Ordinal Regression Diagnostics in R: An Introduction to the ordr package

by Brandon M. Greenwell, Author Two and Author Three

Abstract An abstract of less than 150 words.

Introduction

Coming soon!

Ordinal regression (OR) models...

Ordinal regression

Coming soon!

- Provide brief background on OR models.
- Provide brief background on relevant packages.

Li-Shepherd residuals

Coming soon! These are available in package **rms**.

Surrogate-based residuals

Coming soon!

Graphical properties

Coming soon!

Residual-based OR diagnostics in R

Coming soon!

```
library(MASS)
houses.polr <- polr(Sat ~ Infl + Type + Cont, weights = Freq, data = housing)
```

Talk about model.

```
res <- resids(houses.polr)
```

Drawing multiple samples

```
res <- resids(houses.polr, nsim = 50)
```

Detecting heteroscedasticty

For this example, we generated $n = 2000$ observations from the following ordered probit model:

$$Pr\left\{\mathcal{Y} \leq j\right\} = \Phi\left\{\left(\alpha_j + \beta X\right)/\sigma_X\right\}, \quad j = 1, 2, 3, 4, 5,$$

where $\alpha_1 = -36$, $\alpha_2 = -6$, $\alpha_3 = 34$, $\alpha_4 = 64$, $\beta = -4$, $X \sim \mathcal{U}(2,7)$, and $\sigma_X = X^2$.

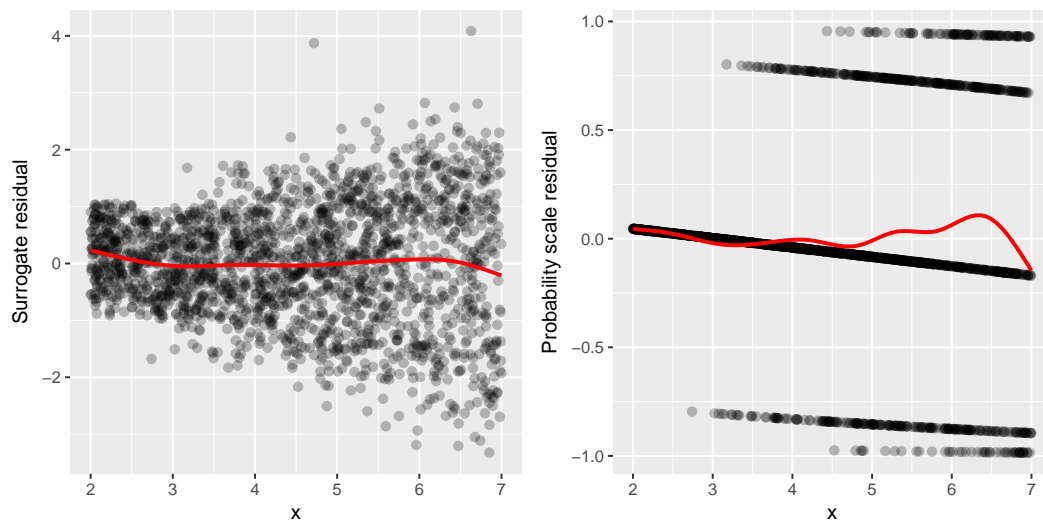The following block of code uses the **MASS** package function `polr` to fit a probit model to the `hd` data.

Figure 1: Residual vs. covariate plots for the simulated heteroscedastid data. *Left*: Surrogate residuals. *Right*: Probability scale residuals.

```
library(ggplot2)
library(MASS)
library(ordr)
fit.polr <- polr(y ~ x, data = hd, method = "probit")
set.seed(101)  # for reproducibility
sur.res <- resids(fit.polr)  # surrogate-based residuals

# Figure 1 (left)
ggplot(data.frame(x = hd$x, y = sur.res), aes(x, y)) +
  geom_point(size = 2, alpha = 0.25) +
  geom_smooth(color = "red", se = FALSE) +
  ylab("Surrogate residual")
```

Alternatively, we can plot the residuals directly from the fitted model using the autoplot function:

```
autoplot(fit.polr, what = "covariate", x = hd$x)  # plot not shown
```

We can also easily obtain and plot the standard Li-Shepherd residuals against x using the **PResiduals** package function presid:

```
library(PResiduals)
ls.res <- presid(fit.polr)  # probability scale residuals

# Figure 1 (right)
ggplot(data.frame(x = hd$x, y = ls.res), aes(x, y)) +
  geom_point(size = 2, alpha = 0.25) +
  geom_smooth(color = "red", se = FALSE) +
  ylab("Probability scale residual")
```

Detecting a misspecified mean structure

Coming soon!

Detecting a misspecified link function

Coming soon!

Checking the proportionality assumption

Coming soon!

Assessing goodness-of-fit

Coming soon!

```
plot(gof(houses.polr, nsim = 1000))
```

Summary

This file is only a basic article template. For full details of *The R Journal* style and information on how to prepare your article for submission, see the Instructions for Authors.

Acknowledgments

TBD.

Bibliography

Author One
Affiliation
Address
Country
(ORCiD if desired)
author1@work

Author Two
Affiliation
Address
Country
(ORCiD if desired)
author2@work

Author Three
Affiliation
Address
Country
(ORCiD if desired)
author3@work