

Modeling Censored Immunological Data

Zane Billings, Andreas Handel https://tinyurl.com/hg-cens



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- Limits of Detection/Quantification (LoD/LoQ)
- Binning/discretizing/rounding/etc. a continuous measurement

E.g., HAI titer data for flu research



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 - Frequentist: "tobit" model, survival models in R
 - Bayesian: brms R package makes it easy
- Censored predictors are harder.

Problem: reading stats papers and package documentation is hard/annoying.

(Even for mathematicians/statisticians!)

(Partial) Solution: we're writing a series of tutorials with examples.



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Modeling with Censored Data

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Preface

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- 2 One censored outcome
- 3 One censored predictor

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Modeling with Censored Data

AUTHOR handelgroup

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Preface

This book contains our notes on dealing with censored data, including methods for dealing with both censored outcomes and predictors. Where possible, we try to include both frequentist and Bayesian models.

- The short link to this website is: https://tinyurl.com/hg-cens.
- The full link is currently: https://wzbillings.github.io/Censored-Data-Tutorials/.
- For source code, go here.
- Please submit bug reports, typos, and comments here.

Contributors:

Zane Billings (https://wzbillings.com/)

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2.3 Integration method for censored data \mathscr{S}

We can regain some measure of our lost diginity using the integration trick we discussed in the introduction. Of course, in the introduction, we only talked about adjusting for censoring in the univariate case, but fortunately we are modeling the **conditional distribution of** y so we can use the same trick:

$$egin{aligned} \mathcal{L}\left(heta \mid y_i, x_i
ight) &= f_{Y_i \mid X_i = x_i}(y_i \mid heta, x_i) \ &= \left(f(y_i \mid heta, x)
ight)^{1-c_i} igg(P(Y_i = y_i \mid x)igg)^{c_i} \ &= \left(f(y_i \mid heta, x_i)
ight)^{1-c_i} igg(\int_{-\infty}^{y_{\min}} f(y_i \mid heta, x_i) \ dy_iigg)^{c_i} \ &= \left(f(y_i \mid heta, x_i)
ight)^{1-c_i} igg(F(y_{\min} \mid heta, x_i)igg)^{c_i}. \end{aligned}$$

The likelihood for y_i is easy to write out here since the censoring structure is (relatively) simple. This gives rise to the likelihood of the sample, which (under the assumption of mutual conditional independence) is

$$\mathcal{L}\left(heta \mid x,y
ight) = \prod_{i=1}^{n} \mathcal{L}\left(heta \mid y_{i},x_{i}
ight).$$

```
# First we have to transform the outcome
surv model <- survival::survreg(</pre>
    # Creating the "survival time" outcome
    survival::Surv(
        # If the value is lower than LoD, replace it w/ LoD, then take the
        pmax(y, LoD) |> log(),
        # The censoring indicator needs to be the opposite of what makes
        # zero for censored, one for uncensored -- it's actually an indic
        # an "event" occurring, for us this is the event
        # "getting a reliable measurement."
        !c,
        # Specify left censoring
        type = 'left'
    )~
        # All the other linear model stuff as usual
        dist_from_farm + personal_gly_use + water_filter_use,
    data = gly_data_obs,
    dist = "gaussian"
```

```
tobit_model <- AER::tobit(
    log(y) ~ dist_from_farm + personal_gly_use + water_filter_use,
    data = gly_data_obs,
    left = log(LoD),
    right = Inf.</pre>
```

Explanation + code examples!

Conclusions and future work

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- Our tutorials for censored data analysis are available free and online.
- They're still under construction though!
- Models for censored outcomes are more straightforward, but we're still experimenting with the best methods for censored predictors.



Thank you! https://tinyurl.com/hg-cens