = yes)

SexF an indicator variable representing gender (0 = female; 1 = male)

SexItem1 Gender by Item1 interaction

SexItem2 Gender by Item2 interaction

SexItem3 Gender by Item3 interaction

SexItem4 Gender by Item4 interaction

freq frequency weight of pattern

**References**

Mislevy R.J. (1985) Estimation of latent group effects *Journal of the American Statistical Association* 80, 993-997.

**Examples**

```

library("mixor")
data("irt.data")
## Sort data by ID
irt.data<-irt.data[order(irt.data$ID),]
# 2 parameter logistic IRT model
Fitted.irt<-mixor(Resp~Item1+Item2+Item3+Item4-1, data=irt.data, id=ID,
  weights=freq, which.random.slope=1:4, link="logit", nAGQ=10,
  random.effect.mean=FALSE, UNID=1, vcov=FALSE)
summary(Fitted.irt)
# 2 parameter logistic IRT model with Sex interations on item parameters
Fitted.irt2<-mixor(Resp~Item1+Item2+Item3+Item4+SexItem1+SexItem2+SexItem3+SexItem4-1,
  data=irt.data, id=ID, weights=freq, which.random.slope=1:8, link="logit",
  nAGQ=10, random.effect.mean=FALSE, UNID=1, vcov=FALSE)
summary(Fitted.irt2)

```

---

logLik.mixor

*Return the log-likelihood for a Fitted Mixor Model*


---

**Description**

Returns the log-likelihood of a fitted mixor model.

**Usage**

```

## S3 method for class 'mixor'
logLik(object, ...)

```

**Arguments**

object	a mixor object.
...	other arguments.

**Value**

Log-likelihood of the fitted mixor model.

**Author(s)**

Kellie J. Archer, Donald Hedeker, Rachel Nordgren, Robert D. Gibbons

**See Also**

See Also as [mixor](#), [summary.mixor](#), [deviance.mixor](#)

## Examples

```
library("mixor")
data("schizophrenia")
### Random intercept
SCHIZ01.fit<-mixor(imps79o ~ TxDrug + SqrtWeek + TxSWeek, data=schizophrenia,
  id=id, link="probit")
summary(SCHIZ01.fit)
logLik(SCHIZ01.fit)
```

---

 mixor

*Mixed-Effects Ordinal Regression Analysis*


---

## Description

This function fits mixed-effects ordinal and binary response models. Various link functions are supported including probit, logistic, and complementary log-log. For longitudinal data, the `mixor` function allows for individual varying intercepts and slopes across times.

## Usage

```
mixor(formula, data, id, which.random.slope = NA, subset, weights,
  exclude.fixed.effect = NA, CONV = 1e-04, empirical.prior = FALSE,
  quadrature.dist = "Normal", nAGQ = 11, adaptive.quadrature = TRUE,
  link = "probit", KG = 0, KS = 0, IADD = -1, indep.re = FALSE,
  random.effect.mean = TRUE, UNID = 0, vcov = TRUE)
```

## Arguments

<code>formula</code>	an object of class " <code>formula</code> " (or one that can be coerced to that class): a symbolic description of the model to be fitted.
<code>data</code>	an optional <code>data.frame</code> containing the variables in the model. Note the <code>data.frame</code> must be sorted by <code>id</code> prior to invoking the <code>mixor</code> function.
<code>id</code>	name of clustering variable in the <code>data.frame</code>
<code>which.random.slope</code>	<code>which.random.slope=NA</code> means no random slope, only a random intercept is fit. To specify a random slope, <code>which.random.slope</code> is the number of the predictor variable on the RHS of the model formula. More than one variable can have a random slope.
<code>subset</code>	an optional vector specifying a subset of observations to be used in the fitting process.
<code>weights</code>	when supplied, indicates differential weights are used; otherwise each <code>id</code> is weighted equally. <code>weights</code> are the frequency weights to be assigned to each <code>id</code> .

<code>exclude.fixed.effect</code>	the RHS of the model includes both fixed and random effects. Variables are identified as random effects using <code>which.random.slope</code> . If it is desired that a variable be included in the model without a fixed effect (random only), the number of that variable(s) in the RHS formula should be passed to <code>exclude.fixed.effects</code> .
<code>CONV</code>	convergence criteria, default is 0.0001.
<code>empirical.prior</code>	logical. If TRUE, uses empirical prior for random effects.
<code>quadrature.dist</code>	distribution for random effects. Either "Normal" (default) or "Uniform".
<code>nAGQ</code>	number of quadrature nodes per dimension. For one random effect, <code>nAGQ=20</code> is reasonable but should be reduced to 5-10 for multiple random effects.
<code>adaptive.quadrature</code>	logical indicating whether adaptive quadrature (default) or non-adaptive quadrature is performed.
<code>link</code>	Link function, either "probit", "logit", or "cloglog"
<code>KG</code>	an optional integer reflecting the number of covariates to interact with threshold parameters (the first KG variables on the RHS of the model formula, so the order of the variables on the RHS of the model formula is important when using KG). Note that if KG is non-zero, KS must be zero.
<code>KS</code>	an optional integer reflecting the number of covariates used in scaling (the first KS variables on the RHS of the model formula, so the order of the variables on the RHS of the model formula is important when using KS). Note that if KS is non-zero, KG must be zero.
<code>IADD</code>	indicates how XB part of model is included; -1 subtract covariates and mean of random effects from thresholds; 1 add covariates and mean of random effects to thresholds. Default is -1 (subtract XB).
<code>indep.re</code>	logical. If TRUE, independent random effects. Default is FALSE which assumes correlated random effects.
<code>random.effect.mean</code>	logical. If TRUE, estimate the mean of the random effects.
<code>UNID</code>	indicator variable where 0 = random effects are multi-dimensional; 1 = random effects are variables related to a uni-dimensional random effect (e.g., item indicators of a latent variable).
<code>vcov</code>	logical. Default is <code>vcov=TRUE</code> which returns estimates of the the random-effect variance-covariance matrix. When <code>vcov=FALSE</code> , then estimates of the Cholesky (matrix square-root) of the random-effect variance-covariance matrix are returned.

## Details

A typical model has the form  $\text{response} \sim \text{terms}$  where response is the (numeric) response vector and terms is a series of terms which specifies a linear predictor for response. The response can also be a censored survival response, of the form `Surv(time,censorvariable)`

**Value**

A list with components:

call	Model call formula
Deviance	Model deviance
Quadrature.points	number of quadrature nodes per dimension used in fit
Model	a matrix summarizing the model fit including columns Estimate, SE, Z, and P-value
varcov	The variance-covariance matrix
EBmean	empirical Bayes estimates of the means of the posterior distribution for each id
EBvar	empirical Bayes estimates of posterior variance/covariance for each id)
RIDGEMAX	Ridge
RLOGL	Log-likelihood
SE	a matrix corresponding the standard errors of the parameters estimates in coef
AIC	AIC
SBC	Schwarz criterion
AICD	Akaike information criterion
SBCD	deviance information criterion
MU	mean of random effects
ALPHA	fixed effects estimates
SIGMA	random effects variance-covariance matrix
GAM	thresholds
TAU	scaling parameter estimates when proportional odds are not assumed. Returns when KG is non-zero.
IADD	indicates how the XB part of model was included; -1 subtract covariates and mean of random effects from thresholds; 1 add covariates and mean of random effects to thresholds.
Y	the response from the fitted model.
X	the random effects terms from the fitted model.
W	the fixed effects terms from the fitted model.
MAXJ	the number of ordinal levels.
random.effect.mean	If TRUE, the mean of the random effects was estimated.
KS	integer reflecting the number of covariates that were specified to use in scaling (the first KS variables on the RHS of the model formula).
KG	integer reflecting the number of covariates that were specified to interact with the threshold parameters (the first KG variables on the RHS of the model formula).
id	name of clustering variable in the data.frame

which.random.slope	the number of the predictor variable on the RHS of the model formula having a random slope. When which.random.slope=NA, only a random intercept model was fit.
ICEN	if 1 indicates right-censoring was considered in the model fit.
link	Link function, either "probit", "logit", or "cloglog"
terms	terms from the fitted model.

### Note

This function is essentially a wrapper for the MIXOR stand-alone program by Hedeker and Gibbons with added generic methods in R to enhance functionality. Note that the Fortran wrapper requires missing values to be denoted by -9 rather than NA.

### Author(s)

Kellie J. Archer, Donald Hedeker, Rachel Nordgren, Robert D. Gibbons

### References

Hedeker D. and Gibbons R.D. (1996) A computer program for mixed-effects ordinal regression analysis. *Computer Methods and Programs in Biomedicine* 49, 157-176. Hedeker D and Gibbons R.D. (2006) *Longitudinal Data Analysis*, Wiley, Hoboken, New Jersey.

### See Also

See Also as [summary.mixor](#), [predict.mixor](#), [coef.mixor](#), [vcov.mixor](#), [print.mixor](#)

### Examples

```
library("mixor")
data("SmokingPrevention")
# data frame must be sorted by id variable
SmokingPrevention<-SmokingPrevention[order(SmokingPrevention$class),]
# school model
Fitted.school<-mixor(thksord~thkspre+cc+tv+cctv, data=SmokingPrevention,
  id=school, link="logit")
summary(Fitted.school)
vcov(Fitted.school)
# students in classrooms analysis
Fitted.students<-mixor(thksord~thkspre+cc+tv+cctv, data=SmokingPrevention,
  id=class, link="logit")
summary(Fitted.students)
coef(Fitted.students)
vcov(Fitted.students)
cm<-matrix(c(-1,-1,-1,0,0,0,0,0,
             0, 0, 0,0,0,0,0,0,
             0, 0, 0,1,0,0,0,1),ncol=3,byrow=TRUE)
Contrasts(Fitted.students, contrast.matrix=cm)
```

---

mixor-deprecated	<i>Deprecated Functions in Package mixor</i>
------------------	--

---

**Description**

These functions are provided for compatibility with older versions of `mixor` only, and will be defunct at the next release.

**Details**

The following functions are deprecated and will be made defunct; use the replacement indicated below:

- mixord: [mixor](#)

**Author(s)**

Kellie J. Archer, Donald Hedeker, Rachel Nordgren, Robert D. Gibbons, Maintainer: Kellie J. Archer <kjarcher@vcu.edu>

---

mixord	<i>Old Function Name Replaced with mixor</i>
--------	--

---

**Description**

The `mixord` function has been deprecated. Please use the `mixor` function for fitting longitudinal/clustered ordinal response models

**Author(s)**

Kellie J. Archer, Donald Hedeker, Rachel Nordgren, Robert D. Gibbons

**See Also**

See Also as [mixor](#), [summary.mixor](#)



**Description**

Each subject provided ordinal responses on three items concerning their opinion on early teens (age 14-16) having sex before marriage (Item1), a man and a woman having sex before marriage (Item2), and a married person having sex with someone other than their spouse (Item3). Data are provided as frequencies by response pattern.

**Usage**

```
data(norcag)
```

**Format**

A data frame with 105 observations on the following 6 variables.

ID a numeric vector indicating unique patient identifier

SexItems ordinal item response coded as 1 = always wrong; 2 = almost always wrong; 3 = wrong only sometimes; 4 = not wrong

int a numeric vector of ones; used in the stand-alone MIXOR program to indicate the intercept

Item2vs1 attitude towards premarital vs teenage sex

Item3vs1 attitude towards extramarital vs teenage sex

freq frequency weight of the pattern

**Source**

Agresti A. and Lang J.B. (1993) A proportional odds model with subject-specific effects for repeated ordered categorical responses, *Biometrika* 80, 527-534.

**References**

Hedeker D. and Mermelstein R.J. (1998) A multilevel thresholds of change model for analysis of stages of change data, *Multivariate Behavioral Research* 33, 427-455.

**Examples**

```
library("mixor")
data("norcag")
# random intercepts model assuming proportional odds for differences in item responses
Fitted.norcag<-mixor(SexItems~Item2vs1+Item3vs1, data=norcag, id=ID,
  weights=freq, link="logit", nAGQ=20)
summary(Fitted.norcag)
# random intercepts model assuming non-proportional odds for differences in item responses
Fitted.norcag.np<-mixor(SexItems~Item2vs1+Item3vs1, data=norcag, id=ID,
  weights=freq, link="logit", nAGQ=10, KG=2)
```

```
summary(Fitted.norcag.np)
# SCALING model
Fitted.norcag.scale<-mixor(SexItems~Item2vs1+Item3vs1, data=norcag, id=ID,
  weights=freq, link="logit", nAGQ=10, KS=2)
summary(Fitted.norcag.scale)
```

---

plot.mixor	<i>Plot empirical Bayes estimates of random effects for a Mixor Model Object</i>
------------	--

---

### Description

Plot of empirical Bayes estimates of random effects from a fitted mixor model object.

### Usage

```
## S3 method for class 'mixor'
plot(x, ...)
```

### Arguments

x	a mixor object.
...	other arguments.

### Value

For each random effect, a histogram and normal quantile-quantile plot of empirical Bayes estimates.

### Author(s)

Kellie J. Archer, Donald Hedeker, Rachel Nordgren, Robert D. Gibbons

### See Also

See Also as [mixor](#), [summary.mixor](#)

### Examples

```
library("mixor")
data("schizophrenia")
### Random intercept
SCHIZ01.fit<-mixor(imps79o ~ TxDrug + SqrtWeek + TxSWeek, data=schizophrenia,
  id=id, link="probit")
plot(SCHIZ01.fit)
```

---

predict.mixor	<i>Predict Outcome From Mixor Fitted Model</i>
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**Description**

predict method for class mixor.

**Usage**

```
## S3 method for class 'mixor'  
predict(object, newdata = NULL, na.action = na.fail, ...)
```

**Arguments**

object	an object of class mixor.
newdata	an optional data frame to be used for obtaining predictions when the random effects are zero. When newdata is not supplied, the random effects estimates are used in obtaining model predictions. All variables used in the mixor model, the fixed and the random effects models, as well as the grouping factors, must be present in the data frame.
na.action	a function that indicates what should happen when newdata contains NAs. The default action (na.fail) causes the function to print an error message and terminate if there are any incomplete observations.
...	other arguments.

**Details**

This function returns fitted probabilities and the predicted class from a fitted mixor object. When the newdata parameter is specified, the random effects are taken to be zero and predictions are returned. Otherwise conditional predictions, which includes both fixed and random effects terms, for the observed data are returned.

**Value**

predicted	class specific probabilities from the fitted model.
class	predicted class, that having the largest fitted probability, from the fitted model.

**Author(s)**

Kellie J. Archer, Donald Hedeker, Rachel Nordgren, Robert D. Gibbons

**See Also**

See Also [mixor](#), [print.mixor](#)

## Examples

```
library("mixor")
data("schizophrenia")
### Random intercept
SCHIZ01.fit<-mixor(imps79o ~ TxDrug + SqrtWeek + TxSWeek, data=schizophrenia,
  id=id, link="probit")
pihat<-predict(SCHIZ01.fit)
table(pihat$class, schizophrenia$imps79o)
head(pihat$predicted)
```

---

print.mixor

*Printing Mixor Model Fits*

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## Description

print method for class mixor.

## Usage

```
## S3 method for class 'mixor'
print(x, digits = max(3L, getOption("digits") - 3L), ...)
```

## Arguments

x                    an object of class mixor.  
digits                the number of significant digits to use when printing.  
...                   further arguments passed to or from other methods.

## Value

The function `print.mixor` prints the model call and coefficients from the `mixor` object.

## Author(s)

Kellie J. Archer, Donald Hedeker, Rachel Nordgren, Robert D. Gibbons

## See Also

See Also as [mixor](#), [summary.mixor](#), [coef.mixor](#)

**Examples**

```

library("mixor")
data("schizophrenia")
### Random intercept
SCHIZO1.fit<-mixor(imps79o ~ TxDrug + SqrtWeek + TxSWeek, data=schizophrenia,
  id=id, link="probit")
print(SCHIZO1.fit)
### Random intercept and slope
SCHIZO2.fit<-mixor(imps79o ~ TxDrug + SqrtWeek + TxSWeek, data=schizophrenia,
  id=id, which.random.slope=2, link="probit")
print(SCHIZO2.fit)

```

---

schizophrenia

*National Institute of Mental Health Schizophrenia Collaborative Study*


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**Description**

In the NIMH Schizophrenia Collaborative Study, patients were randomized to receive one of four medications, either placebo or one of three different anti-psychotic drugs. The protocol indicated subjects were to then be evaluated at weeks 0, 1, 3, 6 to assess severity of illness; additionally some measurements were made at weeks 2, 4, and 5.

**Usage**

```
data(schizophrenia)
```

**Format**

A data frame with 1603 observations on the following 9 variables.

`id` a numeric vector indicating the unique patient identifier

`imps79` a numeric vector from item 79 on the Inpatient Multidimensional Psychiatric Scale indicating severity of illness. The scores were applied to be interpreted as follows: 1 = normal, not ill at all; 2 = borderline mentally ill; 3 = mildly ill; 4 = moderately ill; 5 = markedly ill; 6 = severely ill; 7 = among the most extremely ill

`imps79b` a binary version of `imps79`

`imps79o` an ordinally scaled version of `imps79`

`int` a numeric vector of ones; used in stand-alone package to indicate intercept

`TxDrug` a numeric vector indicating treatment with drug (1) or placebo (0)

`Week` a numeric vector indicating time, in weeks

`SqrtWeek` the square root of the `Week` variable

`TxSWeek` a variable representing the `TxDrug` x `Week` interaction

**Source**

From <http://tigger.uic.edu/~hedeker/SCHIZX1.DAT.txt>

## References

Hedeker D. and Gibbons R.D. (1996) A computer program for mixed-effects ordinal regression analysis. *Computer Methods and Programs in Biomedicine* 49, 157-176. Hedeker D and Gibbons R.D. (2006) *Longitudinal Data Analysis*, Wiley, Hoboken, New Jersey.

## Examples

```
library("mixor")
data("schizophrenia")
### Random intercept
SCHIZ01.fit<-mixor(imps79o ~ TxDrug + SqrtWeek + TxSWeek, data=schizophrenia,
  id=id, link="probit")
summary(SCHIZ01.fit)
### Random intercept and slope
SCHIZ02.fit<-mixor(imps79o ~ TxDrug + SqrtWeek + TxSWeek, data=schizophrenia,
  id=id, which.random.slope=2, link="probit")
summary(SCHIZ02.fit)
# random intercept and trend with independent random effects; using logit link
SCHIZ03.fit<-mixor(imps79o ~ TxDrug + SqrtWeek + TxSWeek, data=schizophrenia,
  id=id, which.random.slope=2, indep.re=TRUE, link="logit")
summary(SCHIZ03.fit)
```

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SmokeOnset

*Smoking Onset Data*

---

## Description

From the Television School and Family Smoking Prevention and Cessation Project, a study designed to increase knowledge of the effects of tobacco use in school-age children.

## Usage

```
data(SmokeOnset)
```

## Format

A data frame with 1556 observations on the following 10 variables.

`school` a numeric vector identifying the unique school in the Los Angeles area

`class` a numeric vector identifying classroom

`student` a numeric vector identifying student

`smkonset` a numeric vector indicating time to smoking or right-censoring (post-intervention=1, 1 year follow-up=2, and 2 year follow-up=3). For these data right-censoring means that the observation was observed at the indicated timepoint (and had not smoked at that timepoint or at earlier timepoints), but was not observed at subsequent timepoints or thereafter.

`event` a numeric vector indicating whether the student smoked (1) or did not (0)

`int` a numeric vector of ones; used in stand-alone MIXOR program to represent the intercept

SexMale a numeric vector indicating gender of the student (0=Female, 1=Male)

cc a numeric vector indicating whether the school was randomized to a social-resistance classroom curriculum (1=Yes, 0=No)

tv a numeric vector indicating whether the school was randomized to a media (television) intervention (1=Yes, 0=No)

cctv a numeric vector indicating whether the school was randomized to CC combined with TV

## References

Flay B.R., Brannon B.R., Johnson C.A. et al. (1989) The television, school and family smoking cessation and prevention project: I. Theoretical basis and program development, *Preventive Medicine* 17, 585-607.

Hedeker D., Siddiqui O. and Hu F.B. Random-effects regression analysis of correlated grouped-time survival data, *Statistical Methods in Medical Research* 9,161-179.

Hedeker D and Gibbons R.D. (2006) *Longitudinal Data Analysis*, Wiley, Hoboken, New Jersey.

## Examples

```
library("mixor")
data("SmokeOnset")
require("survival")
### Grouped survival time example
### students in classrooms analysis
Surv.mixor<-mixor(Surv(smkonset,event)~SexMale+cc+tv, data=SmokeOnset,
  id=class, link="cloglog", nAGQ=20, IADD=1)
Surv.mixor
vcov(Surv.mixor)
### students in schools analysis
School.mixor<-mixor(Surv(smkonset,event)~SexMale+cc+tv, data=SmokeOnset,
  id=school, link="cloglog", nAGQ=20, IADD=1)
School.mixor
vcov(School.mixor)
### students in classrooms analysis with varying Sex effect across time intervals
students.mixor<-mixor(Surv(smkonset,event)~SexMale+cc+tv, data=SmokeOnset,
  id=class, link="cloglog", KG=1, nAGQ=20, IADD=1)
students.mixor
```

---

SmokingPrevention	<i>Television School and Family Smoking Prevention and Cessation Project Data</i>
-------------------	---

---

## Description

From the Television School and Family Smoking Prevention and Cessation Project, a study designed to increase knowledge of the effects of tobacco use in school-age children.

**Usage**

```
data(SmokingPrevention)
```

**Format**

A data frame with 1600 observations on the following 9 variables.

school a numeric vector identifying the Los Angeles school

class a numeric vector identifying classroom

thksord a numeric vector reflecting quartiles of the post-intervention tobacco and health knowledge scale score

thksbin a binary version of the post-intervention tobacco and health knowledge scale score

int a numeric vector of ones; used in the stand-alone MIXOR program to represent the intercept

thkspre the pre-intervention tobacco and health knowledge scale score

cc a numeric vector indicating whether the school was randomized to a social-resistance classroom curriculum (1=Yes, 0=No)

tv a numeric vector indicating whether the school was randomized to a media (television) intervention (1=Yes, 0=No)

cctv a numeric vector indicating whether the school was randomized to CC combined with TV

**References**

Flay B.R., Brannon B.R., Johnson C.A. et al. (1988) The television, school and family smoking cessation and prevention project: I. Theoretical basis and program development, *Preventive Medicine* 17, 585-607.

Hedeker D. and Gibbons R.D. (1996) A computer program for mixed-effects ordinal regression analysis. *Computer Methods and Programs in Biomedicine* 49, 157-176.

Hedeker D and Gibbons R.D. (2006) *Longitudinal Data Analysis*, Wiley, Hoboken, New Jersey.

**Examples**

```
library("mixor")
data("SmokingPrevention")
# sort dataset by id; note for these data sorting by class will also sort by school
SmokingPrevention<-SmokingPrevention[order(SmokingPrevention$class),]
# school model
Fitted.school<-mixor(thksord~thkspre+cc+tv+cctv, data=SmokingPrevention,
  id=school, link="logit")
summary(Fitted.school)
vcov(Fitted.school)
# students in classrooms analysis; not run
#Fitted.students<-mixor(thksord~thkspre+cc+tv+cctv, data=SmokingPrevention,
#   id=class, link="logit")
#summary(Fitted.students)
#vcov(Fitted.students)
```



---

summary.mixor	<i>Summarize Mixor Model Fit</i>
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---

## Description

summary method for class mixor.

## Usage

```
## S3 method for class 'mixor'
summary(object, digits=max(3, getOption("digits") - 2),
        signif.stars=TRUE, dig.tst = max(1, min(5, digits - 1)), ...)
```

## Arguments

object	an object of class mixor.
digits	minimum number of significant digits to be used for most numbers.
signif.stars	logical; if TRUE, P-values are additionally encoded visually as "significance stars" in order to help scanning of long coefficient tables.
dig.tst	minimum number of significant digits for the test statistics.
...	other arguments.

## Value

Prints the following items extracted from the fitted mixor object: the call to mixor (model formula), mode Deviance, Log-likelihood, RIDGEMAX, AIC, SBC, and model parameter estimates along with their SE, Z, and p-value.

## Author(s)

Kellie J. Archer, Donald Hedeker, Rachel Nordgren, Robert D. Gibbons

## See Also

See Also [mixor](#), [print.mixor](#), [coef.mixor](#)

## Examples

```
library("mixor")
data("schizophrenia")
### Random intercept
SCHIZ01.fit<-mixor(imps79o ~ TxDrug + SqrtWeek + TxSWeek, data=schizophrenia,
                 id=id, link="probit")
summary(SCHIZ01.fit)
```

---

`vcov.mixed`*Return Variance-Covariance Matrix for a Mixed Model Object*

---

**Description**

Returns the variance-covariance matrix of a fitted `mixed` model object.

**Usage**

```
## S3 method for class 'mixed'  
vcov(object, ...)
```

**Arguments**

`object` a `mixed` object.  
`...` other arguments.

**Value**

A matrix of the estimated covariances between the parameter estimates in the model.

**Author(s)**

Kellie J. Archer, Donald Hedeker, Rachel Nordgren, Robert D. Gibbons

**See Also**

See Also as [mixed](#), [summary.mixed](#)

**Examples**

```
library("mixed")  
data("schizophrenia")  
### Random intercept  
SCHIZ01.fit<-mixed(imps79o ~ TxDrug + SqrtWeek + TxSWeek, data=schizophrenia,  
  id=id, link="probit")  
summary(SCHIZ01.fit)  
vcov(SCHIZ01.fit)
```

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