
Zelig Documentation

Release 5.0.1

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Zelig is a framework for interfacing with a wide range of statistical models and analytic methods in a common and simple way. Above and beyond estimation, it adds considerable infrastructure to existing heterogeneous R implementations by translating coefficient estimates into interpretable quantities of interest and automating statistical procedures (e.g., bootstrapping) through an intelligible call structure.

To get started, we recommend following the [Installation & Quickstart](#) guide. More information about the software, including our technical vision and goals for the project, can be found at the [About Zelig](#) page.

To view the code-base, visit the source repository at <https://github.com/IQSS/Zelig> and for regular updates and release information be sure to follow us on twitter at [@IQSS](#). We also recommend joining the [Zelig Google Group](#), where we are encouraging users to ask questions, report bugs, and help others.

IMPLEMENTED MODELS IN ZELIG 5.0.1

Inheritance Tree

1.1 Installation & Quickstart

This guide is designed to get you up and running with the current *beta* release of Zelig (5.0.1).

1.1.1 Installing R & Zelig

Before using Zelig, you will need to download and install both the R statistical program and the Zelig package:

Installing R

To install R, go to <http://www.r-project.org/>. Select the CRAN option from the left-hand menu (CRAN is the Comprehensive R Archive Network where all files related to R can be found). Pick a CRAN mirror closest to your current geographic location (there are multiple mirrors of this database in various locations, selecting the one closest to you will be sure to maximize your the speed of your download). Follow the instructions for downloading R for Linux, Mac OS X, or Windows.

Installing Zelig

Because Zelig 5 is still a *beta* release and is not yet available on CRAN (with other R software packages), it must be downloaded from Github using the `devtools` package.

Once you've successfully installed R, open it, and at the terminal prompt, type in the following commands verbatim:

```
# This installs devtools package, if not already installed
install.packages("devtools")
# This loads devtools
library(devtools)
# This downloads Zelig 5.0.1 from the IQSS Github repo
install_github('IQSS/Zelig')
```

If you have successfully installed the program, you will see a the following message: *"DONE (Zelig5)"*.

1.1.2 Quickstart Guide

Now that we have successfully downloaded and installed Zelig from Github, we will load the package and walk through an example. The scenario is a simple one: imagine you want to estimate the distance a car has traveled given its speed and you have a dataset of cars, distance and speed. Throughout the rest of this guide, we will walk you through building a statistical model from this data using Zelig.

Loading Zelig

First, we have to load Zelig into R. After installing both R and Zelig, open R and type:

```
library(Zelig5)
```

Building Models

Now, let's build a statistical model that captures the relationship between a car's distance and speed, where distance is the outcome (dependent) variable and speed is the only explanatory (independent) variable. Given that distance (the DV) is a continuous variable, we should use a least squares regression.

To do so, we must first create a Zelig least squares object, then specify our model, and finally regress distance on speed to estimate the relationship between speed and distance:

```
# load toy dataset (when you install R, example datasets are also installed)
data(cars)
# initialize Zelig5 least squares object
z5 <- zls$new()
# estimate ls model
z5$zelig(dist ~ speed, data = cars)
# you can now get model summary estimates
z5

## Model: 1
## Call:
## stats::lm(formula = dist ~ speed, data = .)
##
## Coefficients:
## (Intercept)          speed
##      -17.58           3.93
##
## Next step: Use 'setx' method
```

So what do our model estimates tell us? First, off we can see that the positive 3.93 estimate for speed suggests a positive relationship between speed and distance. In particular, we would interpret this coefficient as a one unit increase in speed (e.g., mph) leads to a 3 unit increase in distance (e.g., miles). This interpretation is not very intuitive. Perhaps, we want to know how the distance a car can travel changes over a range of speed (e.g., 10 to 20 mph).

Zelig makes this simple, by automating the translation of model estimates in interpretable quantities of interest (more on this below) using Monte Carlo simulations. To get this process started we need to set explanatory variables in our model (i.e., speed) using the `$setx()` or `$setrange()` method:

```
# simulate over a range of speed between 10 and 20 mph
z5$setrange(speed = 10:20)

# you can also set covariates at particular value using $setx()
z5$setx(speed = 30)
```

Now that we've set our variables, all we have to do is run our simulations:


```
#run 10 simulations and estimate quantities of interest
z5$sim(num = 10)
# default is 1,000 simulations
```

Now we've estimated a model and calculated interpretable estimates across a range of speed (e.g., 10 - 20 mph). What can we do with them? Zelig gives you access to estimated quantities of interest and makes plotting and presenting them particularly easy.

Quantities of Interest

As mentioned earlier, a major feature of Zelig is the translation of model estimates into easy to interpret quantities of interest (QIs). These QIs (e.g., expected and predicted values) can be accessed via the `$sim.out` field:

```
z5$sim.out$range

## [[1]]
## Source: local data frame [1 x 2]
## Groups: <by row>
##
##           ev           pv
## 1 <dbl[10,1]> <dbl[10,1]>
##
## [[2]]
## Source: local data frame [1 x 2]
## Groups: <by row>
##
##           ev           pv
## 1 <dbl[10,1]> <dbl[10,1]>
##
## [[3]]
## Source: local data frame [1 x 2]
## Groups: <by row>
##
##           ev           pv
## 1 <dbl[10,1]> <dbl[10,1]>
##
## [[4]]
## Source: local data frame [1 x 2]
## Groups: <by row>
##
##           ev           pv
## 1 <dbl[10,1]> <dbl[10,1]>
##
## [[5]]
## Source: local data frame [1 x 2]
## Groups: <by row>
##
##           ev           pv
## 1 <dbl[10,1]> <dbl[10,1]>
##
## [[6]]
## Source: local data frame [1 x 2]
## Groups: <by row>
##
##           ev           pv
## 1 <dbl[10,1]> <dbl[10,1]>
##
```

```
## [[7]]
## Source: local data frame [1 x 2]
## Groups: <by row>
##
##           ev           pv
## 1 <dbl[10,1]> <dbl[10,1]>
##
## [[8]]
## Source: local data frame [1 x 2]
## Groups: <by row>
##
##           ev           pv
## 1 <dbl[10,1]> <dbl[10,1]>
##
## [[9]]
## Source: local data frame [1 x 2]
## Groups: <by row>
##
##           ev           pv
## 1 <dbl[10,1]> <dbl[10,1]>
##
## [[10]]
## Source: local data frame [1 x 2]
## Groups: <by row>
##
##           ev           pv
## 1 <dbl[10,1]> <dbl[10,1]>
##
## [[11]]
## Source: local data frame [1 x 2]
## Groups: <by row>
##
##           ev           pv
## 1 <dbl[10,1]> <dbl[10,1]>
```

Plots

A second major Zelig feature is how easy it is to plot QIs for presentation in slides or an article. Using the `plot()` function on the `z5$s.out` will produce ready-to-use plots with labels and confidence intervals.

Plots of QI's from binary choice model:

```
z5$graph()
```

Plot of expected values across range of simulations:

1.2 Model Reference and Vignettes

This section includes technical information on the models currently implemented in Zelig (5.0.1). This includes a reference with a list of supported models as well as individual model vignettes with detailed information on the model, quantities of interest and syntax.

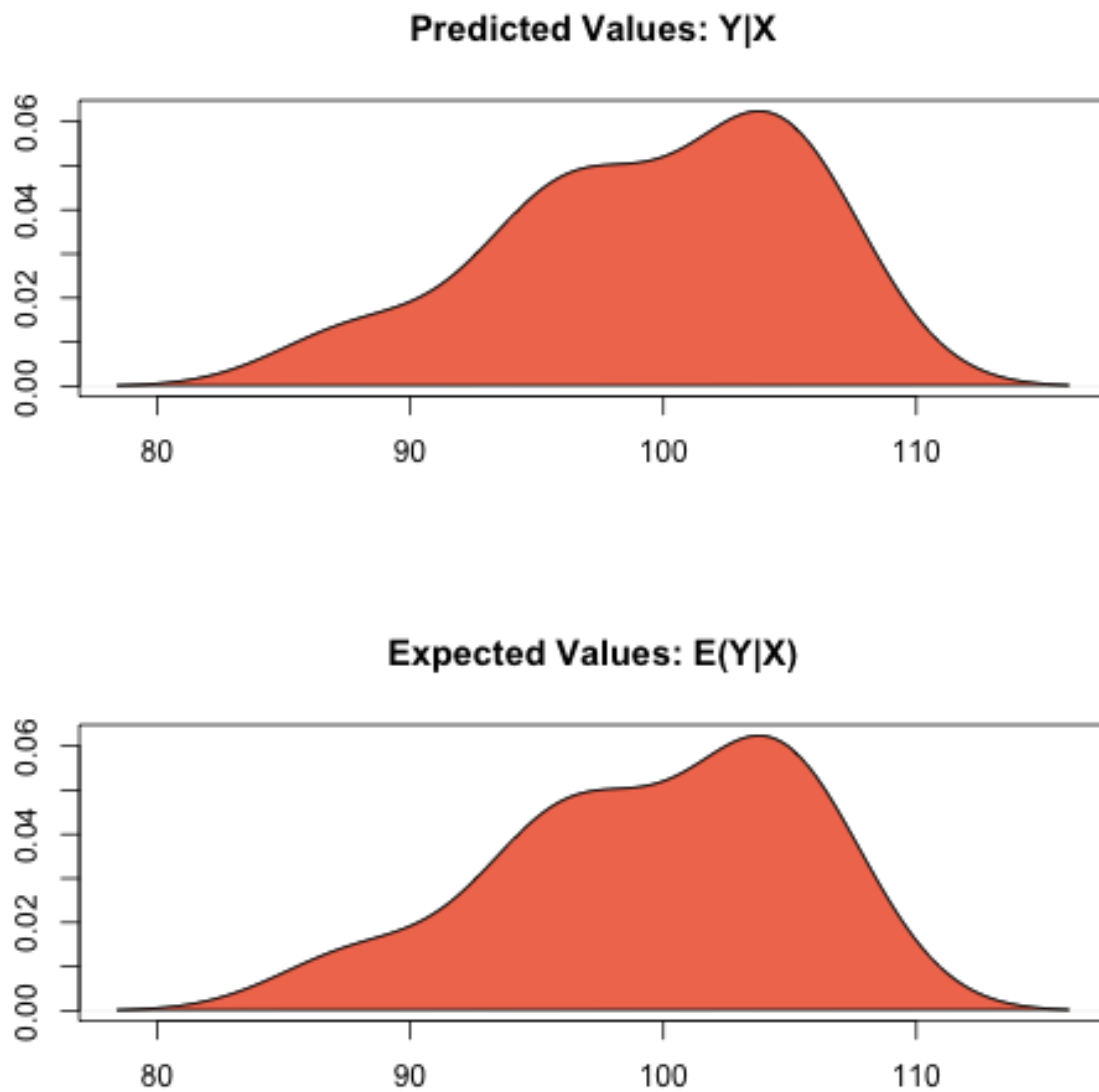


Figure 1.1: plot of chunk unnamed-chunk-8

1.2.1 Reference

The following models are currently supported in Zelig 5:

- Exponential Regression: `zexp$new()`
 - Gamma Regression: `zgamma()`
 - Logistic Regression: `zlogit$new()`
 - Log-Normal Regression: `zlognorm$new()`
 - Least Squares Regression: `zls$new()`
 - Negative Binomial Regression: `zbinom$new()`
 - Normal Regression: `znormal$new()`
 - Poisson Regression: `zpoisson$new()`
 - Probit Regression: `zprobit$new()`
 - Quantile Regression: `zquantile$new()`
 - Rare Events Logistic Regression: `zrelogit$new()`
 - Tobit Regression: `ztobit$new()`
-

1.2.2 zelig-exp

Exponential Regression for Duration Dependent Variables

Use the exponential duration regression model if you have a dependent variable representing a duration (time until an event). The model assumes a constant hazard rate for all events. The dependent variable may be censored (for observations have not yet been completed when data were collected).

Syntax

```
z.out <- zelig(Surv(Y, C) ~ X, model = "exp", data = mydata)
x.out <- setx(z.out)
s.out <- sim(z.out, x = x.out)

z5 <- zexp$new()
z5$zelig(Surv(Y, C) ~ X, data = mydata)
z5$setx()
z5$sim()
```

Exponential models require that the dependent variable be in the form `Surv(Y, C)`, where `Y` and `C` are vectors of length n . For each observation i in $1, \dots, n$, the value y_i is the duration (lifetime, for example), and the associated c_i is a binary variable such that $c_i = 1$ if the duration is not censored (*e.g.*, the subject dies during the study) or $c_i = 0$ if the duration is censored (*e.g.*, the subject is still alive at the end of the study and is known to live at least as long as y_i). If c_i is omitted, all `Y` are assumed to be completed; that is, time defaults to 1 for all observations.

Input Values

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

- `robust`: defaults to `FALSE`. If `TRUE`, `zelig()` computes robust standard errors based on sandwich estimators (see [here](#) and [here](#)) and the options selected in `cluster`.
- `cluster`: if `robust = TRUE`, you may select a variable to define groups of correlated observations. Let `x3` be a variable that consists of either discrete numeric values, character strings, or factors that define strata. Then

```
z.out <- zelig(y ~ x1 + x2, robust = TRUE, cluster = "x3",
              model = "exp", data = mydata)
```

means that the observations can be correlated within the strata defined by the variable `x3`, and that robust standard errors should be calculated according to those clusters. If `robust = TRUE` but `cluster` is not specified, `zelig()` assumes that each observation falls into its own cluster.

Example

Attach the sample data:

```
data(coalition)
```

Estimate the model:

```
z.out <- zelig(Surv(duration, ciepl2) ~ fract + numst2, model = "exp", data = coalition)
```

```
## How to cite this model in Zelig:
##   Olivia Lau, Kosuke Imai, Gary King. 2011.
##   exp: Exponential Regression for Duration Dependent Variables
##   in Kosuke Imai, Gary King, and Olivia Lau, "Zelig: Everyone's Statistical Software,"
##   http://datascience.iq.harvard.edu/zelig
```

View the regression output:

```
summary(z.out)

## Model: 1Call:
##   survival::survreg(formula = Surv(duration, ciepl2) ~ fract +
##     numst2, data = ., dist = "exponential", model = FALSE)
##
## Coefficients:
##   (Intercept)      fract      numst2
##    5.535873   -0.003909    0.461179
##
## Scale fixed at 1
##
## Loglik(model)= -1077   Loglik(intercept only)= -1101
##   Chisq= 46.66 on 2 degrees of freedom, p= 7.4e-11
## n= 314
## Next step: Use 'setx' method
```

Set the baseline values (with the ruling coalition in the minority) and the alternative values (with the ruling coalition in the majority) for `X`:

```
x.low <- setx(z.out, numst2 = 0)
x.high <- setx(z.out, numst2 = 1)
```

Simulate expected values (`qi$ev`) and first differences (`qi$fd`):

```
s.out <- sim(z.out, x = x.low, x1 = x.high)
```

Summarize quantities of interest and produce some plots:

```
summary(s.out)

##
##   sim x :
##   -----
##   ev
##      mean      sd    50%   2.5% 97.5%
## 1 15.34 1.426 15.34 12.61 18.25
##   pv
##      mean      sd    50%   2.5% 97.5%
## [1,] 15.7 17.52 10.08 0.4039 59.97
##
##   sim x1 :
##   -----
##   ev
##      mean      sd    50%   2.5% 97.5%
## 1 24.35 1.86 24.24 20.97 28.1
##   pv
##      mean      sd    50%   2.5% 97.5%
## [1,] 24.09 24.17 16.49 0.6458 85.44
##   fd
##      mean      sd    50%   2.5% 97.5%
## 1 9.007 2.38 8.943 4.64 13.83

plot(s.out)
```

Model

Let Y_i^* be the survival time for observation i . This variable might be censored for some observations at a fixed time y_c such that the fully observed dependent variable, Y_i , is defined as

$$Y_i = \begin{cases} Y_i^* & \text{if } Y_i^* \leq y_c \\ y_c & \text{if } Y_i^* > y_c \end{cases}$$

- The *stochastic component* is described by the distribution of the partially observed variable Y^* . We assume Y_i^* follows the exponential distribution whose density function is given by

$$f(y_i^* | \lambda_i) = \frac{1}{\lambda_i} \exp\left(-\frac{y_i^*}{\lambda_i}\right)$$

for $y_i^* \geq 0$ and $\lambda_i > 0$. The mean of this distribution is λ_i .

In addition, survival models like the exponential have three additional properties. The hazard function $h(t)$ measures the probability of not surviving past time t given survival up to t . In general, the hazard function is equal to $f(t)/S(t)$ where the survival function $S(t) = 1 - \int_0^t f(s)ds$ represents the fraction still surviving at time t . The cumulative hazard function $H(t)$ describes the probability of dying before time t . In general, $H(t) = \int_0^t h(s)ds = -\log S(t)$. In the case of the exponential model,

$$\begin{aligned} h(t) &= \frac{1}{\lambda_i} \\ S(t) &= \exp\left(-\frac{t}{\lambda_i}\right) \\ H(t) &= \frac{t}{\lambda_i} \end{aligned}$$

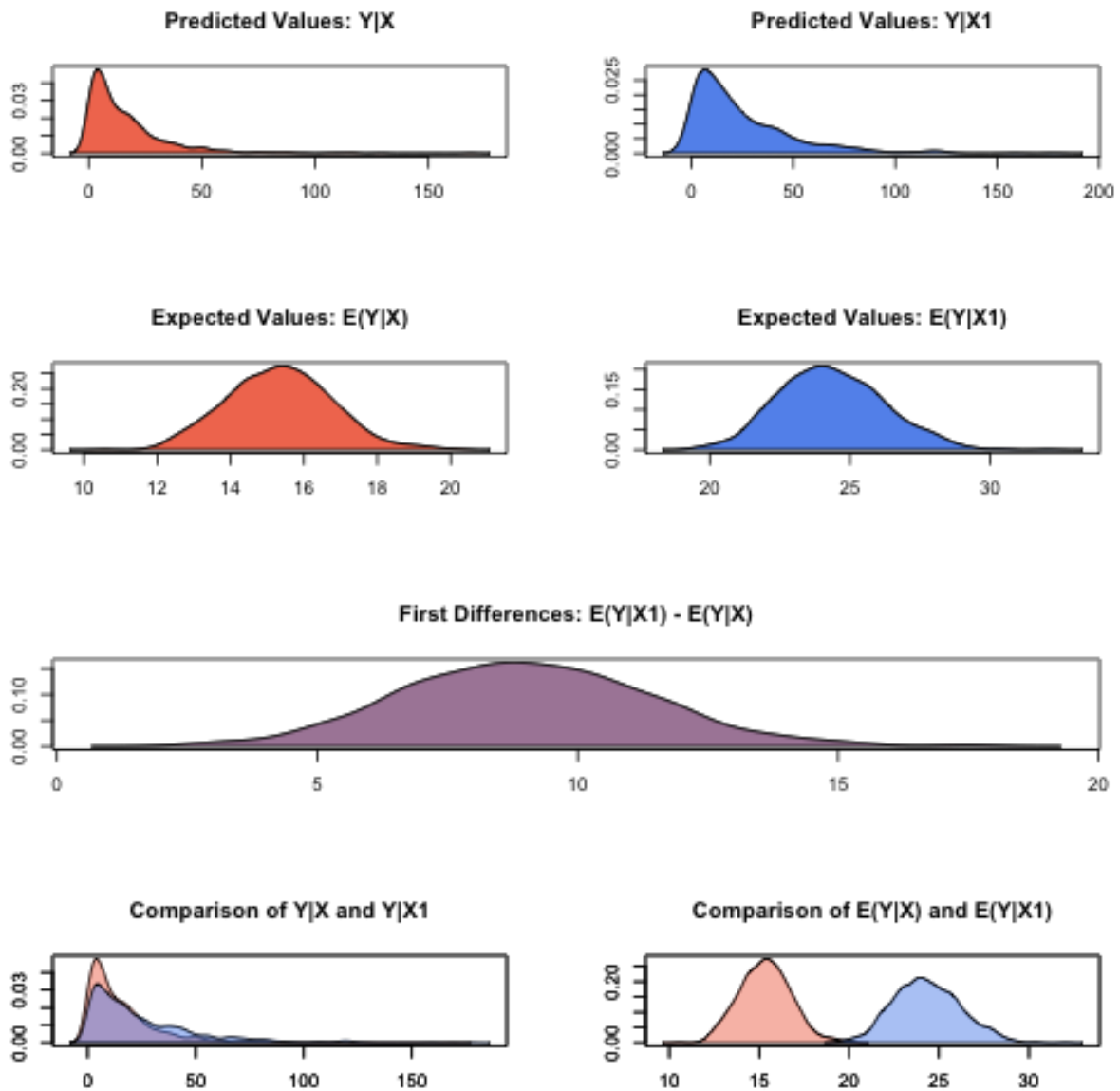


Figure 1.2: plot of chunk unnamed-chunk-11

For the exponential model, the hazard function $h(t)$ is constant over time. The Weibull model and lognormal models allow the hazard function to vary as a function of elapsed time (see and respectively).

- The *systematic component* λ_i is modeled as

$$\lambda_i = \exp(x_i\beta),$$

where x_i is the vector of explanatory variables, and β is the vector of coefficients.

Quantities of Interest

- The expected values (qi\$ev) for the exponential model are simulations of the expected duration given x_i and draws of β from its posterior,

$$E(Y) = \lambda_i = \exp(x_i\beta).$$

- The predicted values (qi\$pr) are draws from the exponential distribution with rate equal to the expected value.
- The first difference (or difference in expected values, qi\$ev.diff), is

$$FD = E(Y \mid x_1) - E(Y \mid x),$$

where x and x_1 are different vectors of values for the explanatory variables.

- 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. When $Y_i(t_i = 1)$ is censored rather than observed, we replace it with a simulation from the model given available knowledge of the censoring process. Variation in the simulations is due to two factors: uncertainty in the imputation process for censored y_i^* and 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

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

where t_i is a binary explanatory variable defining the treatment ($t_i = 1$) and control ($t_i = 0$) groups. When $Y_i(t_i = 1)$ is censored rather than observed, we replace it with a simulation from the model given available knowledge of the censoring process. Variation in the simulations is due to two factors: uncertainty in the imputation process for censored y_i^* and 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(Surv(Y, C) ~ X, model = exp, 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.

See also

The exponential function is part of the survival library by Terry Therneau, ported to R by Thomas Lumley. Advanced users may wish to refer to `help(survfit)` in the survival library.

1.2.3 zelig-gamma

Gamma Regression for Continuous, Positive Dependent Variables

Use the gamma regression model if you have a positive-valued dependent variable such as the number of years a parliamentary cabinet endures, or the seconds you can stay airborne while jumping. The gamma distribution assumes that all waiting times are complete by the end of the study (censoring is not allowed).

Syntax

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

Example

Attach the sample data:

```
data(coalition)
```

Estimate the model:

```
z.out <- zelig(duration ~ fract + numst2, model = "gamma", data =
coalition)
```

View the regression output:

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

Set the baseline values (with the ruling coalition in the minority) and the alternative values (with the ruling coalition in the majority) for X:

```
x.low <- setx(z.out, numst2 = 0) RRR> x.high <- setx(z.out, numst2
= 1)
```

Simulate expected values (qi\$ev) and first differences (qi\$fd):

```
s.out <- sim(z.out, x = x.low, x1 = x.high)
```

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

```
plot(s.out)
```

Model

- The Gamma distribution with scale parameter α has a *stochastic component*:

$$Y \sim \text{Gamma}(y_i \mid \lambda_i, \alpha)$$
$$f(y) = \frac{1}{\alpha^{\lambda_i} \Gamma \lambda_i} y_i^{\lambda_i-1} \exp - \left\{ \frac{y_i}{\alpha} \right\}$$

for $\alpha, \lambda_i, y_i > 0$.

- The *systematic component* is given by

$$\lambda_i = \frac{1}{x_i \beta}$$

Quantities of Interest

- The expected values (qi\$ev) are simulations of the mean of the stochastic component given draws of α and β from their posteriors:

$$E(Y) = \alpha \lambda_i.$$

- The predicted values (qi\$pr) are draws from the gamma distribution for each given set of parameters (α, λ_i) .
- If x1 is specified, sim() also returns the differences in the expected values (qi\$fd),

$$E(Y \mid x_1) - E(Y \mid x)$$

.

- 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

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

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 $\widehat{Y_i(t_i = 0)}$, 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 = gamma, 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`: the vector of fitted values.
 - `linear.predictors`: the 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.
 - `zelig.data`: the input data frame if `save.data = TRUE`.
- 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 `x-observation` (for more than one `x-observation`). Available quantities are:
 - `qi$ev`: the simulated expected values for the specified values of `x`.
 - `qi$pr`: the simulated predicted values drawn from a distribution defined by (α, λ_i) .
 - `qi$fd`: the simulated first difference in the expected values for the specified values in `x` and `x1`.
 - `qi$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.

See also

The gamma model is part of the `stats` package by . Advanced users may wish to refer to `help(glm)` and `help(family)`.

1.2.4 zelig-logit

Logistic Regression for Dichotomous Dependent Variables

Logistic regression specifies a dichotomous dependent variable as a function of a set of explanatory variables.

Syntax

```
z.out <- zelig(Y ~ X1 + X2, model = "logit", 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 logistic 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

1. Basic Example

Attaching the sample turnout dataset:

```
data(turnout)
```

Estimating parameter values for the logistic regression:

```
z.out1 <- zelig(vote ~ age + race, model = "logit", data = turnout)
```

Setting values for the explanatory variables:

```
x.out1 <- setx(z.out1, age = 36, race = "white")
```

Simulating quantities of interest from the posterior distribution.

```
s.out1 <- sim(z.out1, x = x.out1)
```

```
summary(s.out1)
```

```
plot(s.out1)
```

1. Simulating First Differences

Estimating the risk difference (and risk ratio) between low education (25th percentile) and high education (75th percentile) while all the other variables held at their default values.

```
z.out2 <- zelig(vote ~ race + educate, model = "logit", data =  
turnout) > x.high <- setx(z.out2, educate = quantile(turnout$educate, prob = 0.75))  
x.low <- setx(z.out2, educate = quantile(turnout$educate, prob = 0.25))
```

```
s.out2 <- sim(z.out2, x = x.high, x1 = x.low)
```

```
summary(s.out2)
```

```
plot(s.out2)
```

1. Presenting Results: An ROC Plot [ROC]

One can use an ROC plot to evaluate the fit of alternative model specifications. (Use `demo(roc)` to view this example, or see King and Zeng (2002).)

```
z.out1 <- zelig(vote ~ race + educate + age, model = "logit", +
  data = turnout) > z.out2 <- zelig(vote ~ race + educate, model =
  "logit", data = turnout)

rocplot(z.out1\ :math:`y`, z.out2\` y, fitted(z.out1),
  fitted(z.out2))
```

Model

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

- The *stochastic component* is given by

$$\begin{aligned} Y_i &\sim \text{Bernoulli}(y_i \mid \pi_i) \\ &= \pi_i^{y_i} (1 - \pi_i)^{1-y_i} \end{aligned}$$

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

- The *systematic component* is given by:

$$\pi_i = \frac{1}{1 + \exp(-x_i\beta)}.$$

where x_i is the vector of k explanatory variables for observation i and β is the vector of coefficients.

Quantities of Interest

- The expected values (`qi$ev`) for the logit model are simulations of the predicted probability of a success:

$$E(Y) = \pi_i = \frac{1}{1 + \exp(-x_i\beta)},$$

given draws of β from its sampling distribution.

- The predicted values (`qi$pr`) are draws from the Binomial distribution with mean equal to the simulated expected value π_i .
- The first difference (`qi$fd`) for the logit model 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 = logit, 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)`.

See also

The logit model is part of the stats package. Advanced users may wish to refer to `help(glm)` and `help(family)`.

1.2.5 zelig-lognorm

Log-Normal Regression for Duration Dependent Variables

The log-normal model describes an event's duration, the dependent variable, as a function of a set of explanatory variables. The log-normal model may take time censored dependent variables, and allows the hazard rate to increase and decrease.

Syntax

```
z.out <- zelig(Surv(Y, C) ~ X, model = "lognorm", data = mydata)
x.out <- setx(z.out)
s.out <- sim(z.out, x = x.out)
```

Log-normal models require that the dependent variable be in the form `Surv(Y, C)`, where `Y` and `C` are vectors of length n . For each observation i in $1, \dots, n$, the value y_i is the duration (lifetime, for example) of each subject, and the associated c_i is a binary variable such that $c_i = 1$ if the duration is not censored (*e.g.*, the subject dies during the study) or $c_i = 0$ if the duration is censored (*e.g.*, the subject is still alive at the end of the study). If c_i is omitted, all `Y` are assumed to be completed; that is, time defaults to 1 for all observations.

Input Values

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

- `robust`: defaults to `FALSE`. If `TRUE`, `zelig()` computes robust standard errors based on sandwich estimators (see [here](#) and [here](#)) based on the options in `cluster`.
- `cluster`: if `robust = TRUE`, you may select a variable to define groups of correlated observations. Let `x3` be a variable that consists of either discrete numeric values, character strings, or factors that define strata. Then

```
z.out <- zelig(y ~ x1 + x2, robust = TRUE, cluster = "x3", model = "exp", data = mydata)
```

means that the observations can be correlated within the strata defined by the variable `x3`, and that robust standard errors should be calculated according to those clusters. If `robust = TRUE` but `cluster` is not specified, `zelig()` assumes that each observation falls into its own cluster.

Example

Attach the sample data:

```
data(coalition)
```

Estimate the model:

```
RRR> z.out <- zelig(Surv(duration, ciepl2) ~ fract + numst2, model =
"lognorm", data = coalition)
```

View the regression output:

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

Set the baseline values (with the ruling coalition in the minority) and the alternative values (with the ruling coalition in the majority) for `X`:

```
x.low <- setx(z.out, numst2 = 0) RRR> x.high <- setx(z.out, numst2
= 1)
```

Simulate expected values (`qi$ev`) and first differences (`qi$fd`):

```
s.out <- sim(z.out, x = x.low, x1 = x.high)
```

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

```
plot(s.out)
```

Model

Let Y_i^* be the survival time for observation i with the density function $f(y)$ and the corresponding distribution function $F(t) = \int_0^t f(y)dy$. This variable might be censored for some observations at a fixed time y_c such that the fully observed dependent variable, Y_i , is defined as

$$Y_i = \begin{cases} Y_i^* & \text{if } Y_i^* \leq y_c \\ y_c & \text{if } Y_i^* > y_c \end{cases}$$

- The *stochastic component* is described by the distribution of the partially observed variable, Y^* . For the lognormal model, there are two equivalent representations:

$$Y_i^* \sim \text{LogNormal}(\mu_i, \sigma^2) \text{ or } \log(Y_i^*) \sim \text{Normal}(\mu_i, \sigma^2)$$

where the parameters μ_i and σ^2 are the mean and variance of the Normal distribution. (Note that the output from `zelig()` parameterizes `scale=math:' = sigma'`.)

In addition, survival models like the lognormal have three additional properties. The hazard function $h(t)$ measures the probability of not surviving past time t given survival up to t . In general, the hazard function is equal to $f(t)/S(t)$ where the survival function `math:'S(t) =`

`1 - int_{0}^t f(s) ds'` represents the fraction still surviving at

time t . The cumulative hazard function $H(t)$ describes the probability of dying before time t . In general, $H(t) = \int_0^t h(s)ds = -\log S(t)$. In the case of the lognormal model,

$$\begin{aligned} h(t) &= \frac{1}{\sqrt{2\pi} \sigma t S(t)} \exp \left\{ -\frac{1}{2\sigma^2} (\log \lambda t)^2 \right\} \\ S(t) &= 1 - \Phi \left(\frac{1}{\sigma} \log \lambda t \right) \\ H(t) &= -\log \left\{ 1 - \Phi \left(\frac{1}{\sigma} \log \lambda t \right) \right\} \end{aligned}$$

where $\Phi(\cdot)$ is the cumulative density function for the Normal distribution.

- The *systematic component* is described as:

$$\mu_i = x_i \beta.$$

Quantities of Interest

- The expected values (`qi$ev`) for the lognormal model are simulations of the expected duration:

$$E(Y) = \exp \left(\mu_i + \frac{1}{2} \sigma^2 \right),$$

given draws of β and σ from their sampling distributions.

- The predicted value is a draw from the log-normal distribution given simulations of the parameters (λ_i, σ) .
- The first difference (`qi$fd`) is

$$FD = E(Y \mid x_1) - E(Y \mid x).$$

- 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. When $Y_i(t_i = 1)$ is censored rather than observed, we replace it with a simulation from the model given available knowledge of the censoring process. Variation in the simulations is due to two factors: uncertainty in the imputation process for censored y_i^* and 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

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

where t_i is a binary explanatory variable defining the treatment ($t_i = 1$) and control ($t_i = 0$) groups. When $Y_i(t_i = 1)$ is censored rather than observed, we replace it with a simulation from the model given available knowledge of the censoring process. Variation in the simulations are due to two factors: uncertainty in the imputation process for censored y_i^* and uncertainty in simulating $Y_i(\widehat{t_i = 0})$, 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(Surv(Y, C) ~ X, model = lognorm, 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.
 - `icoef`: parameter estimates for the intercept and σ .
 - `var`: Variance-covariance matrix.
 - `loglik`: Vector containing the log-likelihood for the model and intercept only (respectively).
 - `linear.predictors`: the vector of $x_i\beta$.
 - `df.residual`: the residual degrees of freedom.
 - `df.null`: the residual degrees of freedom for the null model.
 - `zelig.data`: the input data frame if `save.data = TRUE`.
- Most of this may be conveniently summarized using `summary(z.out)`. From `summary(z.out)`, you may additionally extract:
 - `table`: the parameter estimates with their associated standard errors, p -values, and t -statistics.
- From the `sim()` output object `s.out`, you may extract quantities of interest arranged as matrices indexed by simulation \times x-observation (for more than one x-observation). Available quantities are:
 - `qi$ev`: the simulated expected values for the specified values of x .
 - `qi$pr`: the simulated predicted values drawn from the distribution defined by (λ_i, σ) .
 - `qi$fd`: the simulated first differences between the simulated expected values for x and $x1$.
 - `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.

See also

The exponential function is part of the survival library by Terry Therneau, ported to R by Thomas Lumley. Advanced users may wish to refer to `help(survfit)` in the survival library.

1.2.6 zelig-ls

Least Squares Regression for Continuous Dependent Variables

Use least squares regression analysis to estimate the best linear predictor for the specified dependent variables.

Syntax

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

Examples

1. Basic Example with First Differences

Attach sample data:

```
data(macro)
```

Estimate model:

```
z.out1 <- zelig(unem ~ gdp + capmob + trade, model = "ls", data =
macro)
```

Summarize regression coefficients:

```
summary(z.out1)
```

Set explanatory variables to their default (mean/mode) values, with high (80th percentile) and low (20th percentile) values for the trade variable:

```
x.high <- setx(z.out1, trade = quantile(macro$trade, 0.8))
x.low <- setx(z.out1, trade = quantile(macro$trade, 0.2))
```

Generate first differences for the effect of high versus low trade on GDP:

```
s.out1 <- sim(z.out1, x = x.high, x1 = x.low)
```

```
summary(s.out1)
```

```
plot(s.out1)
```

1. Using Dummy Variables

Estimate a model with fixed effects for each country (see for help with dummy variables). Note that you do not need to create dummy variables, as the program will automatically parse the unique values in the selected variable into discrete levels.

```
z.out2 <- zelig(unem ~ gdp + trade + capmob + as.factor(country), +
model = "ls", data = macro)
```

Set values for the explanatory variables, using the default mean/mode values, with country set to the United States and Japan, respectively:

```
x.US <- setx(z.out2, country = "United States")
x.Japan <- setx(z.out2, country = "Japan")
```

Simulate quantities of interest:

```
s.out2 <- sim(z.out2, x = x.US, x1 = x.Japan)

plot(s.out2)
```

Model

- The *stochastic component* is described by a density with mean μ_i and the common variance σ^2

$$Y_i \sim f(y_i | \mu_i, \sigma^2).$$

- The *systematic component* models the conditional mean as

$$\mu_i = x_i \beta$$

where x_i is the vector of covariates, and β is the vector of coefficients.

The least squares estimator is the best linear predictor of a dependent variable given x_i , and minimizes the sum of squared residuals, $\sum_{i=1}^n (Y_i - x_i \beta)^2$.

Quantities of Interest

- The expected value (qi\$ev) is the mean of simulations from the stochastic component,

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

given a draw of β from its sampling distribution.

- 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 $t_i = 0$.

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 = ls, 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`: fitted values.
 - `df.residual`: the residual degrees of freedom.
 - `zelig.data`: the input data frame if `save.data = TRUE`.

- From `summary(z.out)`, you may extract:
 - coefficients: the parameter estimates with their associated standard errors, p -values, and t -statistics.

$$\hat{\beta} = \left(\sum_{i=1}^n x_i' x_i \right)^{-1} \sum x_i y_i$$

- sigma: the square root of the estimate variance of the random error e :

$$\hat{\sigma} = \frac{\sum (Y_i - x_i \hat{\beta})^2}{n - k}$$

- r.squared: the fraction of the variance explained by the model.

$$R^2 = 1 - \frac{\sum (Y_i - x_i \hat{\beta})^2}{\sum (y_i - \bar{y})^2}$$

- adj.r.squared: the above R^2 statistic, penalizing for an increased number of explanatory variables.
- 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 x-observation (for more than one x-observation). Available quantities are:
 - `qi$ev`: the simulated expected values for the specified values of x .
 - `qi$fd`: the simulated first differences (or differences in expected values) for the specified values of x and $x1$.
 - `qi$att.ev`: the simulated average expected treatment effect for the treated from conditional prediction models.

See also

The least squares regression is part of the `stats` package by William N. Venables and Brian D. Ripley. In addition, advanced users may wish to refer to `help(lm)` and `help(lm.fit)`.

1.2.7 zelig-negbin

Negative Binomial Regression for Event Count Dependent Variables

Use the negative binomial regression if you have a count of events for each observation of your dependent variable. The negative binomial model is frequently used to estimate over-dispersed event count models.

Syntax

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

Example

Load sample data:

```
data(sanction)
```

Estimate the model:

```
z.out <- zelig(num    target + coop, model = "negbin", data = sanction)
```

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

Set values for the explanatory variables to their default mean values:

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

Simulate fitted values:

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

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

```
plot(s.out)
```

Model

Let Y_i be the number of independent events that occur during a fixed time period. This variable can take any non-negative integer value.

- The negative binomial distribution is derived by letting the mean of the Poisson distribution vary according to a fixed parameter ζ given by the Gamma distribution. The *stochastic component* is given by

$$\begin{aligned} Y_i \mid \zeta_i &\sim \text{Poisson}(\zeta_i \mu_i), \\ \zeta_i &\sim \frac{1}{\theta} \text{Gamma}(\theta). \end{aligned}$$

The marginal distribution of Y_i is then the negative binomial with mean μ_i and variance $\mu_i + \mu_i^2/\theta$:

$$\begin{aligned} Y_i &\sim \text{NegBin}(\mu_i, \theta), \\ &= \frac{\Gamma(\theta + y_i)}{y! \Gamma(\theta)} \frac{\mu_i^{y_i} \theta^\theta}{(\mu_i + \theta)^{\theta + y_i}}, \end{aligned}$$

where θ is the systematic parameter of the Gamma distribution modeling ζ_i .

- The *systematic component* is given by

$$\mu_i = \exp(x_i \beta)$$

where x_i is the vector of k explanatory variables and β is the vector of coefficients.

Quantities of Interest

- The expected values (qi\$ev) are simulations of the mean of the stochastic component. Thus,

$$E(Y) = \mu_i = \exp(x_i \beta),$$

given simulations of β .

- The predicted value (qi\$pr) drawn from the distribution defined by the set of parameters (μ_i, θ) .
- The first difference (qi\$fd) is

$$FD = E(Y|x_1) - E(Y | x)$$

- 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

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

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 $Y_i(\widehat{t_i = 0})$, 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 = negbin, 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)`.

See also

The negative binomial model is part of the MASS package by William N. Venable and Brian D. Ripley . Advanced users may wish to refer to “`help(glm.nb)`”.

1.2.8 zelig-normal

Normal Regression for Continuous Dependent Variables

The Normal regression model is a close variant of the more standard least squares regression model (see). Both models specify a continuous dependent variable as a linear function of a set of explanatory variables. The Normal model reports maximum likelihood (rather than least squares) estimates. The two models differ only in their estimate for the stochastic parameter σ .

Syntax

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

Examples

1. Basic Example with First Differences

Attach sample data:

```
data(macro)
```

Estimate model:

```
z.out1 <- zelig(unem ~ gdp + capmob + trade, model = "normal", data = macro)
```

Summarize of regression coefficients:

```
summary(z.out1)
```

Set explanatory variables to their default (mean/mode) values, with high (80th percentile) and low (20th percentile) values for trade:

```
x.high <- setx(z.out1, trade = quantile(macro$trade, 0.8))
x.low <- setx(z.out1, trade = quantile(macro$trade, 0.2))
```

Generate first differences for the effect of high versus low trade on GDP:

```
s.out1 <- sim(z.out1, x = x.high, x1 = x.low)
```

```
summary(s.out1)
```

A visual summary of quantities of interest:

```
plot(s.out1)
```

Model

Let Y_i be the continuous dependent variable for observation i .

- The *stochastic component* is described by a univariate normal model with a vector of means μ_i and scalar variance σ^2 :

$$Y_i \sim \text{Normal}(\mu_i, \sigma^2).$$

- The *systematic component* is

$$\mu_i = x_i\beta,$$

where x_i is the vector of k explanatory variables and β is the vector of coefficients.

Quantities of Interest

- The expected value (qi\$ev) is the mean of simulations from the the stochastic component,

$$E(Y) = \mu_i = x_i\beta,$$

given a draw of β from its posterior.

- The predicted value (`qi$pr`) is drawn from the distribution defined by the set of parameters (μ_i, σ) .
- The first difference (`qi$fd`) is:

$$FD = E(Y | x_1) - E(Y | x)$$

- 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

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

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 $\widehat{Y_i(t_i = 0)}$, 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 = normal, 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)`.

See also

The normal model is part of the stats package by . Advanced users may wish to refer to `help(glm)` and `help(family)`.

1.2.9 zelig-poisson

Poisson Regression for Event Count Dependent Variables

Use the Poisson regression model if the observations of your dependent variable represents the number of independent events that occur during a fixed period of time (see the negative binomial model, , for over-dispersed event counts.) For a Bayesian implementation of this model, see .

Syntax

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


Example

Load sample data:

```
data(sanction)
```

Estimate Poisson model:

```
z.out <- zelig(num    target + coop, model = "poisson", data =
sanction)
```

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

Set values for the explanatory variables to their default mean values:

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

Simulate fitted values:

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

Model

Let Y_i be the number of independent events that occur during a fixed time period. This variable can take any non-negative integer.

- The Poisson distribution has *stochastic component*

$$Y_i \sim \text{Poisson}(\lambda_i),$$

where λ_i is the mean and variance parameter.

- The *systematic component* is

$$\lambda_i = \exp(x_i\beta),$$

where x_i is the vector of explanatory variables, and β is the vector of coefficients.

Quantities of Interest

- The expected value (qi\$ev) is the mean of simulations from the stochastic component,

$$E(Y) = \lambda_i = \exp(x_i\beta),$$

given draws of β from its sampling distribution.

- The predicted value (qi\$pr) is a random draw from the poisson distribution defined by mean λ_i .
- The first difference in the expected values (qi\$fd) is given by:

$$\text{FD} = E(Y|x_1) - E(Y|x)$$

- 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 = poisson, 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)`.

See also

The `poisson` model is part of the `stats` package by . Advanced users may wish to refer to `help(glm)` and `help(family)`.

1.2.10 zelig-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.

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)
```

Example

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

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

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 $Y_i(\widehat{t_i = 0})$, 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)`.

See also

The probit model is part of the stats package by . Advanced users may wish to refer to `help(glm)` and `help(family)`.

1.2.11 zelig-relogit

Rare Events Logistic Regression for Dichotomous Dependent Variables

The relogit procedure estimates the same model as standard logistic regression (appropriate when you have a dichotomous dependent variable and a set of explanatory variables; see), but the estimates are corrected for the bias that occurs when the sample is small or the observed events are rare (i.e., if the dependent variable has many more 1s than 0s or the reverse). The relogit procedure also optionally uses prior correction for case-control sampling designs.

Syntax

```
z.out <- zelig(Y ~ X1 + X2, model = "relogit", tau = NULL,
             case.control = c("prior", "weighting"),
             bias.correct = TRUE, robust = FALSE,
             data = mydata, ...)
x.out <- setx(z.out)
s.out <- sim(z.out, x = x.out)
```

Arguments

The relogit procedure supports four optional arguments in addition to the standard arguments for `zelig()`. You may additionally use:

- `tau`: a vector containing either one or two values for τ , the true population fraction of ones. Use, for example, `tau = c(0.05, 0.1)` to specify that the lower bound on τ is 0.05 and the upper bound is 0.1. If left unspecified, only finite-sample bias correction is performed, not case-control correction.

- `case.control`: if `tau` is specified, choose a method to correct for case-control sampling design: “prior” (default) or “weighting”.
- `bias.correct`: a logical value of TRUE (default) or FALSE indicating whether the intercept should be corrected for finite sample (rare events) bias.
- `robust`: defaults to FALSE (except when `case.control` = “weighting”; the default in this case becomes `robust` = TRUE). 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.

Note that if `tau` = NULL, `bias.correct` = FALSE, the `relogit` procedure performs a standard logistic regression without any correction.

Example 1: One Tau with Prior Correction and Bias Correction

Due to memory and space considerations, the data used here are a sample drawn from the full data set used in King and Zeng, 2001, The proportion of militarized interstate conflicts to the absence of disputes is $\tau = 1,042/303,772 \approx 0.00343$. To estimate the model,

```
data(mid)
```

```
z.out1 <- zelig(conflict ~ major + contig + power + maxdem + mindem + years, + data = mid, model = "relogit")
```

Summarize the model output:

```
summary(z.out1)
```

Set the explanatory variables to their means:

```
x.out1 <- setx(z.out1)
```

Simulate quantities of interest:

```
s.out1 <- sim(z.out1, x = x.out1) RRR> summary(s.out1)
```

```
plot(s.out1)
```

Example 2: One Tau with Weighting, Robust Standard Errors, and Bias Correction

Suppose that we wish to perform case control correction using weighting (rather than the default prior correction). To estimate the model:

```
z.out2 <- zelig(conflict ~ major + contig + power + maxdem + mindem + years, + data = mid, model = "relogit", tau = 1042/303772, + case.control = "weighting", robust = TRUE)
```

Summarize the model output:

```
summary(z.out2)
```

Set the explanatory variables to their means:

```
x.out2 <- setx(z.out2)
```

Simulate quantities of interest:

```
s.out2 <- sim(z.out2, x = x.out2)
summary(s.out2)
```

Example 3: Two Taus with Bias Correction and Prior Correction

Suppose that we did not know that $\tau \approx 0.00343$, but only that it was somewhere between (0.002, 0.005). To estimate a model with a range of feasible estimates for τ (using the default prior correction method for case control correction):

```
z.out2 <- zelig(conflict major + contig + power + maxdem + mindem
+ + years, data = mid, model = "relogit", + tau = c(0.002, 0.005))
```

Summarize the model output:

```
summary(z.out2)
```

Set the explanatory variables to their means:

```
x.out2 <- setx(z.out2)
```

Simulate quantities of interest:

```
s.out <- sim(z.out2, x = x.out2)
```

```
summary(s.out2)
```

```
plot(s.out2)
```

The cost of giving a range of values for τ is that point estimates are not available for quantities of interest. Instead, quantities are presented as confidence intervals with significance less than or equal to a specified level (e.g., at least 95% of the simulations are contained in the nominal 95% confidence interval).

Model

- Like the standard logistic regression, the *stochastic component* for the rare events logistic regression is:

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

where Y_i is the binary dependent variable, and takes a value of either 0 or 1.

- The *systematic component* is:

$$\pi_i = \frac{1}{1 + \exp(-x_i\beta)}.$$

- If the sample is generated via a case-control (or choice-based) design, such as when drawing all events (or “cases”) and a sample from the non-events (or “controls”) and going backwards to collect the explanatory variables, you must correct for selecting on the dependent variable. While the slope coefficients are approximately unbiased, the constant term may be significantly biased. Zelig has two methods for case control correction:

1. The “prior correction” method adjusts the intercept term. Let τ be the true population fraction of events, \bar{y} the fraction of events in the sample, and $\hat{\beta}_0$ the uncorrected intercept term. The corrected intercept β_0 is:

$$\beta = \hat{\beta}_0 - \ln \left[\left(\frac{1 - \tau}{\tau} \right) \left(\frac{\bar{y}}{1 - \bar{y}} \right) \right].$$

2. The “weighting” method performs a weighted logistic regression to correct for a case-control sampling design. Let the 1 subscript denote observations for which the dependent variable is observed as a 1, and the 0 subscript denote observations for which the dependent variable is observed as a 0. Then the vector of weights w_i

$$\begin{aligned} w_1 &= \frac{\tau}{\bar{y}} \\ w_0 &= \frac{(1 - \tau)}{(1 - \bar{y})} \\ w_i &= w_1 Y_i + w_0 (1 - Y_i) \end{aligned}$$

If τ is unknown, you may alternatively specify an upper and lower bound for the possible range of τ . In this case, the relogit procedure uses “robust Bayesian” methods to generate a confidence interval (rather than a point estimate) for each quantity of interest. The nominal coverage of the confidence interval is at least as great as the actual coverage.

- By default, estimates of the coefficients β are bias-corrected to account for finite sample or rare events bias. In addition, quantities of interest, such as predicted probabilities, are also corrected of rare-events bias. If $\hat{\beta}$ are the uncorrected logit coefficients and $\text{bias}(\hat{\beta})$ is the bias term, the corrected coefficients $\tilde{\beta}$ are

$$\hat{\beta} - \text{bias}(\hat{\beta}) = \tilde{\beta}$$

The bias term is

$$\text{bias}(\hat{\beta}) = (X'WX)^{-1}X'W\xi$$

where

$$\begin{aligned} \xi_i &= 0.5Q_{ii}((1 + w - 1)\hat{\pi}_i - w_1) \\ Q &= X(X'WX)^{-1}X' \\ W &= \text{diag}\{\hat{\pi}_i(1 - \hat{\pi}_i)w_i\} \end{aligned}$$

where w_i and w_1 are given in the “weighting” section above.

Quantities of Interest

- For either one or no τ :
 - The expected values (qi\$ev) for the rare events logit are simulations of the predicted probability

$$E(Y) = \pi_i = \frac{1}{1 + \exp(-x_i\beta)},$$

given draws of β from its posterior.

- The predicted value (qi\$pr) is a draw from a binomial distribution with mean equal to the simulated π_i .
- The first difference (qi\$fd) is defined as

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

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

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

- For a range of τ defined by $[\tau_1, \tau_2]$, each of the quantities of interest are $n \times 2$ matrices, which report the lower and upper bounds, respectively, for a confidence interval with nominal coverage at least as great as the actual coverage. At worst, these bounds are conservative estimates for the likely range for each quantity of interest. Please refer to for the specific method of calculating bounded quantities of interest.
- 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

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

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 $\widehat{Y_i(t_i = 0)}$, 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 = relogit, 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)`.

Differences with Stata Version

The Stata version of ReLogit and the R implementation differ slightly in their coefficient estimates due to differences in the matrix inversion routines implemented in R and Stata. Zelig uses orthogonal-triangular decomposition (through `lm.influence()`) to compute the bias term, which is more numerically stable than standard matrix calculations.

See also

1.2.12 zelig-tobit

Linear Regression for a Left-Censored Dependent Variable

Tobit regression estimates a linear regression model for a left-censored dependent variable, where the dependent variable is censored from below. While the classical tobit model has values censored at 0, you may select another censoring point. For other linear regression models with fully observed dependent variables, see Bayesian regression (), maximum likelihood normal regression (), or least squares ().

Syntax

```
> z.out <- zelig(Y ~ X1 + X2, below = 0, above = Inf,
               model = "tobit", data = mydata)
> x.out <- setx(z.out)
> s.out <- sim(z.out, x = x.out)
```

Inputs

`zelig()` accepts the following arguments to specify how the dependent variable is censored.

- `below`: (defaults to 0) The point at which the dependent variable is censored from below. If any values in the dependent variable are observed to be less than the censoring point, it is assumed that that particular observation is censored from below at the observed value. (See for a Bayesian implementation that supports both left and right censoring.)
- `robust`: defaults to `FALSE`. If `TRUE`, `zelig()` computes robust standard errors based on sandwich estimators (see [and](#)) and the options selected in `cluster`.
- `cluster`: if `robust = TRUE`, you may select a variable to define groups of correlated observations. Let `x3` be a variable that consists of either discrete numeric values, character strings, or factors that define strata. Then

```
> z.out <- zelig(y ~ x1 + x2, robust = TRUE, cluster = "x3",
               model = "tobit", data = mydata)
```

means that the observations can be correlated within the strata defined by the variable `x3`, and that robust standard errors should be calculated according to those clusters. If `robust = TRUE` but `cluster` is not specified, `zelig()` assumes that each observation falls into its own cluster.

Zelig users may wish to refer to `help(survreg)` for more information.

Examples

1. Basic Example

Attaching the sample dataset:

```
data(tobin)
```

Estimating linear regression using `tobit`:

```
z.out <- zelig(durable ~ age + quant, model = "tobit", data = tobin)
```

Setting values for the explanatory variables to their sample averages:

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

Simulating quantities of interest from the posterior distribution given `x.out`.

```
s.out1 <- sim(z.out, x = x.out)
```

```
summary(s.out1)
```

1. Simulating First Differences

Set explanatory variables to their default(mean/mode) values, with

high (80th percentile) and low (20th percentile) liquidity ratio (`quant`):

```
x.high <- setx(z.out, quant = quantile(tobin\` :math:`quant, prob = 0.8))
x.low <- setx(z.out, quant = quantile(tobin\` quant, prob = 0.2))
```

Estimating the first difference for the effect of high versus low liquidity ratio on duration(durable):

```
s.out2 <- sim(z.out, x = x.high, x1 = x.low)

summary(s.out2)
```

Model

- Let Y_i^* be a latent dependent variable which is distributed with *stochastic* component

$$Y_i^* \sim \text{Normal}(\mu_i, \sigma^2)$$

where μ_i is a vector means and σ^2 is a scalar variance parameter. Y_i^* is not directly observed, however. Rather we observed Y_i which is defined as:

$$Y_i = \begin{cases} Y_i^* & \text{if } c < Y_i^* \\ c & \text{if } c \geq Y_i^* \end{cases}$$

where c is the lower bound below which Y_i^* is censored.

- The *systematic component* is given by

$$\mu_i = x_i \beta,$$

where x_i is the vector of k explanatory variables for observation i and β is the vector of coefficients.

Quantities of Interest

- The expected values (`qi$ev`) for the tobit regression model are the same as the expected value of Y^* :

$$E(Y^*|X) = \mu_i = x_i \beta$$

- The first difference (`qi$fd`) for the tobit regression model is defined as

$$\text{FD} = E(Y^* | x_1) - E(Y^* | x).$$

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

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

where t_i is a binary explanatory variable defining the treatment ($t_i = 1$) and control ($t_i = 0$) groups.

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 = "tobit", data)
```

then you may examine the available information in “`z.out`”.

See also

The tobit function is part of the survival library by Terry Therneau, ported to R by Thomas Lumley. Advanced users may wish to refer to `help(survfit)` in the survival library.

1.3 Frequently Asked Questions

If you find a bug, or cannot figure something out after reading through the FAQs below, please send your question to the Zelig listserv at: <https://groups.google.com/forum/#!forum/zelig-statistical-software>. Please explain exactly what you did and include the full error message, including the traceback(). You should get an answer from the developers or another user in short order.

1.3.1 How do I cite Zelig?

We would appreciate if you would cite Zelig as:

Imai, Kosuke, Gary King and Olivia Lau. 2006. “Zelig: Everyone’s Statistical Software,”
<http://GKing.Harvard.Edu/zelig>.

Please also cite the contributors for the models or methods you are using. These citations can be found in each individual model’s vignette which can be found in the the *vignettes*:

1.3.2 Why can’t I install Zelig?

We recommend that you first check your internet connection, as you must be connected to install packages. In addition, there are a few platform-specific reasons why you may be having installation problems:

- **On Windows:** If you are using the very latest version of R, you may not be able to install Zelig until we update Zelig to work with this latest release. Currently Zelig 5.0.1 is compatible with R(3.0.2). If you wish to install Zelig in the interim, install the appropriate version of R and try to reinstall Zelig.
- **On Mac or Linux systems:** If you get the following warning message at the end of your installation:

```
> Installation of package VGAM had non-zero exit status in ...
```

this means that you were not able to install VGAM properly. Make sure that you have the g77 Fortran compiler. For Intel Macs, download the Apple developer tools. After installation, try to install Zelig again.

If neither solution works, feel free email the Zelig mailing list directly at: <https://groups.google.com/forum/#!forum/zelig-statistical-software>.

1.3.3 Why can’t I install R?

If you have problems installing R, you should search the internet for the R help mailing list, check out technical Q & A forums (e.g., StackOverflow), or email the Zelig mailing list directly at: <https://groups.google.com/forum/#!forum/zelig-statistical-software>.

1.3.4 Why can't I load data?

It is likely that the reason you are unable to load data because you have not specified the correct working directory (e.g., the location of the data you are trying to load). You should specify your working directory using the `setwd()` function in which you will include the file path to your working director. For example, if I wanted to load a file that is my *Documents* folder, I must first:

```
> setwd("path/to/Documents")
```

File paths can be found by right clicking the working directory folder in any file browser and clicking “Get Info” (on Mac) or “Properties” (on Windows). Black-slashes (\) in file paths copied from the “Properties” link on Windows machines must be replaced with forward-slashes (/). For example, the Windows path: `C:\Program Files\R`, would be typed as `C:/Program Files/R`.

1.3.5 How do I increase the memory for R?

Windows users may get the error that R has run out of memory. If you've installed more memory on your machine, you may have to reinstall R in order to take advantage of the additional capacity.

You may also set the amount of available memory manually. Close R, then right-click on your R program icon (the icon on your desktop or in your programs directory). Select “Properties”, and then select the “Shortcut” tab. Look for the “Target” field and after the closing quotes around the location of the R executable, add

```
--max-mem-size=500M
```

You may increase this value up to 2GB or the maximum amount of physical RAM you have installed. If you get the error that R cannot allocate a vector of length x, close out of R and add the following line to the “Target” field:

```
--max-vsize=500M
```

or as appropriate.

You can always check to see how much memory R has available by typing at the R prompt

```
> round(memory.limit()/2^20, 2)
```

which gives you the amount of available memory in MB.

1.3.6 Why doesn't the pdf print properly?

Zelig uses several special LaTeX environments. If the pdf looks right on the screen, there are two possible reasons why it's not printing properly:

- Adobe Acrobat isn't cleaning up the document. Updating to Acrobat Reader 6.0.1 or higher should solve this problem.
 - Your printer doesn't support PostScript Type 3 fonts. Updating your print driver should take care of this problem.
-

1.3.7 R is neat. How can I find out more?

R is a collective project with contributors from all over the world. Their website (r-project.org) has more information on the R project, R packages, conferences, and other learning material.

1.4 About Zelig

Zelig is an open source project development and maintained by the Data Science group at the [Data Science group](#) at Harvard's Institute for Quantitative Social Science (IQSS). It was originally conceived and created by Kosuke Imai, Gary King, and Olivia Lau in 2007. The name is borrowed from Woody Allen's movie with the same name, Zelig. Leonard Zelig is a fictional character who takes on the characteristics of any strong personality around. Likewise, the Zelig statistical software easily adapts to any statistical model written in R, and in essence, takes the characteristics of any model.

It leverages (R) code from many researchers and is designed to allow anyone to contribute their methods to it. Hence, we often refer to Zelig as “everyone’s statistical software” and our aim is to make it, as well as the models it wraps, as accessible as possible. As such, Zelig comes with self-contained documentation that minimizes startup costs, automates model summaries and graphics, and bridges existing R implementations through an intelligible call structure.

License: GPL-2 | GPL-3 [expanded from: GPL (2)]

Contact: For questions, please join the Zelig mailing list: <https://groups.google.com/forum/#!forum/zelig-statistical-software>

The Zelig Team:

- Gary King (*Principle Investigator*)
- James Honaker (*Project Lead*)
- Christine Choirat (*Lead Author*)
- Kosuke Imai
- Olivia Lau
- Muhammed Y. Idris

1.4.1 Technical Vision

Zelig is a framework for interfacing a wide range of statistical models and analytic methods in a common and simple way. Above and beyond estimation, Zelig adds considerable infrastructure to existing heterogeneous R implementations by translating hard-to-interpret coefficients into quantities of interest (e.g., expected and predicted values) through a simple call structure. This includes many specific methods, based on likelihood, frequentist, Bayesian, robust Bayesian and nonparametric theories of inference. Developers are encouraged to add their R packages to the Zelig toolkit by writing a few simple bridge functions.

Additional features include:

- Dealing with missing data by combining multiply imputed datasets
- Automating statistical bootstrapping
- Improving parametric procedures by leveraging nonparametric matching methods
- Evaluating counterfactuals
- Allowing conditional population and super population inferences
- Automating the creation of replication data files

1.4.2 Release Notes

v 5.0.1

This release expands the set of models available, while simplifying the model wrapping process, and solving architectural problems by completely rewriting into R's Reference Classes for a fully object-oriented architecture.