

0.1 probit: Probit Regression for Dichotomous Dependent Variables

Use probit regression to model binary dependent variables specified as a function of a set of explanatory variables. For a Bayesian implementation of this model, see Section ??.

Syntax

```
> z.out <- zelig(Y ~ X1 + X2, model = "probit", data = mydata)
> x.out <- setx(z.out)
> s.out <- sim(z.out, x = x.out, x1 = NULL)
```

Additional Inputs

In addition to the standard inputs, `zelig()` takes the following additional options for probit regression:

- **robust**: defaults to **FALSE**. If **TRUE** is selected, `zelig()` computes robust standard errors via the **sandwich** package (see ?). The default type of robust standard error is heteroskedastic and autocorrelation consistent (HAC), and assumes that observations are ordered by time index.

In addition, **robust** may be a list with the following options:

- **method**: Choose from
 - * **"vcovHAC"**: (default if **robust** = **TRUE**) HAC standard errors.
 - * **"kernHAC"**: HAC standard errors using the weights given in ?).
 - * **"weave"**: HAC standard errors using the weights given in ?).
- **order.by**: defaults to **NULL** (the observations are chronologically ordered as in the original data). Optionally, you may specify a vector of weights (either as **order.by** = **z**, where **z** exists outside the data frame; or as **order.by** = **~z**, where **z** is a variable in the data frame). The observations are chronologically ordered by the size of **z**.
- **...**: additional options passed to the functions specified in **method**. See the **sandwich** library and ?) for more options.

Examples

Attach the sample turnout dataset:

```
> data(turnout)
```

Estimate parameter values for the probit regression:

```
> z.out <- zelig(vote ~ race + educate, model = "probit", data = turnout)
```

```
> summary(z.out)
```

Set values for the explanatory variables to their default values.

```
> x.out <- setx(z.out)
```

Simulate quantities of interest from the posterior distribution.

```
> s.out <- sim(z.out, x = x.out)
```

```
> summary(s.out)
```

Model

Let Y_i be the observed binary dependent variable for observation i which takes the value of either 0 or 1.

- The *stochastic component* is given by

$$Y_i \sim \text{Bernoulli}(\pi_i),$$

where $\pi_i = \Pr(Y_i = 1)$.

- The *systematic component* is

$$\pi_i = \Phi(x_i\beta)$$

where $\Phi(\mu)$ is the cumulative distribution function of the Normal distribution with mean 0 and unit variance.

Quantities of Interest

- The expected value (`qi$ev`) is a simulation of predicted probability of success

$$E(Y) = \pi_i = \Phi(x_i\beta),$$

given a draw of β from its sampling distribution.

- The predicted value (`qi$pr`) is a draw from a Bernoulli distribution with mean π_i .
- The first difference (`qi$fd`) in expected values is defined as

$$\text{FD} = \Pr(Y = 1 \mid x_1) - \Pr(Y = 1 \mid x).$$

- The risk ratio (`qi$rr`) is defined as

$$\text{RR} = \Pr(Y = 1 \mid x_1) / \Pr(Y = 1 \mid x).$$

- In conditional prediction models, the average expected treatment effect (**att.ev**) for the treatment group is

$$\frac{1}{\sum_{i=1}^n t_i} \sum_{i:t_i=1}^n \{Y_i(t_i = 1) - E[Y_i(t_i = 0)]\},$$

where t_i is a binary explanatory variable defining the treatment ($t_i = 1$) and control ($t_i = 0$) groups. Variation in the simulations are due to uncertainty in simulating $E[Y_i(t_i = 0)]$, the counterfactual expected value of Y_i for observations in the treatment group, under the assumption that everything stays the same except that the treatment indicator is switched to $t_i = 0$.

- In conditional prediction models, the average predicted treatment effect (**att.pr**) for the treatment group is

$$\frac{1}{\sum_{i=1}^n t_i} \sum_{i:t_i=1}^n \left\{ Y_i(t_i = 1) - \widehat{Y_i(t_i = 0)} \right\},$$

where t_i is a binary explanatory variable defining the treatment ($t_i = 1$) and control ($t_i = 0$) groups. Variation in the simulations are due to uncertainty in simulating $\widehat{Y_i(t_i = 0)}$, the counterfactual predicted value of Y_i for observations in the treatment group, under the assumption that everything stays the same except that the treatment indicator is switched to $t_i = 0$.

Output Values

The output of each `Zelig` command contains useful information which you may view. For example, if you run `z.out <- zelig(y ~ x, model = "probit", data)`, then you may examine the available information in `z.out` by using `names(z.out)`, see the `coefficients` by using `z.out$coefficients`, and a default summary of information through `summary(z.out)`. Other elements available through the `$` operator are listed below.

- From the `zelig()` output object `z.out`, you may extract:
 - **coefficients**: parameter estimates for the explanatory variables.
 - **residuals**: the working residuals in the final iteration of the IWLS fit.
 - **fitted.values**: a vector of the in-sample fitted values.
 - **linear.predictors**: a vector of $x_i\beta$.
 - **aic**: Akaike's Information Criterion (minus twice the maximized log-likelihood plus twice the number of coefficients).
 - **df.residual**: the residual degrees of freedom.
 - **df.null**: the residual degrees of freedom for the null model.

- `data`: the name of the input data frame.
- From `summary(z.out)`, you may extract:
 - `coefficients`: the parameter estimates with their associated standard errors, p -values, and t -statistics.
 - `cov.scaled`: a $k \times k$ matrix of scaled covariances.
 - `cov.unscaled`: a $k \times k$ matrix of unscaled covariances.
- From the `sim()` output object `s.out`, you may extract quantities of interest arranged as matrices indexed by simulation \times \mathbf{x} -observation (for more than one \mathbf{x} -observation). Available quantities are:
 - `qi$ev`: the simulated expected values, or predicted probabilities, for the specified values of \mathbf{x} .
 - `qi$pr`: the simulated predicted values drawn from the distributions defined by the predicted probabilities.
 - `qi$fd`: the simulated first differences in the predicted probabilities for the values specified in \mathbf{x} and $\mathbf{x1}$.
 - `qi$rr`: the simulated risk ratio for the predicted probabilities simulated from \mathbf{x} and $\mathbf{x1}$.
 - `qi$att.ev`: the simulated average expected treatment effect for the treated from conditional prediction models.
 - `qi$att.pr`: the simulated average predicted treatment effect for the treated from conditional prediction models.

Contributors

The probit model is part of the base package by William N. Venables and Brian D. Ripley. Please cite the model as:

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In addition, advanced users may wish to refer to `help(glm)` and `help(family)`, as well as `?`).

Robust standard errors are implemented via the `sandwich` package by Achim Zeileis. Please cite as

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Sample data are a selection of 2,000 observations from

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Kosuke Imai, Gary King, and Olivia Lau added `Zelig` functionality.