

## 0.1 weibull: Weibull Regression for Duration Dependent Variables

Choose the Weibull regression model if the values in your dependent variable are duration observations. The Weibull model relaxes the exponential model's (see Section ??) assumption of constant hazard, and allows the hazard rate to increase or decrease monotonically with respect to elapsed time.

### Syntax

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

Weibull 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). 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 weibull 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, ciepl2) ~ fract + numst2, model = "weibull",  
+ 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:

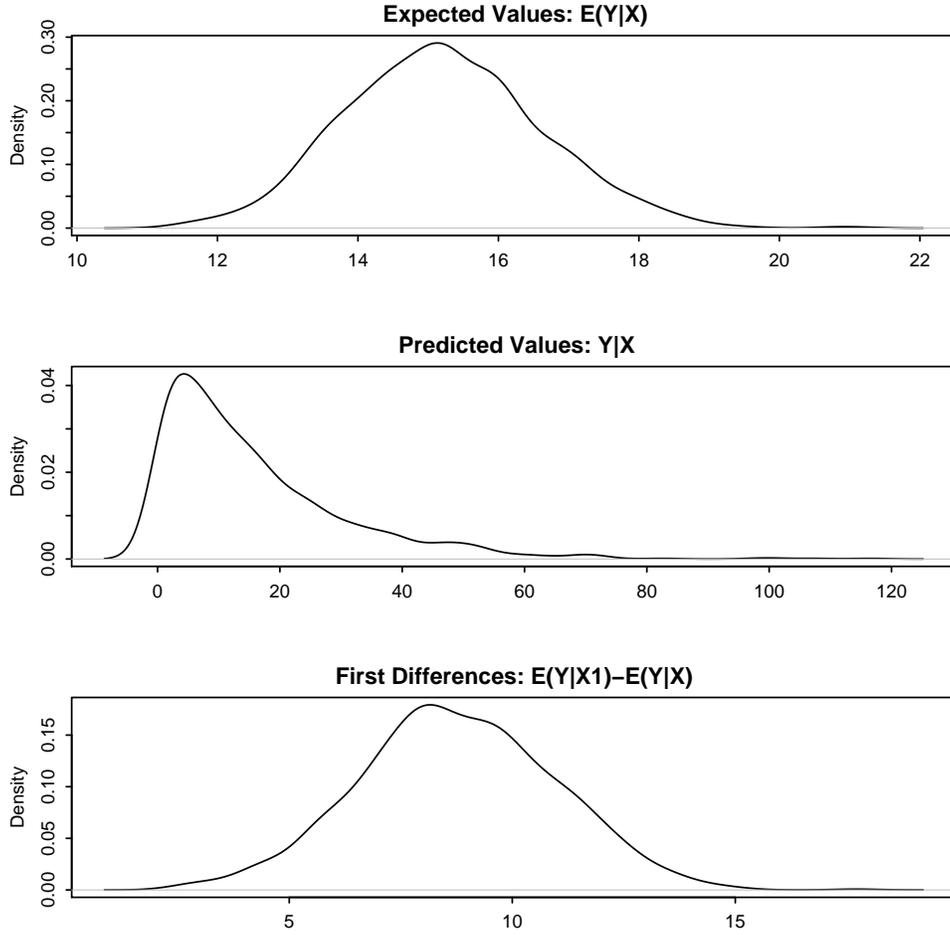
```
> x.low <- setx(z.out, numst2 = 0)  
> x.high <- setx(z.out, numst2 = 1)
```

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  $i$ . 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 Weibull distribution whose density function is given by

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

for  $y_i^* \geq 0$ , the scale parameter  $\lambda_i > 0$ , and the shape parameter  $\alpha > 0$ . The mean of this distribution is  $\lambda_i \Gamma(1 + 1/\alpha)$ . When  $\alpha = 1$ , the distribution reduces to the exponential distribution (see Section ??). (Note that the output from `zelig()` parameterizes `scale=1/\alpha`.)

In addition, survival models like the Weibull 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 Weibull model,

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

For the Weibull model, the hazard function  $h(t)$  can increase or decrease monotonically over time.

- The *systematic component*  $\lambda_i$  is modeled as

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

where  $x_i$  is the vector of explanatory variables, and  $\beta$  is the vector of coefficients.

### Quantities of Interest

- The expected values (**qi\$ev**) for the Weibull model are simulations of the expected duration:

$$E(Y) = \lambda_i \Gamma(1 + \alpha^{-1}),$$

given draws of  $\beta$  and  $\alpha$  from their sampling distributions.

- The predicted value (**qi\$pr**) is drawn from a distribution defined by  $(\lambda_i, \alpha)$ .
- The first difference (**qi\$fd**) in expected value 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. 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 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. 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 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 = "weibull", 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 “scale” parameter  $1/\alpha$ .
  - `var`: the variance-covariance matrix.
  - `loglik`: a vector containing the log-likelihood for the model and intercept only (respectively).
  - `linear.predictors`: a vector of the  $x_i\beta$ .
  - `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  $\times$   $\mathbf{x}$ -observation (for more than one  $\mathbf{x}$ -observation). Available quantities are:
  - `qi$ev`: the simulated expected values for the specified values of  $\mathbf{x}$ .
  - `qi$pr`: the simulated predicted values drawn from a distribution defined by  $(\lambda_i, \alpha)$ .
  - `qi$fd`: the simulated first differences between the simulated expected values for  $\mathbf{x}$  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 Weibull model 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, and

Sample data are from

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