0.1 `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 $1, \ldots, n$, 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 log-normal regression:

- `robust`: defaults to `FALSE`. If `TRUE`, `zelig()` computes robust standard errors based on sandwich estimators (see **?**) and **?**)) 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:

```
> z.out <- zelig(Surv(duration, ciep12) ~ 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:

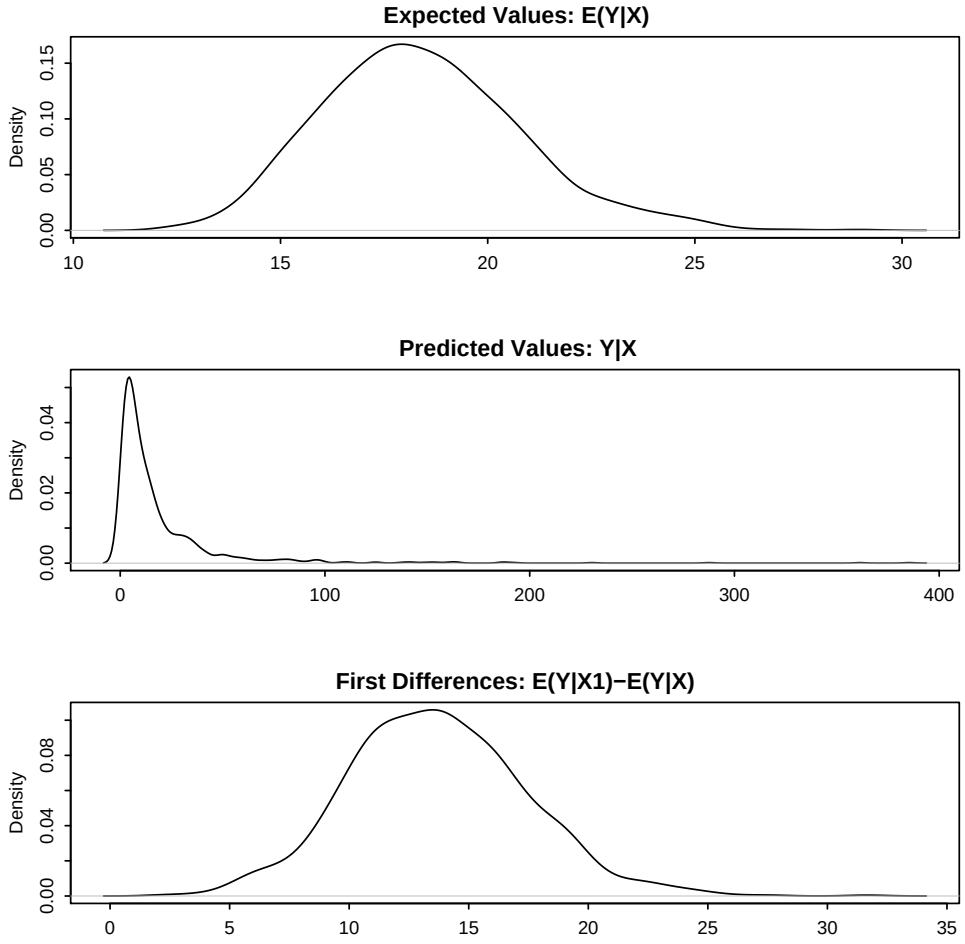
```
> x.low <- setx(z.out, numst2 = 0)
> x.high <- setx(z.out, numst2 = 1)
```

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:

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

  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`$= \sigma$.)

  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 $S(t) = 1 - \int_0^t f(s)ds$ 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

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

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

Contributors

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

.

Sample data are from

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