Package 'ordinalgmifs'

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Title Ordinal Regression for High-Dimensional Data

Depends R (>= 4.2.0), survival

Description

Provides a function for fitting cumulative link, adjacent category, forward and backward continuation ratio, and stereotype ordinal response models when the number of parameters exceeds the sample size, using the the generalized monotone incremental forward stagewise method.

License GPL (>= 2)

Imports methods

BuildResaveData best

SystemRequirements C++11

NeedsCompilation yes

BuildVignettes TRUE

LazyData true

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ordinalgmifs-package   *Ordinal Response Regression for High-Dimensional Data*

Description

This package provides a function, ordinalgmifs, for fitting cumulative link, adjacent category, forward and backward continuation ratio, and stereotype ordinal response models when the number of parameters exceeds the sample size, using the the generalized monotone incremental forward stagewise method.

Details

Package:	ordinalgmifs
Version:	1.0.8
Date:	2023-05-01
Title:	Ordinal Regression for High-Dimensional Data
Authors@R:	c(person(c("Kellie", "J."), "Archer", email = "archer.43@osu.edu", role = c("aut", "cre"), comment =
Depends:	R (>= 4.2.0), survival
Description:	Provides a function for fitting cumulative link, adjacent category, forward and backward continuation
License:	GPL (>= 2)
Imports:	methods
BuildResaveData:	best
SystemRequirements:	C++11
NeedsCompilation:	yes
BuildVignettes:	TRUE
LazyData:	true
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```

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summary.ordinalgmifs      Summarize an Ordinal GMIFS Object.
```

This package contains generic methods (coef, plot, predict, print, summary) that can be invoked for an object fitted using ordinalgmifs.

Author(s)

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References

Hastie T., Taylor J., Tibshirani R., and Walther G. (2007) Forward stagewise regression and the monotone lasso. *Electronic Journal of Statistics*, 1, 1-29.

See Also

See Also ordinalgmifs. For models where no predictor is penalized see vglm

---

coef.ordinalgmifs   *Extract Model Coefficients*

Description

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

Usage

```
## S3 method for class 'ordinalgmifs'
coef(object, model.select = "AIC", ...)
```

Arguments

object	an ordinalgmifs object.
model.select	when x is specified any model along the solution path can be selected. The default is model.select="AIC" which extracts the coefficients from the model having the lowest AIC. Other options are model.select="BIC" or any numeric value from the solution path.
...	other arguments.

Value

Coefficients extracted from the model object.

Author(s)

Kellie J. Archer

References

Hastie T., Taylor J., Tibshirani R., and Walther G. (2007) Forward stagewise regression and the monotone lasso. *Electronic Journal of Statistics*, 1, 1-29.

See Also

See Also `ordinalgmifs`, `summary.ordinalgmifs`, `plot.ordinalgmifs`, `predict.ordinalgmifs`

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eyedisease   *Eye Disease Risk Factors*

Description

Eye Disease Risk Factors data from Section 9.1 of Agresti's Analysis of Ordinal Categorical Data. The primary data are from the Wisconsin Epidemiological Study of Diabetic Retinopathy. The primary outcome is severity of retinopathy which was measured in the left and right eye of every subject.

Usage

```
data(eyedisease)
```

Format

A data frame with 720 observations on the following 19 variables.

rme right eye macular oedema (absent = 0, present = 1)

lme left eye macular oedema (absent = 0, present = 1)

rre right eye refraction index

lre left eye refraction index

riop right eye intraocular eye pressure

liop left eye intraocular eye pressure

age age

diab duration of diabetes (in years)

gh glycosylated haemoglobin level

sbp systolic blood pressure

dbp diastolic blood pressure

bmi body mass index

pr pulse rate?

sex gender (male=1, female=2)

prot proteinuria (absent = 0, present = 1)

dose a numeric vector

rerl right eye severity of retinopathy, an ordered factor with levels None < Mild < Moderate < Proliferative

lerl left eye severity of retinopathy, an ordered factor with levels None < Mild < Moderate < Proliferative

id subject identifier

References

R. Klein and B.E.K. Klein and S.E. Moss and M.D. Davis and D.L. DeMets. (1984) The Wisconsin Epidemiologic Study of Diabetic Retinopathy II. Prevalence and risk of diabetic retinopathy when age at diagnosis is less than 30 years. *Archives of Opthalmology* 101, 520-526.

J. Williamson and K. Kim. (1996) A global odds ratio regression model for bivariate ordered categorical data from opthalmologic studies. *Statistics in Medicine* 15: 1507-1518.

A. Agresti. (2010) *Analysis of Ordered Categorical Data*, Second Edition. Wiley. Hoboken, NJ.

See Also

See Also as `ordinalgmifs`

Examples

```
data(eyedisease)
```

---

hccframe   *Liver Cancer Methylation Data*

Description

These data are a subset of subjects and CpG sites reported in the original paper where liver samples were assayed using the Illumina GoldenGate Methylation BeadArray Cancer Panel I. Technical replicate samples were removed to ensure all samples were independent. The matched cirrhotic samples from subjects with hepatocellular carcinoma (HCC, labeled Tumor) were also excluded. Therefore methylation levels in liver tissue are provided for independent subjects whose liver was Normal (N=20), cirrhotic but not having HCC (N=16, Cirrhosis non-HCC), and HCC (N=20, Tumor).

Usage

```
data(hccframe)
```

Format

A data frame with 56 observations on the following 46 variables.

group an ordered factor with levels Normal < Cirrhosis non-HCC < Tumor

CDKN2B_seq_50_S294_F a numeric vector representing a CpG site proportion methylation for CDKN2B

DDIT3_P1313_R a numeric vector representing a CpG site proportion methylation for DDIT3

ERN1_P809_R a numeric vector representing a CpG site proportion methylation for ERN1

GML_E144_F a numeric vector representing a CpG site proportion methylation for GML

HDAC9_P137_R a numeric vector representing a CpG site proportion methylation for HDAC9

HLA.DPA1_P205_R a numeric vector representing a CpG site proportion methylation for HLA.DPA1

HOXB2_P488_R a numeric vector representing a CpG site proportion methylation for HOXB2

IL16_P226_F a numeric vector representing a CpG site proportion methylation for IL16

IL16_P93_R a numeric vector representing a CpG site proportion methylation for IL16

IL8_P83_F a numeric vector representing a CpG site proportion methylation for IL8

MPO_E302_R a numeric vector representing a CpG site proportion methylation for MPO

MPO_P883_R a numeric vector representing a CpG site proportion methylation for MPO

PADI4_P1158_R a numeric vector representing a CpG site proportion methylation for PADI4

SOX17_P287_R a numeric vector representing a CpG site proportion methylation for SOX17

TJP2_P518_F a numeric vector representing a CpG site proportion methylation for TJP2

WRN_E57_F a numeric vector representing a CpG site proportion methylation for WRN

CRIP1_P874_R a numeric vector representing a CpG site proportion methylation for CRIP1

SLC22A3_P634_F a numeric vector representing a CpG site proportion methylation for SLC22A3

CCNA1_P216_F a numeric vector representing a CpG site proportion methylation for CCNA1

SEPT9_P374_F a numeric vector representing a CpG site proportion methylation for SEPT9

ITGA2_E120_F a numeric vector representing a CpG site proportion methylation for ITGA2

ITGA6_P718_R a numeric vector representing a CpG site proportion methylation for ITGA6

HGF_P1293_R a numeric vector representing a CpG site proportion methylation for HGF

DLG3_E340_F a numeric vector representing a CpG site proportion methylation for DLG3

APP_E8_F a numeric vector representing a CpG site proportion methylation for APP

SFTPB_P689_R a numeric vector representing a CpG site proportion methylation for SFTPB

PENK_P447_R a numeric vector representing a CpG site proportion methylation for PENK

COMT_E401_F a numeric vector representing a CpG site proportion methylation for COMT

NOTCH1_E452_R a numeric vector representing a CpG site proportion methylation for NOTCH1

EPHA8_P456_R a numeric vector representing a CpG site proportion methylation for EPHA8

WT1_P853_F a numeric vector representing a CpG site proportion methylation for WT1

KLK10_P268_R a numeric vector representing a CpG site proportion methylation for KLK10

PCDH1_P264_F a numeric vector representing a CpG site proportion methylation for PCDH1

TDGF1_P428_R a numeric vector representing a CpG site proportion methylation for TDGF1

EFNB3_P442_R a numeric vector representing a CpG site proportion methylation for EFNB3

MMP19_P306_F a numeric vector representing a CpG site proportion methylation for MMP19

FGFR2_P460_R a numeric vector representing a CpG site proportion methylation for FGFR2

RAF1_P330_F a numeric vector representing a CpG site proportion methylation for RAF1

BMPR2_E435_F a numeric vector representing a CpG site proportion methylation for BMPR2

GRB10_P496_R a numeric vector representing a CpG site proportion methylation for GRB10

CTSH_P238_F a numeric vector representing a CpG site proportion methylation for CTSH

SLC6A8_seq_28_S227_F a numeric vector representing a CpG site proportion methylation for SLC6A8

PLXDC1_P236_F a numeric vector representing a CpG site proportion methylation for PLXDC1

TFE3_P421_F a numeric vector representing a CpG site proportion methylation for TFE3

TSG101_P139_R a numeric vector representing a CpG site proportion methylation for TSG101

Source

The full dataset is available as GSE18081 from Gene Expression Omnibus at `https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE18081`

References

Archer KJ, Mas VR, Maluf DG, Fisher RA. High-throughput assessment of CpG site methylation for distinguishing between HCV-cirrhosis and HCV-associated hepatocellular carcinoma. Molecular Genetics and Genomics, 283(4): 341-349, 2010.

See Also

See Also as `ordinalgmifs`

Examples

```
data(hccframe)
```

---

ordinalgmifs	*Ordinal Generalized Monotone Incremental Forward Stagewise Regression*

Description

This function can fit a cumulative link, adjacent category, forward and backward continuation ratio, and stereotype ordinal response model when the number of parameters exceeds the sample size, using the the generalized monotone incremental forward stagewise method.

Usage

```
ordinalgmifs(formula, data, x = NULL, subset, epsilon = 0.001, tol = 1e-05,
scale = TRUE, probability.model = "Cumulative", link = "logit",
verbose=FALSE, assumption=NULL, ...)
```

Arguments

formula	an object of class `"formula"` (or one that can be coerced to that class): a symbolic description of the model to be fitted. The left side of the formula is the ordinal outcome while the variables on the right side of the formula are the covariates that are not included in the penalization process. Note that if all variables in the model are to be penalized, an intercept only model formula should be specified.
data	an optional data frame, list or environment (or object coercible by `as.data.frame` to a data frame) containing the variables in the model.
x	an optional matrix of predictors that are to be penalized in the model fitting process.
subset	an optional vector specifying a subset of observations to be used in the fitting process.
epsilon	small incremental amount used to update a coefficient at a given step.
tol	the iterative process stops when the difference between successive log-likelihoods is less than this specified level of tolerance.
scale	logical, if TRUE the penalized predictors are centered and scaled.
probability.model	
	the type of ordinal response model to be fit. Can be `"Cumulative"`, `"AdjCategory"`, `"ForwardCR"`, `"BackwardCR"`, or `"Stereotype"`
link	the link function used. Allowable links for `"Cumulative"`, `"ForwardCR"`, and `"BackwardCR"` are `"logit"`, `"probit"`, and `"cloglog"`. For an `"AdjCategory"` model only a `"loge"` link is allowed; for a `"Stereotype"` model only a `"logit"` link is allowed.
verbose	logical, if TRUE the step number is printed to the console (default is FALSE).
assumption	integer, only use with `probability.model = "ForwardCR"` and `link = "cloglog"` to denote the assumption to use for discrete censored survival modeling. If `assumption = 1`, assume the observation was censored at the end of the discrete time interval in which the censoring occurred; if `assumption = 2`, assume the observation was censored at the beginning of the interval in which censoring occurred; if `assumption = 3`, assume constant hazard rate within the interval in which the censoring occurred; if no censoring occurs, do not specify a value for `assumption`.
...	additional arguments

Details

A model specified as `response~terms, x=penalized.terms` where `response` is the ordinal response vector and `terms` is the series of variables in the model that are not to be penalized and `x` is a matrix of variables that are to be penalized. For example, `terms` may include the variables age and gender while `x` includes hundreds to thousands of features from a high-throughput genomic experiment. In the event that no baseline demographic/clinical characteristics/subject level variables are available or needed in `terms` (all variables are to be penalized) then the model is specified as `response~1, x=penalized.terms`.

Value

AIC	a vector of AIC values for each step (if x is specified).
BIC	a vector of BIC values for each step (if x is specified).
alpha	the ordinal threshold estimates for the fitted model.
theta	the coefficient estimates for the unpenalized variables (if terms are specified on the right hand side of the model formula).
beta	the coefficient estimates for the penalized variables (if x is specified in the model).
phi	the scaling coefficient estimates (if a "Stereotype" logit model is fit).
logLik	a vector of log-likelihood values for each step(if terms are specified on the right hand side of the model formula).
link	the link function used in the model fit.
model.select	the step at which the minimum AIC was observed (if terms are specified on the right hand side of the model formula).
probability.model	
	the model fit.
scale	logical indicating whether penalized variables were centered and scaled.
w	the unpenalized variables in the model (if any).
x	the penalized variables in the model (if any).
y	the ordinal response.

Author(s)

Kellie J. Archer, Jiayi Hou, Qing Zhou, Kyle Ferber, John G. Layne, Amanda Gentry

References

Hastie T., Taylor J., Tibshirani R., and Walther G. (2007) Forward stagewise regression and the monotone lasso. *Electronic Journal of Statistics*, 1, 1-29.

See Also

See Also coef.ordinalgmifs, summary.ordinalgmifs, plot.ordinalgmifs, predict.ordinalgmifs

Examples

```
data(hccframe)
# To minimize processing time, MPO_E302_R is coerced into the model and only a subset of
# two CpG sites (DDIT3_P1313_R and HDAC9_P137_R) are included as penalized covariates
# in this demonstration, and epsilon is set to 0.01
hcc.fit <- ordinalgmifs(group ~ MPO_E302_R, x = c("DDIT3_P1313_R", "HDAC9_P137_R"),
data = hccframe, epsilon = 0.01)
coef(hcc.fit)
summary(hcc.fit)
phat <- predict(hcc.fit)
head(phat$predicted)
table(phat$class, hccframe$group)
```

---

plot.ordinalgmifs   *Plot Solution Path for Ordinal GMIFS Fitted Model.*

Description

This function plots either the coefficient path, the AIC, or the log-likelihood for a fitted `ordinalgmifs` object.

Usage

```
## S3 method for class 'ordinalgmifs'
plot(x, type = "trace", xlab=NULL, ylab=NULL, main=NULL, ...)
```

Arguments

x	an `ordinalgmifs` object.
type	default is `"trace"` which plots the coefficient path for the fitted object. Also available are `"AIC"`, `"BIC"`, and `"logLik"`.
xlab	a default x-axis label will be used which can be changed by specifying a user-defined x-axis label.
ylab	a default y-axis label will be used which can be changed by specifying a user-defined y-axis label.
main	a default main title will be used which can be changed by specifying a user-defined main title.
...	other arguments.

Value

No return value, called for side effects

Author(s)

Kellie J. Archer

See Also

See Also ordinalgmifs, coef.ordinalgmifs, summary.ordinalgmifs, predict.ordinalgmifs

---

predict.ordinalgmifs   *Predicted Probabilities and Class for Ordinal GMIFS Fit.*

Description

This function returns a list the includes the predicted probabilities as well as the predicted class for an `ordinalgmifs` fitted object.

Usage

```
## S3 method for class 'ordinalgmifs'
predict(object, neww = NULL, newdata, newx = NULL, model.select = "AIC", ...)
```

Arguments

`object`	an `ordinalgmifs` fitted object.
`neww`	an optional formula that includes the unpenalized variables to use for predicting the response. If omitted, the training data are used.
`newdata`	an optional data.frame that minimally includes the unpenalized variables to use for predicting the response. If omitted, the training data are used.
`newx`	an optional matrix of penalized variables to use for predicting the response. If omitted, the training data are used.
`model.select`	when x is specified any model along the solution path can be selected. The default is `model.select="AIC"` which calculates the predicted values using the coefficients from the model having the lowest AIC. Other options are `model.select="BIC"` or any numeric value from the solution path.
`...`	other arguments.

Value

`predicted`	a matrix of predicted probabilities from the fitted model.
`class`	a vector containing the predicted class taken as that class having the largest predicted probability.
`...`	other arguments.

Author(s)

Kellie J. Archer, Jiayi Hou, Qing Zhou, Kyle Ferber, John G. Layne, Amanda Gentry

See Also

See Also ordinalgmifs, coef.ordinalgmifs, summary.ordinalgmifs, plot.ordinalgmifs

---

print.ordinalgmifs   *Print the Contents of an Ordinal GMIFS Fitted Object.*

Description

This function prints the names of the list objects from an ordinalgmifs fitted model.

Usage

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

Arguments

x   an ordinalgmifs object.

...   other arguments.

Value

returns the object names in the fitted ordinalgmifs object

Note

The contents of an ordinalgmifs fitted object differ depending upon whether x is specified in the ordinalgmifs model (i.e., penalized variables are included in the model fit hence a solution path is returned) or only terms on the right hand side of the equation are included (unpenalized variables). In the latter case, we recommend using the VGAM package.

Author(s)

Kellie J. Archer

See Also

See Also ordinalgmifs, coef.ordinalgmifs, summary.ordinalgmifs, plot.ordinalgmifs, predict.ordinalgmifs

---

summary.ordinalgmifs   *Summarize an Ordinal GMIFS Object.*

Description

summary method for class ordinalgmifs.

Usage

```
## S3 method for class 'ordinalgmifs'
summary(object, model.select = "AIC", ...)
```

Arguments

object	an ordinalgmifs object.
model.select	when x is specified any model along the solution path can be selected. The default is model.select="AIC" which extracts the model having the lowest AIC. Other options are model.select="BIC" or any numeric value from the solution path.
...	other arguments.

Details

Prints the following items extracted from the fitted ordinalgmifs object: the probability model and link used and model parameter estimates. For models that include x, the parameter estimates, AIC, BIC, and log-likelihood are printed for indicated model.select step or if model.select is not supplied the step at which the minimum AIC was observed.

Value

extracts the relevant information from the step in the solution path that attained the minimum AIC (default) or at the user-defined model.select step

Author(s)

Kellie J. Archer

See Also

See Also ordinalgmifs, coef.ordinalgmifs, plot.ordinalgmifs, predict.ordinalgmifs

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