

Package ‘FuzzyLogit’

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Type Package

Title Fuzzy Logistic Regression

Version 0.1.1

Description Fits logistic regression models in which the binary response is represented by a triangular fuzzy number rather than an exact crisp label, allowing uncertainty in class membership to be encoded directly in the outcome. Model parameters are estimated using the Fuzzy Least Squares approach of Diamond (1988) [doi:10.1016/0020-0255\(88\)90047-3](https://doi.org/10.1016/0020-0255(88)90047-3), following the integrated fuzzy logistic regression method of Yapici Pehlivan and Sahin (2018) <https://dergipark.org.tr/en/pub/jssa/issue/37877/437725>. Provides fitting, prediction, classification, cross-validation, and diagnostic plotting methods, along with tools for comparing model behaviour across different assumed levels of label uncertainty.

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Contents

breast_cancer	2
case.names	4

classify	4
coef.fuzzy_logit	6
coefficients.fuzzy_logit	7
compare_cv_results	7
compare_fuzzy_models	8
confint.fuzzy_logit	9
cv.fuzzy_logit	10
deviance.fuzzy_logit	11
df.residual.fuzzy_logit	11
fitted.fuzzy_logit	12
formula.fuzzy_logit	12
fuzzy_logit	13
is.fuzzy_logit	14
logLik.fuzzy_logit	15
model.frame.fuzzy_logit	15
model.matrix.fuzzy_logit	16
nobs.fuzzy_logit	16
plot.fuzzy_logit	17
plot_binned_residuals	18
plot_fuzzy_membership	19
plot_leverage	20
plot_pearson_residuals	21
plot_scale_location	22
predict.fuzzy_logit	23
print.cv.fuzzy_logit	23
print.fuzzy_logit	24
print.fuzzy_logit_comparison	25
print.summary.fuzzy_logit	25
residuals.fuzzy_logit	26
summary.cv.fuzzy_logit	26
summary.fuzzy_logit	27
terms.fuzzy_logit	27
update.fuzzy_logit	28
variable.names.fuzzy_logit	28
vcov.fuzzy_logit	29
Index	30

breast_cancer

UCI Breast Cancer Wisconsin Dataset

Description

A dataset containing measurements from fine needle aspirates (FNA) of breast masses, used to classify tumours as benign or malignant. This is a cleaned version of the UCI Breast Cancer Wisconsin dataset with 16 rows containing missing values (in the BareNuclei column) removed.

Usage

```
data(breast_cancer)
```

Format

A data frame with 683 rows and 10 columns:

ClumpThickness Clump thickness, integer 1-10.

UniformCellSize Uniformity of cell size, integer 1-10.

UniformCellShape Uniformity of cell shape, integer 1-10.

MarginalAdhesion Marginal adhesion, integer 1-10.

SingleEpithelialCellSize Single epithelial cell size, integer 1-10.

BareNuclei Bare nuclei, integer 1-10.

BlandChromatin Bland chromatin, integer 1-10.

NormalNucleoli Normal nucleoli, integer 1-10.

Mitoses Mitoses, integer 1-10.

Outcome Binary outcome: 0 = Benign (444 cases), 1 = Malignant (239 cases).

Details

The original dataset contains 699 observations and 11 columns (including a sample ID column). The ID column has been removed, 16 rows with missing values in `BareNuclei` have been dropped, and the class variable (originally coded 2 = benign, 4 = malignant) has been recoded to `Outcome` (0 = benign, 1 = malignant).

Source

UCI Machine Learning Repository. [https://archive.ics.uci.edu/ml/datasets/Breast+Cancer+Wisconsin+\(Original\)](https://archive.ics.uci.edu/ml/datasets/Breast+Cancer+Wisconsin+(Original))

Wolberg, W. H. and Mangasarian, O. L. (1990). Multisurface method of pattern separation for medical diagnosis applied to breast cytology. *Proceedings of the National Academy of Sciences*, 87, 9193-9196.

Examples

```
data(breast_cancer)
head(breast_cancer)
table(breast_cancer$Outcome)

model <- fuzzy_logit(
  Outcome ~ ClumpThickness + UniformCellSize + BareNuclei,
  data     = breast_cancer,
  n_alpha = 100
)
summary(model)
```

case.names	<i>Extract case names from fuzzy_logit model</i>
------------	--

Description

This function extracts the row names (case names) from the model frame.

Usage

```
case.names(object, ...)
```

Arguments

object	A fuzzy_logit object
...	Additional arguments

Value

Character vector of case names

classify	<i>Classify Observations Using a Fuzzy Logistic Regression Model</i>
----------	--

Description

Classifies observations as belonging to class 0 or class 1 using a fitted fuzzy_logit model, builds a confusion matrix against the observed outcomes, and computes a set of performance metrics. classify is a generic function; classify.fuzzy_logit is the method used for objects of class "fuzzy_logit".

Usage

```
classify(object, ...)

## S3 method for class 'fuzzy_logit'
classify(
  object,
  newdata = NULL,
  threshold = 0.5,
  type = c("crisp", "fuzzy"),
  metrics = c("accuracy", "sensitivity", "specificity", "precision", "recall", "f1",
    "auc", "kappa"),
  plot = FALSE,
  ...
)
```

```
## S3 method for class 'classify.fuzzy_logit'
print(x, digits = 4, ...)

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

Arguments

object	An object of class "fuzzy_logit" (for classify), or an object of class "classify.fuzzy_logit" (for summary).
...	Further arguments passed to or from other methods.
newdata	An optional data frame of new observations to classify, which must also contain the true outcome column so a confusion matrix can be built. If NULL (the default), the training data used to fit object is classified.
threshold	Numeric value in (0, 1) used as the probability cutoff for assigning class 1. An observation is classified as 1 if its predicted probability is greater than or equal to threshold. Lowering the threshold increases sensitivity (more positives detected) at the cost of specificity. Default is 0.5.
type	Character string. "crisp" (the default) assigns each observation a hard label of 0 or 1. "fuzzy" returns the raw predicted probabilities without thresholding.
metrics	Character vector specifying which performance metrics to compute. Available options are "accuracy", "sensitivity" (true positive rate), "specificity" (true negative rate), "precision", "recall" (identical to sensitivity), "f1", "auc" (area under the ROC curve), and "kappa" (Cohen's kappa). By default all are computed.
plot	Logical. If TRUE, a plot of the classification results is displayed in addition to the numeric output. Default is FALSE.
x	An object of class "classify.fuzzy_logit", for the print method.
digits	Integer. Number of decimal places to display. Default is 4.

Value

An object of class "classify.fuzzy_logit", a list containing predictions (a data frame of predicted probabilities/classes and, if available, observed values), confusion_matrix, metrics (a named numeric vector of the requested performance metrics), threshold, type, and the fitted model.

No return value, called for its side effect of printing the classification results, confusion matrix, and performance metrics to the console. Invisibly returns x.

No return value, called for its side effect of printing detailed classification statistics (TP, TN, FP, FN counts) to the console. Invisibly returns object.

See Also

[fuzzy_logit](#), [predict.fuzzy_logit](#), [cv.fuzzy_logit](#)

Examples

```
data(breast_cancer)
model <- fuzzy_logit(Outcome ~ ClumpThickness + UniformCellSize + BareNuclei,
  data = breast_cancer, n_alpha = 100)

## Classify at the default threshold
cls <- classify(model, threshold = 0.5, type = "crisp")
print(cls)
summary(cls)

## Lower the threshold to increase sensitivity
cls2 <- classify(model, threshold = 0.3)
cls2$metrics["sensitivity"]
```

coef.fuzzy_logit	<i>Extract coefficients from fuzzy_logit model</i>
------------------	--

Description

Extract coefficients from fuzzy_logit model

Usage

```
## S3 method for class 'fuzzy_logit'
coef(object, type = c("a", "s", "both"), ...)
```

Arguments

object	A fuzzy_logit object
type	Type of coefficient to extract
...	Additional arguments

Value

If type = "a" or type = "s", a named numeric vector of coefficients. If type = "both", a list with two named numeric vectors, a (centre coefficients) and s (spread parameters).

coefficients.fuzzy_logit

Extract coefficients from fuzzy_logit model (alias)

Description

This function extracts the central tendency coefficients from a fuzzy_logit model.

Usage

```
## S3 method for class 'fuzzy_logit'
coefficients(object, ...)
```

Arguments

object	A fuzzy_logit object
...	Additional arguments

Value

Named numeric vector of centre coefficients.

compare_cv_results

Compare Multiple Cross-Validation Results

Description

Takes a named list of cv.fuzzy_logit results and displays their performance metrics side by side in a single comparison table. Useful for comparing how different fuzzy membership settings, or different model specifications, affect generalisation performance.

Usage

```
compare_cv_results(cv_list)
```

Arguments

cv_list	A named list containing at least two objects of class "cv.fuzzy_logit", each produced by cv.fuzzy_logit . The names given to the list elements are used as row labels in the comparison table.
---------	--

Value

A data frame of class comparing performance metrics across models, with one row per model/setting and one column per metric. Also printed to the console.

Examples

```

data(breast_cancer)

cv_low <- cv.fuzzy_logit(
  formula = Outcome ~ ClumpThickness + UniformCellSize + BareNuclei,
  data     = breast_cancer, K = 5,
  mu_0 = c(0.01, 0.03, 0.05), mu_1 = c(0.95, 0.97, 0.99),
  n_alpha = 100, seed = 42, verbose = FALSE
)

cv_high <- cv.fuzzy_logit(
  formula = Outcome ~ ClumpThickness + UniformCellSize + BareNuclei,
  data     = breast_cancer, K = 5,
  mu_0 = c(0.10, 0.20, 0.30), mu_1 = c(0.70, 0.80, 0.90),
  n_alpha = 100, seed = 42, verbose = FALSE
)

compare_cv_results(list("Low fuzziness" = cv_low, "High fuzziness" = cv_high))

```

compare_fuzzy_models *Compare Multiple Fuzzy Logit Models with Different Mu Values*

Description

Fits multiple fuzzy logistic regression models with different membership function specifications and compares their results.

Usage

```
compare_fuzzy_models(formula, data, mu_list = NULL, verbose = TRUE, ...)
```

Arguments

formula	A formula object specifying the model
data	A data frame containing the variables
mu_list	A named list of mu specifications, where each element is a list containing mu_0 and mu_1. If NULL, uses default comparisons.
verbose	Logical. If TRUE (the default), a message is printed for each model as it is fitted.
...	Additional arguments passed to fuzzy_logit

Value

A list of class "fuzzy_logit_comparison" containing:

models	List of fitted fuzzy_logit models
comparison_table	Data frame comparing coefficients across models

spread_table Data frame comparing spread parameters across models
 fit_statistics Data frame with AIC, BIC, and other fit statistics

Examples

```
data(breast_cancer)

# Compare three levels of uncertainty
comparison <- compare_fuzzy_models(
  Outcome ~ ClumpThickness + UniformCellSize + BareNuclei,
  data = breast_cancer,
  mu_list = list(
    low = list(mu_0 = c(0.01, 0.03, 0.05), mu_1 = c(0.95, 0.97, 0.99)),
    medium = list(mu_0 = c(0.05, 0.10, 0.15), mu_1 = c(0.85, 0.90, 0.95)),
    high = list(mu_0 = c(0.10, 0.20, 0.30), mu_1 = c(0.70, 0.80, 0.90))
  ),
  n_alpha = 100
)

print(comparison)
```

confint.fuzzy_logit *Confidence intervals for fuzzy_logit model parameters*

Description

Confidence intervals for fuzzy_logit model parameters

Usage

```
## S3 method for class 'fuzzy_logit'
confint(object, parm = NULL, level = 0.95, ...)
```

Arguments

object	A fuzzy_logit object
parm	Parameters to include (default: all)
level	Confidence level (default: 0.95)
...	Additional arguments

Value

A matrix with columns giving the lower and upper confidence limits for each requested parameter, computed as the centre coefficient plus/minus a t-based margin using the spread parameter as an approximate standard error.

cv.fuzzy_logit

Cross-Validation for Fuzzy Logistic Regression

Description

Cross-Validation for Fuzzy Logistic Regression

Usage

```
cv.fuzzy_logit(
  formula,
  data,
  K = 10,
  mu_0 = c(0.01, 0.03, 0.05),
  mu_1 = c(0.95, 0.97, 0.99),
  n_alpha = NULL,
  stratified = TRUE,
  seed = NULL,
  metrics = c("accuracy", "sensitivity", "specificity", "precision", "f1", "auc"),
  threshold = 0.5,
  verbose = TRUE,
  ...
)
```

Arguments

formula	A formula object
data	A data frame
K	Number of folds
mu_0	Fuzzy membership for class 0
mu_1	Fuzzy membership for class 1
n_alpha	Number of alpha-cuts
stratified	Whether to use stratified sampling
seed	Random seed
metrics	Metrics to compute
threshold	Classification threshold
verbose	Whether to print progress
...	Additional arguments

Value

An object of class "cv.fuzzy_logit", a list containing: `metrics` (a data frame of performance metrics per fold), `mean_metrics` and `sd_metrics` (named numeric vectors of metrics averaged and their standard deviation across folds), `predictions` (a data frame of out-of-fold predictions), `confusion_matrix` (the overall confusion matrix pooled across folds), and the fold assignments, formula, and settings used.

`deviance.fuzzy_logit` *Deviance for fuzzy_logit model*

Description

Deviance for fuzzy_logit model

Usage

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

Arguments

<code>object</code>	A fuzzy_logit object
<code>...</code>	Additional arguments

Value

A single numeric value: the sum of squared deviance residuals.

`df.residual.fuzzy_logit`
Extract residual degrees of freedom

Description

Extract residual degrees of freedom

Usage

```
## S3 method for class 'fuzzy_logit'
df.residual(object, ...)
```

Arguments

<code>object</code>	A fuzzy_logit object
<code>...</code>	Additional arguments

Value

A single integer: the number of observations minus the number of estimated coefficients (including the intercept).

fitted.fuzzy_logit	<i>Extract fitted values from fuzzy_logit model</i>
--------------------	---

Description

Extract fitted values from fuzzy_logit model

Usage

```
## S3 method for class 'fuzzy_logit'
fitted(object, type = c("link", "response"), ...)
```

Arguments

object	A fuzzy_logit object
type	Type of fitted values
...	Additional arguments

Value

A numeric vector of fitted values, one per observation used in fitting the model. On the "link" scale these are log-odds; on the "response" scale these are probabilities in [0, 1].

formula.fuzzy_logit	<i>Extract formula from fuzzy_logit model</i>
---------------------	---

Description

Extract formula from fuzzy_logit model

Usage

```
## S3 method for class 'fuzzy_logit'
formula(x, ...)
```

Arguments

x	A fuzzy_logit object
...	Additional arguments

Value

An object of class "formula": the model formula used to fit the object.

Description

Fits a fuzzy logistic regression model using triangular fuzzy numbers for the response variable. Users can customize the fuzzy membership values to control the degree of fuzziness in the model.

Usage

```
fuzzy_logit(
  formula,
  data,
  mu_0 = c(0.01, 0.03, 0.05),
  mu_1 = c(0.95, 0.97, 0.99),
  n_alpha = NULL,
  na.action = na.omit,
  subset = NULL,
  contrasts = NULL,
  ...
)
```

Arguments

formula	A formula object specifying the model, e.g., $y \sim x_1 + x_2 + \dots$. Can include transformations, interactions, and factor variables.
data	A data frame containing the variables in the model
mu_0	A numeric vector of length 3 specifying the triangular fuzzy number for the negative class ($y = 0$) as $c(\text{left}, \text{mode}, \text{right})$. Default is $c(0.01, 0.03, 0.05)$ representing low uncertainty. **Users can modify these values to change the fuzziness level.**
mu_1	A numeric vector of length 3 specifying the triangular fuzzy number for the positive class ($y = 1$) as $c(\text{left}, \text{mode}, \text{right})$. Default is $c(0.95, 0.97, 0.99)$ representing low uncertainty. **Users can modify these values to change the fuzziness level.**
n_alpha	Integer specifying the number of alpha-cut levels for numerical integration. Higher values give more accurate integration but slower computation. Default is the number of rows in the data (can be computationally expensive for large datasets).
na.action	A function which indicates what should happen when the data contain NAs. Default is <code>na.omit</code> .
subset	An optional vector specifying a subset of observations to be used
contrasts	An optional list for factor contrasts
...	Additional arguments (currently unused)

Details

The fuzzy membership values control the degree of uncertainty in class assignment. Narrower triangles (e.g., $\mu_0 = c(0.01, 0.03, 0.05)$) represent low fuzziness, closer to crisp logistic regression. Wider triangles (e.g., $\mu_0 = c(0.10, 0.25, 0.40)$) represent high fuzziness and more uncertainty in classification.

Value

An object of class "fuzzy_logit" containing model results

Examples

```
data(breast_cancer)

# Basic usage with default fuzzy membership
model1 <- fuzzy_logit(Outcome ~ ClumpThickness + UniformCellSize + BareNuclei,
                     data = breast_cancer, n_alpha = 100)
summary(model1)

# Custom fuzzy membership (moderate uncertainty)
model2 <- fuzzy_logit(
  Outcome ~ ClumpThickness + UniformCellSize + BareNuclei,
  data = breast_cancer,
  mu_0 = c(0.05, 0.10, 0.15),
  mu_1 = c(0.85, 0.90, 0.95),
  n_alpha = 100
)
```

is.fuzzy_logit

Check if object is a fuzzy_logit model

Description

Check if object is a fuzzy_logit model

Usage

```
is.fuzzy_logit(x)
```

Arguments

x An object to check

Value

Logical value indicating if object is of class fuzzy_logit

logLik.fuzzy_logit	<i>Log-likelihood for fuzzy_logit model</i>
--------------------	---

Description

Computes an approximate log-likelihood assuming normal errors. Note: This is an approximation as fuzzy regression does not have a standard likelihood function.

Usage

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

Arguments

object	A fuzzy_logit object
...	Additional arguments

Value

An object of class "logLik" with the approximate log-likelihood value and attributes "df" (number of estimated parameters) and "nobs" (number of observations).

model.frame.fuzzy_logit	<i>Extract model frame from fuzzy_logit model</i>
-------------------------	---

Description

Extract model frame from fuzzy_logit model

Usage

```
## S3 method for class 'fuzzy_logit'
model.frame(formula, ...)
```

Arguments

formula	A fuzzy_logit object
...	Additional arguments

Value

A data frame containing the response and predictor variables used in fitting the model (i.e. the original data after applying na.action and any subset).

```
model.matrix.fuzzy_logit
```

Extract model matrix from fuzzy_logit model

Description

Extract model matrix from fuzzy_logit model

Usage

```
## S3 method for class 'fuzzy_logit'
model.matrix(object, ...)
```

Arguments

object	A fuzzy_logit object
...	Additional arguments

Value

A numeric matrix: the design matrix used in estimation, with one row per observation and one column per model parameter (including the intercept).

```
nobs.fuzzy_logit
```

Extract number of observations from fuzzy_logit model

Description

Extract number of observations from fuzzy_logit model

Usage

```
## S3 method for class 'fuzzy_logit'
nobs(object, ...)
```

Arguments

object	A fuzzy_logit object
...	Additional arguments

Value

A single integer: the number of observations used in fitting the model (after any rows with missing values have been removed).

plot.fuzzy_logit	<i>Plot diagnostic plots for fuzzy_logit model</i>
------------------	--

Description

Produces up to four diagnostic plots for a fitted fuzzy_logit model. Plots can be shown all at once or individually using the which argument or the dedicated single-plot functions.

Usage

```
## S3 method for class 'fuzzy_logit'
plot(x, which = 1:4, ...)
```

Arguments

x	A fuzzy_logit object
which	Integer vector specifying which plots to produce. 1 = Pearson Residuals vs Fitted, 2 = Binned Residual Plot, 3 = Scale-Location, 4 = Residuals vs Leverage. Default is 1:4 (all plots).
...	Additional arguments (currently unused)

Details

Diagnostic plots are adapted from classical logistic regression for convenience. They are approximate tools for model checking and are not theoretically derived from the fuzzy least squares estimation framework.

Value

Invisibly returns a named list of ggplot objects: pearson, binned, scale_location, leverage. Use `p <- plot(model)` then `p$pearson` to access individually.

Examples

```
data(breast_cancer)
model <- fuzzy_logit(Outcome ~ ClumpThickness + BareNuclei,
  data = breast_cancer, n_alpha = 100)

# All four plots
plot(model)

# Individual plots using which
plot(model, which = 1)
plot(model, which = 2)
plot(model, which = 3)
plot(model, which = 4)

# Individual plots using named functions
```

```

plot_pearson_residuals(model)
plot_binned_residuals(model)
plot_scale_location(model)
plot_leverage(model)

# Save a single plot to a temporary file
p <- plot(model)
ggplot2::ggsave(file.path(tempdir(), "pearson.png"), p$pearson,
                 width = 7, height = 5)

```

plot_binned_residuals *Plot Binned Residuals for a Fuzzy Logistic Regression Model*

Description

Groups observations into bins by fitted probability and plots the average residual within each bin, together with an approximate 95% confidence band. Equivalent to `plot(model, which = 2)`, provided as a standalone named function for convenience.

Usage

```
plot_binned_residuals(model)
```

Arguments

model	A fuzzy_logit object
-------	----------------------

Details

This plot is often the most informative of the four diagnostic plots. Bin averages that stay within the grey confidence band indicate the model is reasonably well calibrated. Bins outside the band point to specific probability ranges where the model is systematically over- or under-predicting.

Value

A ggplot object, printed as a side effect and returned invisibly.

See Also

[plot.fuzzy_logit](#), [plot_pearson_residuals](#), [plot_scale_location](#), [plot_leverage](#)

Examples

```

data(breast_cancer)
model <- fuzzy_logit(Outcome ~ ClumpThickness + UniformCellSize + BareNuclei,
                    data = breast_cancer, n_alpha = 100)
plot_binned_residuals(model)

```

`plot_fuzzy_membership` *Visualize Fuzzy Membership Functions*

Description

Creates a visualization of the triangular fuzzy membership functions for both classes to help users understand the effect of mu parameters.

Usage

```
plot_fuzzy_membership(  
  mu_0 = c(0.01, 0.03, 0.05),  
  mu_1 = c(0.95, 0.97, 0.99),  
  main = "Fuzzy Membership Functions"  
)
```

Arguments

<code>mu_0</code>	Triangular fuzzy number for class 0: c(left, mode, right)
<code>mu_1</code>	Triangular fuzzy number for class 1: c(left, mode, right)
<code>main</code>	Title for the plot

Value

A ggplot object showing the fuzzy membership functions

Examples

```
# Default membership functions  
plot_fuzzy_membership()  
  
# Custom membership functions with more uncertainty  
plot_fuzzy_membership(  
  mu_0 = c(0.05, 0.15, 0.25),  
  mu_1 = c(0.75, 0.85, 0.95)  
)
```

plot_leverage

Residuals vs. Leverage Plot for a Fuzzy Logistic Regression Model

Description

Plots deviance residuals against leverage (the diagonal of the hat matrix), highlighting influential observations whose Cook's distance exceeds $4/n$. Equivalent to `plot(model, which = 4)`, provided as a standalone named function for convenience.

Usage

```
plot_leverage(model)
```

Arguments

`model` A fuzzy_logit object

Details

Observations highlighted in red have a Cook's distance greater than $4/n$, a common rule-of-thumb threshold for flagging influential points. High leverage combined with a large residual indicates an observation that may be disproportionately affecting the fitted coefficients and is worth inspecting individually.

Value

A ggplot object, printed as a side effect and returned invisibly.

See Also

[plot.fuzzy_logit](#), [plot_pearson_residuals](#), [plot_binned_residuals](#), [plot_scale_location](#)

Examples

```
data(breast_cancer)
model <- fuzzy_logit(Outcome ~ ClumpThickness + UniformCellSize + BareNuclei,
  data = breast_cancer, n_alpha = 100)
plot_leverage(model)
```

`plot_pearson_residuals`*Plot Pearson Residuals vs. Fitted Probabilities*

Description

Produces a single diagnostic plot of Pearson residuals against fitted probabilities for a fitted `fuzzy_logit` object. Equivalent to `plot(model, which = 1)`, provided as a standalone named function for convenience.

Usage

```
plot_pearson_residuals(model)
```

Arguments

<code>model</code>	A <code>fuzzy_logit</code> object
--------------------	-----------------------------------

Details

Points should scatter without any strong systematic curve. The gentle arch shape typically seen in this plot is a normal artefact of binary outcomes and is not on its own evidence of poor fit. Look instead for isolated extreme outliers (beyond roughly ± 4).

Value

A `ggplot` object, printed as a side effect and returned invisibly.

See Also

[plot.fuzzy_logit](#), [plot_binned_residuals](#), [plot_scale_location](#), [plot_leverage](#)

Examples

```
data(breast_cancer)
model <- fuzzy_logit(Outcome ~ ClumpThickness + UniformCellSize + BareNuclei,
  data = breast_cancer, n_alpha = 100)
plot_pearson_residuals(model)
```

plot_scale_location	<i>Scale-Location Plot for a Fuzzy Logistic Regression Model</i>
---------------------	--

Description

Plots the absolute value of the Pearson residuals against fitted probabilities, used to check for non-constant residual variance (heteroscedasticity). Equivalent to `plot(model, which = 3)`, provided as a standalone named function for convenience.

Usage

```
plot_scale_location(model)
```

Arguments

model	A fuzzy_logit object
-------	----------------------

Details

For binary outcomes, the variance of the Pearson residual is approximately $p(1-p)$, which is maximised at $p = 0.5$. This produces an inverted-U shape in the smooth trend line, which is expected and not a sign of model misspecification.

Value

A ggplot object, printed as a side effect and returned invisibly.

See Also

[plot.fuzzy_logit](#), [plot_pearson_residuals](#), [plot_binned_residuals](#), [plot_leverage](#)

Examples

```
data(breast_cancer)
model <- fuzzy_logit(Outcome ~ ClumpThickness + UniformCellSize + BareNuclei,
  data = breast_cancer, n_alpha = 100)
plot_scale_location(model)
```

predict.fuzzy_logit *Predict method for fuzzy_logit models*

Description

Predict method for fuzzy_logit models

Usage

```
## S3 method for class 'fuzzy_logit'
predict(
  object,
  newdata = NULL,
  type = c("link", "response"),
  se.fit = FALSE,
  ...
)
```

Arguments

object	A fitted fuzzy_logit object
newdata	Optional data frame for predictions
type	Type of prediction
se.fit	Whether to return standard errors
...	Additional arguments

Value

If `se.fit = FALSE`, a numeric vector of predictions. If `se.fit = TRUE`, a list with components `fit` (numeric vector of predicted values) and `se.fit` (numeric vector of corresponding approximate standard errors).

print.cv.fuzzy_logit *Print Cross-Validation Results*

Description

Print Cross-Validation Results

Usage

```
## S3 method for class 'cv.fuzzy_logit'
print(x, digits = 4, ...)
```

Arguments

<code>x</code>	An object of class " <code>cv.fuzzy_logit</code> ".
<code>digits</code>	Integer. Number of decimal places to display. Default is 4.
<code>...</code>	Further arguments passed to or from other methods (currently unused).

Value

No return value, called for its side effect of printing the mean (+/- SD) performance metrics and pooled confusion matrix to the console. Invisibly returns `x`.

<code>print.fuzzy_logit</code>	<i>Print method for fuzzy_logit objects</i>
--------------------------------	---

Description

Print method for `fuzzy_logit` objects

Usage

```
## S3 method for class 'fuzzy_logit'
print(x, digits = 4, ...)
```

Arguments

<code>x</code>	A <code>fuzzy_logit</code> object
<code>digits</code>	Number of digits to display
<code>...</code>	Additional arguments

Value

No return value, called for its side effect of printing the model call, coefficients, and degrees of freedom to the console. Invisibly returns `x`.

```
print.fuzzy_logit_comparison
```

Print method for fuzzy_logit_comparison

Description

Print method for fuzzy_logit_comparison

Usage

```
## S3 method for class 'fuzzy_logit_comparison'
print(x, digits = 4, ...)
```

Arguments

x	A fuzzy_logit_comparison object
digits	Number of digits to display
...	Additional arguments

Value

No return value, called for its side effect of printing the fit statistics and pivoted coefficient/spread comparison tables to the console. Invisibly returns x.

```
print.summary.fuzzy_logit
```

Print method for summary.fuzzy_logit objects

Description

Print method for summary.fuzzy_logit objects

Usage

```
## S3 method for class 'summary.fuzzy_logit'
print(x, digits = 4, signif.stars = TRUE, ...)
```

Arguments

x	A summary.fuzzy_logit object
digits	Number of digits to display
signif.stars	Logical, whether to show significance stars
...	Additional arguments

Value

No return value, called for its side effect of printing the formatted model summary to the console. Invisibly returns x.

`residuals.fuzzy_logit` *Extract residuals from fuzzy_logit model*

Description

Extract residuals from fuzzy_logit model

Usage

```
## S3 method for class 'fuzzy_logit'
residuals(object, type = c("response", "deviance", "pearson"), ...)
```

Arguments

<code>object</code>	A fuzzy_logit object
<code>type</code>	Type of residuals
<code>...</code>	Additional arguments

Value

A numeric vector of residuals, one per observation used in fitting the model. The scale depends on type: "response" residuals are on the log-odds scale, "pearson" residuals are standardised, and "deviance" residuals are signed square roots of each observation's deviance contribution.

`summary.cv.fuzzy_logit`
Summarise Cross-Validation Results

Description

Summarise Cross-Validation Results

Usage

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

Arguments

<code>object</code>	An object of class "cv.fuzzy_logit".
<code>...</code>	Further arguments passed to or from other methods (currently unused).

Value

No return value, called for its side effect of printing the overall results plus per-fold performance metrics to the console. Invisibly returns object.

summary.fuzzy_logit	<i>Summary method for fuzzy_logit objects</i>
---------------------	---

Description

Summary method for fuzzy_logit objects

Usage

```
## S3 method for class 'fuzzy_logit'  
summary(object, digits = 4, ...)
```

Arguments

object	A fuzzy_logit object
digits	Number of digits to display
...	Additional arguments

Value

An object of class "summary.fuzzy_logit", a list containing the model call, a coefficient table (coefficients) with centre estimate, spread, approximate SE, t-value, p-value, and significance code for each variable, the residual standard error, degrees of freedom, number of observations, and the fuzzy membership parameters used to fit the model.

terms.fuzzy_logit	<i>Extract terms from fuzzy_logit model</i>
-------------------	---

Description

Extract terms from fuzzy_logit model

Usage

```
## S3 method for class 'fuzzy_logit'  
terms(x, ...)
```

Arguments

x	A fuzzy_logit object
...	Additional arguments

Value

An object of class "terms" describing the structure of the fitted model.

update.fuzzy_logit	<i>Update fuzzy_logit model</i>
--------------------	---------------------------------

Description

Update fuzzy_logit model

Usage

```
## S3 method for class 'fuzzy_logit'
update(object, formula., ..., evaluate = TRUE)
```

Arguments

object	A fuzzy_logit object
formula.	New formula (optional)
...	Additional arguments to pass to fuzzy_logit
evaluate	Logical, whether to evaluate the call

Value

If evaluate = TRUE, a new object of class "fuzzy_logit" fitted with the updated formula and/or arguments. If evaluate = FALSE, the unevaluated updated call.

variable.names.fuzzy_logit	<i>Extract variable names from fuzzy_logit model</i>
----------------------------	--

Description

Extract variable names from fuzzy_logit model

Usage

```
## S3 method for class 'fuzzy_logit'
variable.names(object, ...)
```

Arguments

object	A fuzzy_logit object
...	Additional arguments

Value

A character vector of variable names, including the intercept.

vcov.fuzzy_logit	<i>Variance-covariance matrix for fuzzy_logit model</i>
------------------	---

Description

Computes an approximate variance-covariance matrix using the spread parameters. Note: This is an approximation for fuzzy regression models.

Usage

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

Arguments

object	A fuzzy_logit object
...	Additional arguments

Value

A square numeric matrix with row and column names matching the model's variable names (including the intercept).

Index

- * **datasets**
 - breast_cancer, [2](#)
- breast_cancer, [2](#)
- case.names, [4](#)
- classify, [4](#)
- coef.fuzzy_logit, [6](#)
- coefficients.fuzzy_logit, [7](#)
- compare_cv_results, [7](#)
- compare_fuzzy_models, [8](#)
- confint.fuzzy_logit, [9](#)
- cv.fuzzy_logit, [5](#), [7](#), [10](#)
- deviance.fuzzy_logit, [11](#)
- df.residual.fuzzy_logit, [11](#)
- fitted.fuzzy_logit, [12](#)
- formula.fuzzy_logit, [12](#)
- fuzzy_logit, [5](#), [13](#)
- is.fuzzy_logit, [14](#)
- logLik.fuzzy_logit, [15](#)
- model.frame.fuzzy_logit, [15](#)
- model.matrix.fuzzy_logit, [16](#)
- nobs.fuzzy_logit, [16](#)
- plot.fuzzy_logit, [17](#), [18](#), [20–22](#)
- plot_binned_residuals, [18](#), [20–22](#)
- plot_fuzzy_membership, [19](#)
- plot_leverage, [18](#), [20](#), [21](#), [22](#)
- plot_pearson_residuals, [18](#), [20](#), [21](#), [22](#)
- plot_scale_location, [18](#), [20](#), [21](#), [22](#)
- predict.fuzzy_logit, [5](#), [23](#)
- print.classify.fuzzy_logit(classify), [4](#)
- print.cv.fuzzy_logit, [23](#)
- print.fuzzy_logit, [24](#)
- print.fuzzy_logit_comparison, [25](#)
- print.summary.fuzzy_logit, [25](#)
- residuals.fuzzy_logit, [26](#)
- summary.classify.fuzzy_logit(classify), [4](#)
- summary.cv.fuzzy_logit, [26](#)
- summary.fuzzy_logit, [27](#)
- terms.fuzzy_logit, [27](#)
- update.fuzzy_logit, [28](#)
- variable.names.fuzzy_logit, [28](#)
- vcov.fuzzy_logit, [29](#)