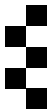


Binary Dependent Variables

Philip Leifeld

GV903: Advanced Research Methods, Week 16



University of Essex

1. Binary Dependent Variables

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How can we analyse these data as dependent variables?

American National Election Survey: Voting for Obama

```
ANES <- read.csv("dataset-anes-2012-subset1.csv")
str(ANES)
## 'data.frame': 3870 obs. of 10 variables:
## $ ft_dem : int 100 100 70 100 50 30 70 0 15 85 ...
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```

vote_obama: DV: Did respondent vote for Obama or Romney?

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ft_dem: Feeling thermometer – Democratic Party

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```

ft_rep: Feeling thermometer – Republican Party

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```

income: 28 ordinal income categories of \$5,000 each

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white: Is the respondent white?

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```

black: Is the respondent black?

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## $ vote_obama : int  1 1 1 1 0 0 1 0 0 1 ...
```

hispanic: Is the respondent hispanic?

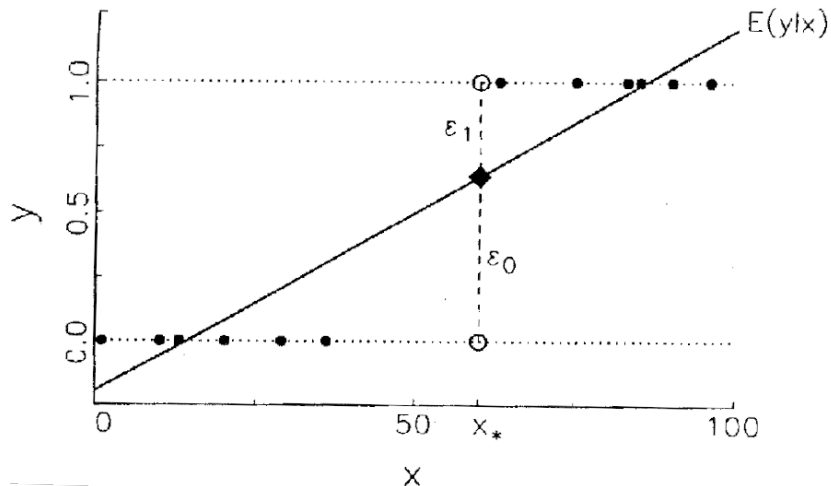
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```

other: Other ethnicity than white/black/hispanic

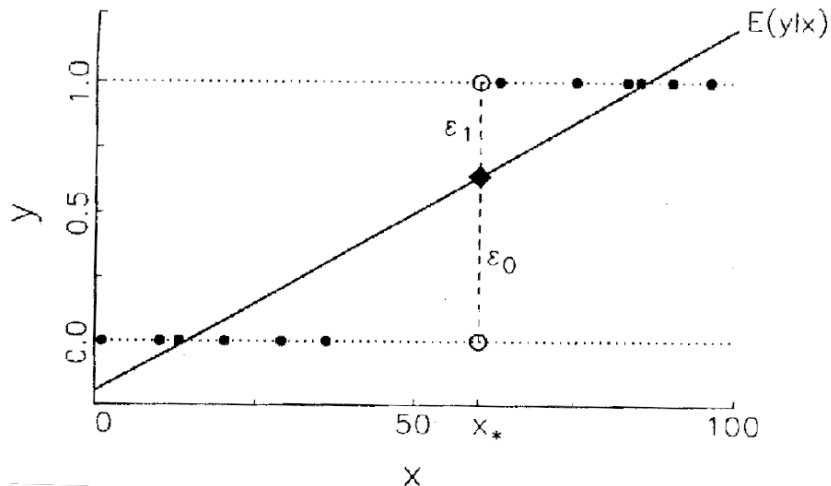
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(= Application of the linear model to binary data. This is usually a bad idea...)



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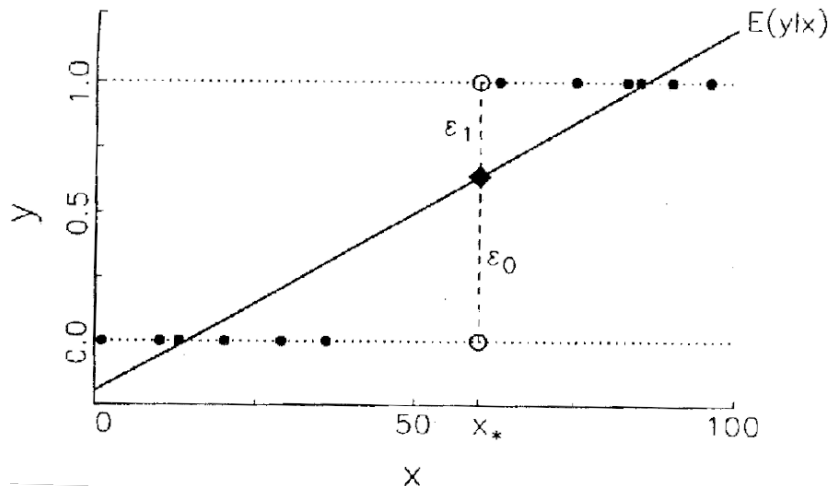
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- Prediction of values outside of $[0; 1]$...

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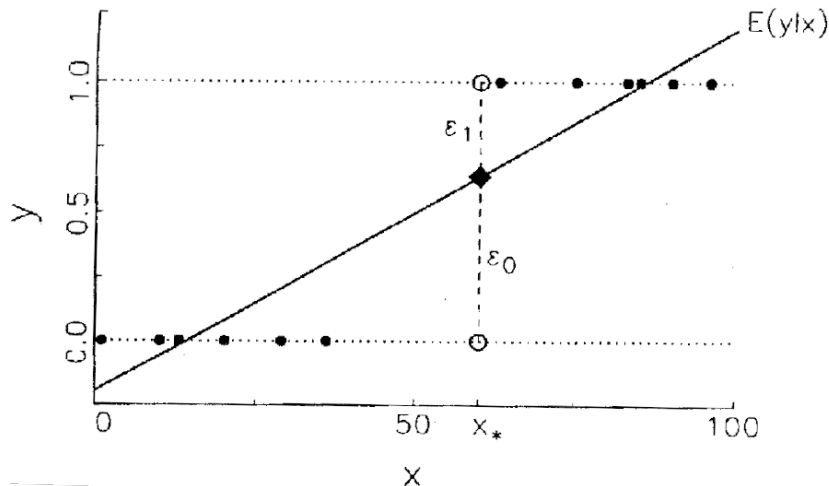
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- ▶ Prediction of values outside of $[0; 1]$...
- ▶ We almost always have heteroskedasticity...
- ▶ Assuming linear increases in probability...

The Generalised Linear Model (GLM)

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- ▶ In this case, we use the binomial distribution for binary data.
- ▶ In R, the GLM is implemented in the `glm` function.
- ▶ It works almost like the `lm` function.

Estimation of a GLM in R

```
model <- glm(vote_obama ~ ft_dem + ft_rep + black + hispanic + other +
             income, family = binomial, data = ANES)
summary(model)
##
## Call:
## glm(formula = vote_obama ~ ft_dem + ft_rep + black + hispanic +
##      other + income, family = binomial, data = ANES)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -4.2260  -0.1350   0.0140   0.1639   4.1982
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.223619   0.253391  -0.883   0.3775
## ft_dem       0.093786   0.004278  21.923 < 2e-16 ***
## ft_rep      -0.090827   0.004182 -21.716 < 2e-16 ***
## black        3.165810   0.394835   8.018 1.07e-15 ***
## hispanic     0.969995   0.189366   5.122 3.02e-07 ***
## other        0.558628   0.254384   2.196  0.0281 *
## income      -0.025063   0.008530  -2.938  0.0033 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 5247.0  on 3869  degrees of freedom
## Residual deviance: 1467.8  on 3863  degrees of freedom
## AIC: 1481.8
##
## Number of Fisher Scoring iterations: 8
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Now how do we interpret these estimates? 🤖

2. Details of the Model

Link Functions

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So what link function maps Y to continuous $F(Y) \in [-\infty; \infty]$?

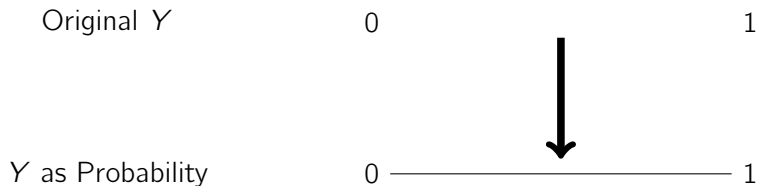
Mapping a Binary DV to a Continuous Scale

Original Y

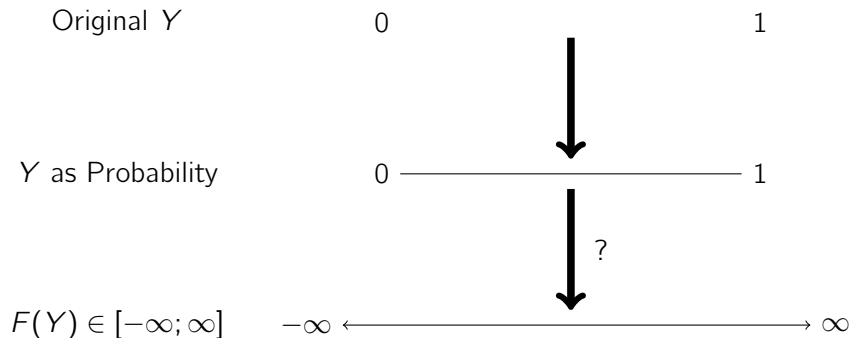
0

1

Mapping a Binary DV to a Continuous Scale



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Or conversely:

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$F(Y) = \Phi^{-1}(Y)$ is known as the probit link function.

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For example, let $p = 0.16$ denote the probability of civil war. I. e., 16 out of 100 countries have a civil war. The odds of civil war are 16:84 or $\frac{16}{84} = 0.19$. The odds of peace are 84:16 or $\frac{84}{16} = 5.25$. These are called odds-ratios.

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Values between 0 and 1 indicate ≤ 0.5 probability. Values above 1 indicate probabilities above 0.5, and there is no upper bound. To avoid this skewness of the odds-ratios, their logarithm can be computed in order to scale them symmetrically around 0.

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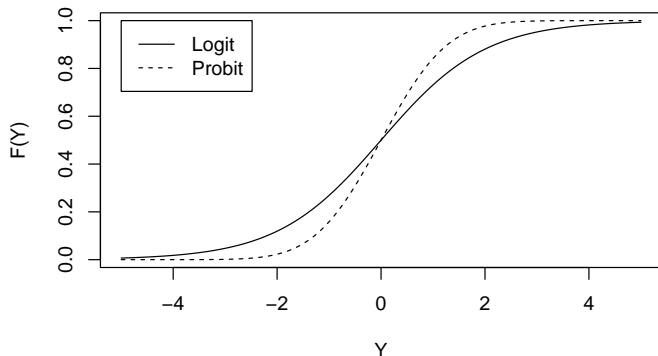
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In practice, it does not matter if we use logit or probit link functions as long as we remember the inverse transformation to get back to the original scale.

Either transformation can be used to map a linear (= additive) model onto the probability scale.

Logit and Probit in Comparison

```
Y <- seq(-5, 5, 0.05)
plot(Y, 1 / (1 + exp(-Y)), type = "l", xlab = "Y",
     ylab = "F(Y)")
lines(Y, pnorm(Y), lty = "dashed")
legend(-5, 1, legend = c("Logit", "Probit"), lty = 1:2)
```



Both transformations indeed have very similar shapes.

The Logit Model

Binary outcomes can be modelled as Bernoulli trials (e. g., coin flip). Bernoulli trials are defined by a single parameter θ for the probability of success. Bernoulli trials are binomial experiments with $n = 1$:

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Now we can plug the linear part into this model through the link function. This is where the different probabilities come from:

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And voilà: we have a logistic model – a non-linear model for binary data! (And similar for the probit model. . .)

3. Estimation

The Likelihood Function of a Logit Model

We have defined the probability for a single observation, $P(Y_i = y_i)$. We can now define the joint probability for all observations:

$$P(\mathbf{Y}|\boldsymbol{\theta}) = \prod_{i=1}^n \theta_i^{y_i} (1 - \theta_i)^{1-y_i}$$

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The corresponding log likelihood (applying the laws of logarithms):

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This can be further simplified (see Ward and Ahlquist 2018) and then solved analytically. Or we can maximise computationally.

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negLL <- function(b, X, y) {  
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Prepare the design matrix, DV, and θ start values:

```
myX <- cbind(1, ANES$ft_dem, ANES$ft_rep, ANES$black,  
             ANES$hispanic, ANES$other, ANES$income)  
myY <- ANES$vote_obama  
startval <- rep(0, ncol(myX))
```

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```

And now we are ready to optimise the function given the data:

```
results <- optim(startval, negLL, hessian = TRUE,  
                 method = "BFGS", X = myX, y = myY)
```

Extract the Results

Extract parameters and SEs (via diagonal of VCOV matrix):

```
data.frame(coef = results$par,  
           SE = sqrt(diag(solve(results$hessian))))  
##           coef           SE  
## 1 -0.22379114 0.253417386  
## 2  0.09382491 0.004277321  
## 3 -0.09086239 0.004182228  
## 4  3.16617989 0.394914617  
## 5  0.97007557 0.189397775  
## 6  0.55869840 0.254419592  
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Extract the log likelihood:

```
results$value  
## [1] 733.8795
```

Compute AIC (recap: $AIC = -2 \log \hat{\mathcal{L}} + 2k$):

```
2 * results$value + 2 * ncol(myX) # (not -2 because negLL)  
## [1] 1481.759
```

Let's Look at the glm Output Again for Comparison...

```
summary(model)
##
## Call:
## glm(formula = vote_obama ~ ft_dem + ft_rep + black + hispanic +
##      other + income, family = binomial, data = ANES)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -4.2260  -0.1350   0.0140   0.1639   4.1982
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.223619   0.253391  -0.883   0.3775
## ft_dem       0.093786   0.004278  21.923 < 2e-16 ***
## ft_rep      -0.090827   0.004182 -21.716 < 2e-16 ***
## black        3.165810   0.394835   8.018 1.07e-15 ***
## hispanic     0.969995   0.189366   5.122 3.02e-07 ***
## other        0.558628   0.254384   2.196  0.0281 *
## income      -0.025063   0.008530  -2.938  0.0033 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 5247.0  on 3869  degrees of freedom
## Residual deviance: 1467.8  on 3863  degrees of freedom
## AIC: 1481.8
##
## Number of Fisher Scoring iterations: 8
```

Estimation of Logit and Probit Models

Logit model again, now specifying logit link function explicitly:

```
model <- glm(vote_obama ~ ft_dem + ft_rep + black +  
             hispanic + other + income,  
             family = binomial(link = logit), data = ANES)
```

Similarly, we can specify the probit link function:

```
model2 <- glm(vote_obama ~ ft_dem + ft_rep + black +  
              hispanic + other + income,  
              family = binomial(link = probit), data = ANES)
```

Logit and Probit Comparison

```
library("texreg")
texreg(list(model, model2), single.row = TRUE, dcolumn = TRUE,
        booktabs = TRUE, use.packages = FALSE, table = FALSE,
        custom.model.names = c("Logit", "Probit"))
```

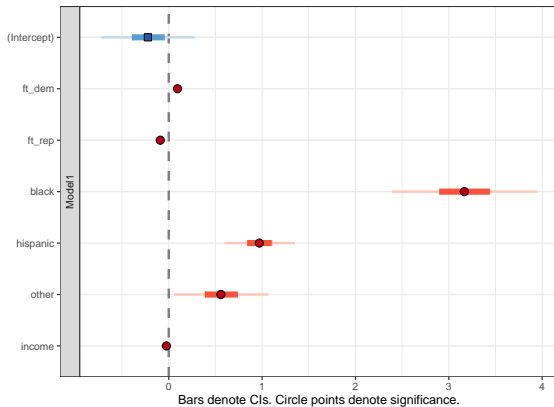
	Logit	Probit
(Intercept)	-0.22 (0.25)	-0.14 (0.14)
ft_dem	0.09 (0.00) ^{***}	0.05 (0.00) ^{***}
ft_rep	-0.09 (0.00) ^{***}	-0.05 (0.00) ^{***}
black	3.17 (0.39) ^{***}	1.66 (0.18) ^{***}
hispanic	0.97 (0.19) ^{***}	0.60 (0.10) ^{***}
other	0.56 (0.25) [*]	0.29 (0.14) [*]
income	-0.03 (0.01) ^{**}	-0.01 (0.00) ^{**}
AIC	1481.76	1542.69
BIC	1525.59	1586.52
Log Likelihood	-733.88	-764.35
Deviance	1467.76	1528.69
Num. obs.	3870	3870

*** $p < 0.001$; ** $p < 0.01$; * $p < 0.05$

4. Interpretation

Coefficient Plots in texreg

```
plotreg(model)
```



Interpretation of Logit Coefficients

Coefficients are log odds-ratios. These are hard to interpret. We can at least convert them into odds-ratios by exponentiating:

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exp(coef(model))  
## (Intercept)      ft_dem      ft_rep      black      hispanic  
##  0.7996197    1.0983245    0.9131759    23.7079342    2.6379315  
##      other      income  
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Or being hispanic (as opposed to white) increases the odds of voting for Obama by $(2.64 - 1) \cdot 100 = 164$ per cent.

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For example, one additional point on the feeling thermometer for Democrats increases the odds of voting for Obama by 9 per cent.

Or being hispanic (as opposed to white) increases the odds of voting for Obama by $(2.64 - 1) \cdot 100 = 164$ per cent.

These are relative statements. Do not confuse with probabilities. They depend on the values of all other variables. We need predicted probabilities to interpret the effects more clearly.

Predicted Probabilities for Logit Models

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```
newdata <- data.frame(ft_dem = mean(ANES$ft_dem, na.rm = TRUE),  
                      ft_rep = mean(ANES$ft_rep, na.rm = TRUE),  
                      black = 0,  
                      hispanic = 0,  
                      other = 0,  
                      income = mean(ANES$income, na.rm = TRUE))
```

```
newdata  
##      ft_dem  ft_rep black hispanic other  income  
## 1 54.72016 42.04109     0         0     0 14.55995
```

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newdata  
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```

We basically create scenarios that we can compare to each other.
newdata serves as our template...

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```
newdata <- newdata[rep(1, 4), ]
newdata$black[2] <- 1
newdata$hispanic[3] <- 1
newdata$other[4] <- 1
rownames(newdata) <- c("white", "black", "hispanic", "other")
newdata
```

##	ft_dem	ft_rep	black	hispanic	other	income
## white	54.72016	42.04109	0	0	0	14.55995
## black	54.72016	42.04109	1	0	0	14.55995
## hispanic	54.72016	42.04109	0	1	0	14.55995
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Based on this, we can now predict the probabilities.

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logodds <- predict(model, newdata = newdata)
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prob <- predict(model, newdata = newdata, type = "response")
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```

Black people have a 98 per cent probability of voting for Obama (at average income etc levels). 20 per cent higher than whites.

Confidence Intervals for the Predictions

```
pred <- predict(model, newdata = newdata, type = "response",
                 se.fit = TRUE)
crit <- qnorm(1 - (0.05 / 2))
crit
## [1] 1.959964

data.frame(prediction = pred$fit,
            upper_ci = pred$fit + crit * pred$se.fit,
            lower_ci = pred$fit - crit * pred$se.fit)
##           prediction upper_ci lower_ci
## white      0.6737035 0.7106951 0.6367118
## black      0.9799799 0.9950438 0.9649159
## hispanic   0.8448778 0.8905384 0.7992171
## other      0.7830639 0.8649926 0.7011353
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## other      0.7830639 0.8649926 0.7011353
```

Note how these point predictions are useful for categorical independent variables. Next, we will look at the continuous case...

Predictions for the Democratic Feeling Thermometer

Create scenarios with varying thermometer levels and all other variables fixed at their means, then predict:

```
dtherm <- seq(from = min(ANES$ft_dem), to = max(ANES$ft_dem),
              length.out = 100)
newdata <- data.frame(ft_dem = dtherm,
                      ft_rep = mean(ANES$ft_rep, na.rm = TRUE),
                      black = mean(ANES$black, na.rm = TRUE),
                      hispanic = mean(ANES$hispanic, na.rm = TRUE),
                      other = mean(ANES$other, na.rm = TRUE),
                      income = mean(ANES$income, na.rm = TRUE))

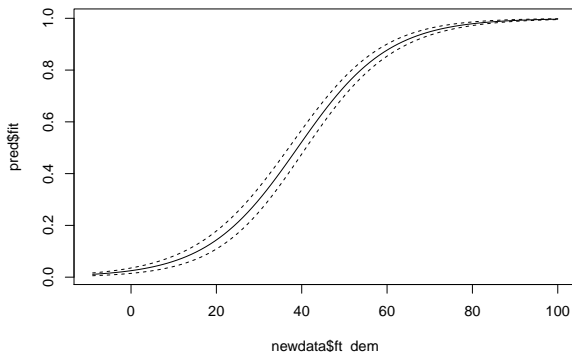
tail(newdata)
##           ft_dem  ft_rep  black  hispanic  other  income
## 95  94.49495 42.04109 0.181137 0.1457364 0.05400517 14.55995
## 96  95.59596 42.04109 0.181137 0.1457364 0.05400517 14.55995
## 97  96.69697 42.04109 0.181137 0.1457364 0.05400517 14.55995
## 98  97.79798 42.04109 0.181137 0.1457364 0.05400517 14.55995
## 99  98.89899 42.04109 0.181137 0.1457364 0.05400517 14.55995
## 100 100.00000 42.04109 0.181137 0.1457364 0.05400517 14.55995

pred <- predict(model, newdata = newdata, type = "response",
                 se.fit = TRUE)
```

Predictions for the Democratic Feeling Thermometer

Plot the predicted probabilities with a 95 per cent CI:

```
plot(newdata$ft_dem, pred$fit, type = "l")  
lines(newdata$ft_dem, pred$fit + crit * pred$se.fit,  
      lty = "dashed")  
lines(newdata$ft_dem, pred$fit - crit * pred$se.fit,  
      lty = "dashed")
```



We can see how the IV is non-linearly related to the probability of voting for Obama, all things being equal.

Predictions for the Democratic Feeling Thermometer

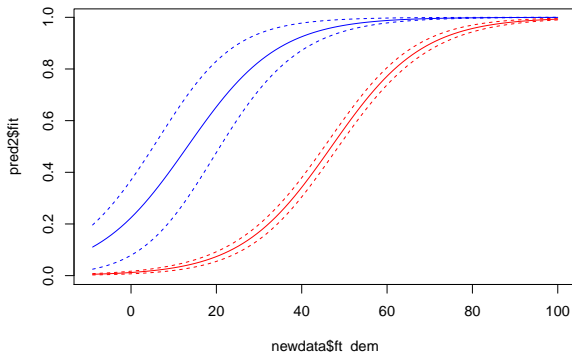
Create thermometer scenarios conditional on ethnicities:

```
newdata$black <- 0
newdata$hispanic <- 0
newdata$other <- 0
newdata$white <- 1
pred2 <- predict(model, newdata = newdata, type = "response",
                  se.fit = TRUE)

newdata$black <- 1
newdata$white <- 0
pred3 <- predict(model, newdata = newdata, type = "response",
                  se.fit = TRUE)
```

Predictions for the Democratic Feeling Thermometer

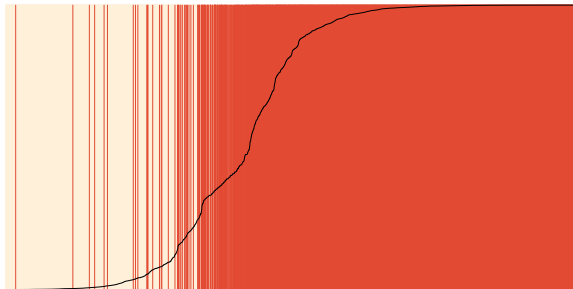
```
plot(newdata$ft_dem, pred2$fit, type = "l", col = "red")
lines(newdata$ft_dem, pred2$fit + crit * pred2$se.fit,
      lty = "dashed", col = "red")
lines(newdata$ft_dem, pred2$fit - crit * pred2$se.fit,
      lty = "dashed", col = "red")
lines(newdata$ft_dem, pred3$fit, type = "l", col = "blue")
lines(newdata$ft_dem, pred3$fit + crit * pred3$se.fit,
      lty = "dashed", col = "blue")
lines(newdata$ft_dem, pred3$fit - crit * pred3$se.fit,
      lty = "dashed", col = "blue")
```



5. Model Fit

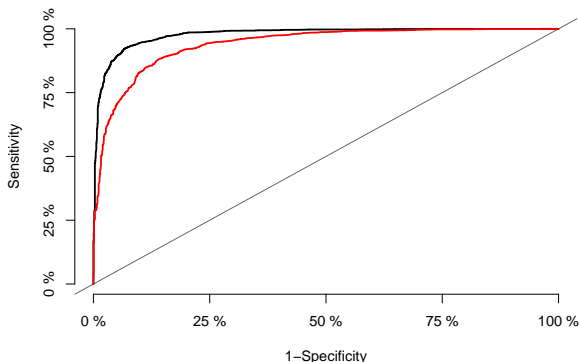
Separation Plots

```
library("separationplot")  
separationplot(pred = model$fitted.values,  
               actual = model$y,  
               line = TRUE,  
               newplot = FALSE)
```



Receiver Operating Characteristics (ROC)

```
library("ModelGood")  
model3 <- glm(vote_obama ~ ft_rep + black + hispanic +  
              other + income, family = binomial,  
              data = ANES) # leaving out ft_dem  
plot(Roc(model))  
lines(Roc(model3), col = "red")
```



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- ▶ The ROC curve shows the trade-off between the two criteria at each level, for many simulations from the estimated model.
- ▶ Simulations were generated by incorporating random fluctuation from the VCOV matrix.
- ▶ ROC can be used for model comparison.

Area Under the Curve (AUC)

The area under the curve is an overall measure of model fit.

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Roc(model)
## Receiver operating characteristic
## Sample size: 3870
##
## Response: '0' (n=1598) '1' (n=2272)
##
## Area under the ROC curve (AUC, higher better):
## full data
##      97.76
##
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```

We can also use this to compare models:

```
Roc(model)$Auc$glm$Auc - Roc(model3)$Auc$glm$Auc
## [1] 0.03816528
```