What is Probit regression and how is it used in R for data analysis?

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June 29, 2024

Probit regression is a statistical method used to analyze the relationship between a binary response variable and one or more independent variables. It is commonly used for data analysis in situations where the dependent variable can only take two possible values, such as yes or no, success or failure, etc.

In R, probit regression is implemented through the "glm" function, which stands for generalized linear model. This function allows users to specify the type of model they want to run, including probit regression, and provides output in the form of coefficients and p-values to assess the significance of the independent variables.

Probit regression is particularly useful in analyzing data where the response variable follows a normal distribution, as it provides a more accurate estimation of the relationship between the variables compared to other methods such as logistic regression.

In conclusion, probit regression is a valuable tool in data analysis, and its implementation in R allows for efficient and accurate modeling of binary response variables.

Probit Regression | R Data Analysis Examples

Probit regression, also called a probit model, is used to model dichotomous or binary outcome variables. In the probit model, the inverse standard normal distribution of the probability is modeled as a linear combination of the predictors.

This page uses the following packages. Make sure that you can load them before trying to run the examples on this page. If you do not have a package installed, run: `install.packages("packagename")`, or

if you see the version is out of date, run: `update.packages()`.

```
require(aod)
require(ggplot2)
```

```
Version info: Code for this page was tested in R Under development (unstable)
(2012-11-16 r61126)
On: 2012-12-15
With: ggplot2 0.9.3; aod 1.3; knitr 0.9
```

Please Note: The purpose of this page is to show how to use various data analysis commands.
It does not cover all aspects of the research process which researchers are expected to do. In particular, it does not cover data cleaning and checking, verification of assumptions, model diagnostics and potential follow-up analyses.

Examples

Example 1: Suppose that we are interested in the factors that influence whether a political candidate wins an election. The outcome (response) variable is binary (0/1); win or lose. The predictor variables of interest are the amount of money spent on the campaign, the amount of

time spent campaigning
negatively and whether the candidate is an incumbent.

Example 2: A researcher is interested in how variables, such as GRE (Graduate Record Exam scores), GPA (grade point average) and prestige of the undergraduate institution, effect
admission into graduate school. The response variable, admit/don't admit, is a
binary variable.

Description of the Data

For our data analysis below, we are going to expand on Example 2 about getting
into graduate school. We have generated hypothetical data, which
can be obtained from our website in R. Note that *R requires forward slashes*
(*/*) not back slashes (\) when specifying a file location even if the file is
on your hard drive.

```
mydata <-
read.csv("https://stats.idre.ucla.edu/stat/data/binary.csv
```

")

convert rank to a factor (categorical variable)
mydata$rank <- factor(mydata$rank)

view first few rowshead(mydata)

admit gre gpa rank
1 0 380 3.61 3
2 1 660 3.67 3
3 1 800 4.00 1
4 1 640 3.19 4
5 0 520 2.93 4
6 1 760 3.00 2

This data set has a binary response (outcome, dependent) variable called `admit`.
There are three predictor variables: `gre`, `gpa` and `rank`. We will treat the
variables `gre` and `gpa` as continuous. The variable `rank` takes on the
values 1 through 4. Institutions with a rank of 1 have the highest prestige,
while those with a rank of 4 have the lowest.

```
summary(mydata)

## admit gre gpa rank
## Min. :0.000 Min. :220 Min. :2.26 1: 61
## 1st Qu.:0.000 1st Qu.:520 1st Qu.:3.13 2:151
## Median :0.000 Median :580 Median :3.40 3:121
## Mean :0.318 Mean :588 Mean :3.39 4: 67
## 3rd Qu.:1.000 3rd Qu.:660 3rd Qu.:3.67
## Max. :1.000 Max. :800 Max. :4.00

xtabs(~rank + admit, data = mydata)

## admit
## rank 0 1
## 1 28 33
## 2 97 54
## 3 93 28
## 4 55 12
```


Analysis methods you might consider

Below is a list of some analysis methods you may have encountered.
Some of the methods listed are quite reasonable while

others have either
fallen out of favor or have limitations.

Using the Probit Model

The code below estimates a probit regression model using the glm (generalized linear model) function. Since we stored our model output in the object "myprobit", R will not print anything to the console. We can use the `summary` function to get a summary of the model and all the estimates.

```
myprobit <- glm(admit ~ gre + gpa + rank, family =
binomial(link = "probit"),
data = mydata)

## model summarysummary(myprobit)


##
## Call:
## glm(formula = admit ~ gre + gpa + rank, family =
binomial(link = "probit"),
## data = mydata)
##
## Deviance Residuals:
```

```
## Min 1Q Median 3Q Max
## -1.616 -0.871 -0.639 1.156 2.103
##
## Coefficients:
## Estimate Std. Error z value Pr(>|z|)
## (Intercept) -2.38684 0.67395 -3.54 0.00040 ***
## gre 0.00138 0.00065 2.12 0.03433 *
## gpa 0.47773 0.19720 2.42 0.01541 *
## rank2 -0.41540 0.19498 -2.13 0.03313 *
## rank3 -0.81214 0.20836 -3.90 9.7e-05 ***
## rank4 -0.93590 0.24527 -3.82 0.00014 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 499.98 on 399 degrees of freedom
## Residual deviance: 458.41 on 394 degrees of freedom
## AIC: 470.4
##
## Number of Fisher Scoring iterations: 4
```

We can use the `confint` function to obtain confidence intervals for the coefficient estimates.
These will be profiled confidence intervals by default, created by profiling the likelihood function. As
such, they are not necessarily symmetric.

```
confint(myprobit)
```

```
## Waiting for profiling to be done...
```

```
## 2.5 % 97.5 %
## (Intercept) -3.7201051 -1.076328
## gre 0.0001104 0.002655
## gpa 0.0960655 0.862610
## rank2 -0.7992114 -0.032995
## rank3 -1.2230956 -0.405008
## rank4 -1.4234218 -0.459539
```

We can test for an overall effect of `rank` using the `wald.test` function of the `aod` library. The
order in which the coefficients are given in the table of coefficients is the
same as the order of the terms in the model. This is important because the

`wald.test` function refers to the coefficients by their order in
the model.
We use the `wald.test` function. `b`
supplies the coefficients, while `Sigma` supplies the variance covariance
matrix of the error terms, finally `Terms` tells R which terms in the model
are to be tested, in this case, terms 4, 5, and 6, are the three terms for the
levels of `rank`.

```
wald.test(b = coef(myprobit), Sigma = vcov(myprobit), Terms = 4:6)


## Wald test:
## ----------
##
## Chi-squared test:
## X2 = 21.4, df = 3, P(> X2) = 8.9e-05
```

The chi-squared test statistic of 21.4 with three degrees of freedom is
associated with a p-value of less than 0.001 indicating

that the overall effect of
`rank` is statistically significant.

We can also test additional hypotheses about the differences in the
coefficients for different levels of rank. Below we
test that the coefficient for `rank`=2 is equal to the coefficient for `rank`=3.
The first line of code below creates a vector `l` that defines the test we
want to perform. In this case, we want to test the difference (subtraction) of
the terms for `rank`=2 and `rank`=3 (i.e. the 4th and 5th terms in the
model). To contrast these two terms, we multiply one of them by 1, and the other
by -1. The other terms in the model are not involved in the test, so they are
multiplied by 0. The second line of code below uses `L=l` to tell R that we
wish to base the test on the vector `l` (rather than using the Terms option
as we did above).

```
l <- cbind(0, 0, 0, 1, -1, 0)
wald.test(b = coef(myprobit), Sigma = vcov(myprobit), L = l)

## Wald test:
## ----------
##
## Chi-squared test:
## X2 = 5.6, df = 1, P(> X2) = 0.018
```

The chi-squared test statistic of 5.5 with 1 degree of freedom is associated with
a p-value of 0.019, indicating that the difference between the coefficient for `rank`=2
and the coefficient for `rank`=3 is statistically significant.

You can also use predicted probabilities to help you understand the model.
To do this, we first create a data frame containing
the values we want for the independent variables.

```
newdata <- data.frame(gre = rep(seq(from = 200, to = 800, length.out = 100),
4 * 4), gpa = rep(c(2.5, 3, 3.5, 4), each = 100 * 4), rank =
```

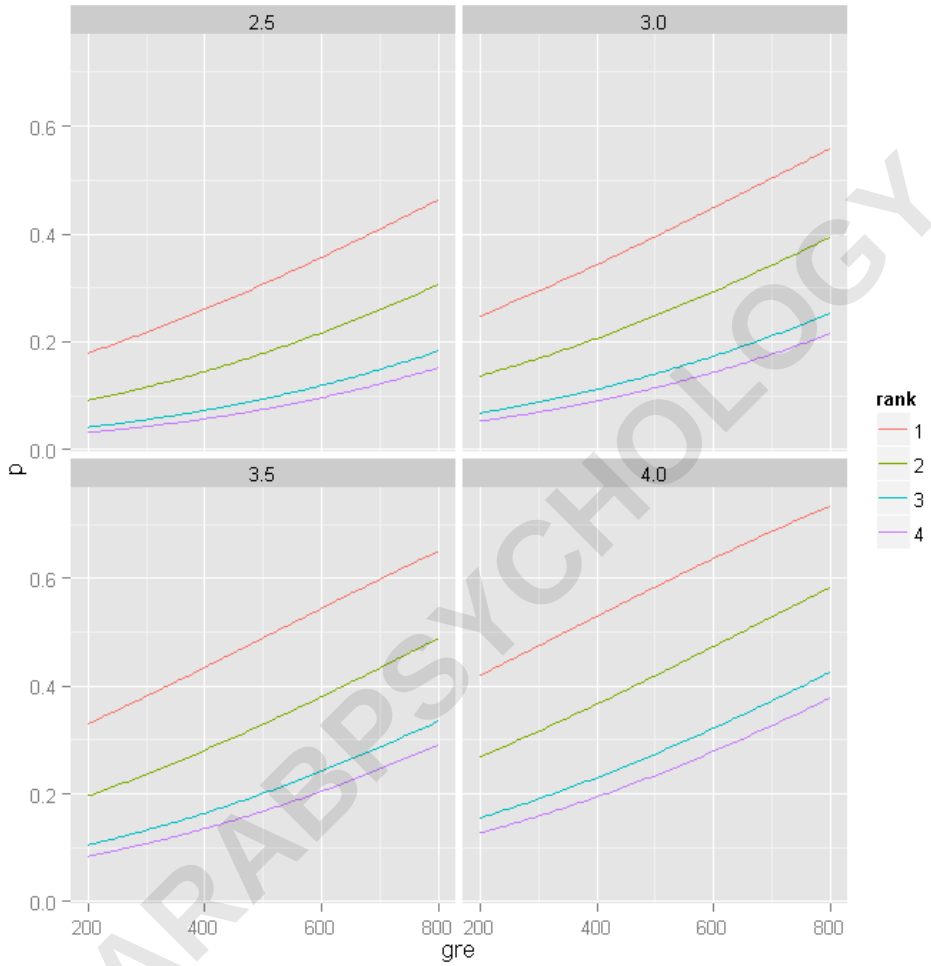
```
factor(rep(rep(1:4,
each = 100), 4)))

head(newdata)


## gre gpa rank
## 1 200.0 2.5 1
## 2 206.1 2.5 1
## 3 212.1 2.5 1
## 4 218.2 2.5 1
## 5 224.2 2.5 1
## 6 230.3 2.5 1
```

Now we can predict the probabilities for our input data as well as their standard errors.
These are stored as new variable in the data frame with the original data, so we can
plot the predicted probabilities for different `gre` scores. We create four plots,
one for each level of `gpa` we used (2.5, 3, 3.5, 4) with the colour of the lines
indicating the rank the predicted probabilities were for.

```
newdata <- predict(myprobit, newdata, type =
```

"response", se.fit = TRUE)

ggplot(newdata, aes(x = gre, y = p, colour = rank)) + geom_line() + facet_wrap(~gpa)



We may also wish to see measures of how well our model fits. This can be particularly useful when comparing competing models. The output produced by

`summary(mylogit)` included indices of fit (shown below the coefficients), including the null and deviance residuals and the AIC. One measure of model fit is the significance of the overall model. This test asks whether the model with predictors fits significantly better than a model with just an intercept (i.e. a null model). The test statistic is the difference between the residual deviance for the model with predictors and the null model. The test statistic is distributed chi-squared with degrees of freedom equal to the differences in degrees of freedom between the current and the null model (i.e. the number of predictor variables in the model). To find the difference in deviance for the two models (i.e. the test statistic) we can compute the change in deviance, and test it using a chi square test--the change in deviance distributed as chi square on the change in degrees of freedom.

change in deviancewith(myprobit, null.deviance - deviance)

41.56

change in degrees of freedomwith(myprobit, df.null - df.residual)

5

chi square test p-valuewith(myprobit, pchisq(null.deviance - deviance, df.null - df.residual, lower.tail = FALSE))

7.219e-08

The chi-square of 41.56 with 5 degrees of freedom and an associated p-value of less than 0.001 tells us that our model as a whole fits
significantly better than an empty model. This is sometimes called a likelihood
ratio test (the deviance residual is -2*log likelihood). To see the

model's log likelihood, we type:

logLik(myprobit)

'log Lik.' -229.2 (df=6)

Things to consider

References

See Also