polr

- In this section we will use the polr command (from the MASS package) to estimate an ordered logistic regression model.
- The command name comes from proportional odds logistic regression, due to the the proportional odds assumption in the model.

polr

- polr uses the standard formula interface in R for specifying a regression model with outcome followed by predictors.
- We will also specify Hess=TRUE to have the model return the observed information matrix from optimization (called the Hessian) which is used to get standard errors.

```
## fit ordered logit model and store results 'm'
m <- polr(apply ~ pared +
          public + gpa, data = dat, Hess=TRUE)
## view a summary of the model
summary(m)
## Call:
## polr(formula = apply ~ pared +
             public + gpa, data = dat, Hess = TRUE)
```

Coefficients:

```
Value Std. Error t value
pared 1.0477 0.266 3.942
public -0.0588 0.298 -0.197
gpa 0.6159 0.261 2.363
```

Intercepts:

	Value	Std. Error	t value
unlikely somewhat likely	2.204	0.780	2.827
somewhat likely very likely	4.299	0.804	5.345

- 1 The "Call", what type of model we ran, what options we specified, etc.
- 2 The usual regression output coefficient table including the value of each coefficient, standard errors, and t-value, which is simply the ratio of the coefficient to its standard error. (Remark: There is no significance test by
 - default.)

- 3 We then have the estimates for the two intercepts, which are sometimes called cutpoints.
- 4 The intercepts indicate where the latent variable is cut to make the three groups that we observe in our data.

- Note that this latent variable is continuous. In general, these are not used in the interpretation of the results.
- The cutpoints are closely related to thresholds, which are reported by other statistical packages.

- ► Finally, we see the residual deviance, -2 * Log Likelihood of the model as well as the AIC.
- Both the deviance and AIC are useful for model comparison.
- Some people are not satisfied without a p−value.
- One way to calculate a p-value in this case is by comparing the t-value against the standard normal distribution, like a z-test.

- Of course this is only true with infinite degrees of freedom, but is reasonably approximated by large samples, becoming increasingly biased as sample size decreases.
- First we store the coefficient table, then calculate the p-values and combine back with the table.

```
# store table
(ctable <- coef(summary(m)))</pre>
                                Value Std. Error t value
pared
                              1.04769
                                           0.2658 3.9418
public
                             -0.05879
                                           0.2979 - 0.1974
                              0.61594
                                           0.2606 2.3632
gpa
 unlikely|somewhat likely
                              2.20391
                                           0.7795 2.8272
 somewhat likely very likely
                              4.29936
                                           0.8043 5.3453
```

```
# calculate and store p values
p <- pnorm(abs(ctable[, "t value"]),</pre>
     lower.tail = FALSE) * 2
# Combined table
(ctable <- cbind(ctable, "p value" = p))</pre>
                     Value Std. Error t value
                                                p value
pared
                   1.04769
                               0.2658 3.9418 8.087e-05
                  -0.05879
                               0.2979 -0.1974 8.435e-01
public
                   0.61594
                               0.2606 2.3632 1.812e-02
gpa
unli...lsome...
                 2.20391 0.7795 2.8272 4.696e-03
               4.29936 0.8043 5.3453 9.027e-08
 some.. | very..
```