Lecture 11: Logistic Regression and Poisson Regression

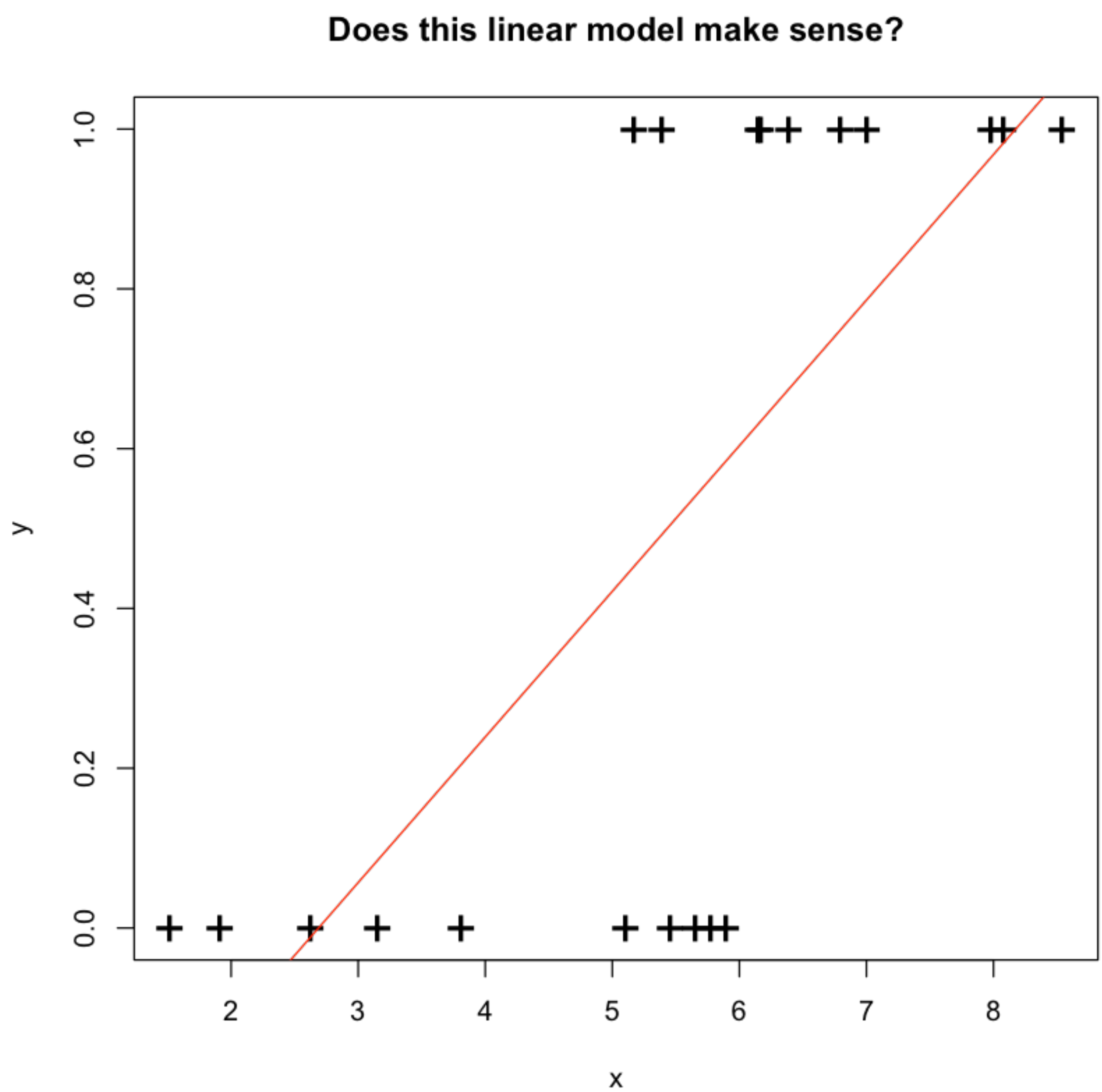
- These are two types of generalized linear models (GLM).
- Generalization to linear models to model binary data and count data.
- Why are they still called linear models?

11.1 Logistic Regression

- Used to model binary outcome.
- More specifically, we model the probabilities.
  - We find the probabilities such that we are mostly likely to observe the actual data.
    - Maximum likelihood estimator (MLE)
- In contrast to linear regression, where we model the outcome directly.
  - We minimized the sum of squares from the model to the actual data.
    - Least squares estimator (LSE)

In [1]:

```
set.seed(613)
x <- c(runif(10, min = 1, max = 6), runif(10, min = 5, max = 10)
)
y <- c(rep(0,10), rep(1,10))
plot(x, y, main = "Does this linear model make sense?", cex = 2,
pch = "+")
abline(lm(y~x), col = "red")
```


Does this linear model make sense?
y
1.0
0.8
0.6
0.4
0.2
0.0
2
3
4
5
6
7
8
x

Solution

- Generalized linear models.
  - Logistic regression in this case.

Model assumptions

- Each sample i follows a bernoulli distribution with probability p_i
  - Bernoulli distribution: Observing a head from tossing a fair coin $\sim Bernoulli(0.5)$
  - $\mathbb{P}(Y_i = 1) = p_i$
  - $\mathbb{P}(Y_i = 0) = 1 - p_i$
- All samples are independent
  - Data: $y_1 = 0,\ y_2 = 1,\ y_3 = 0$
  - Probabilities: $\mathbb{P}(y_1 = 0) = 1 - p_1$, $\mathbb{P}(y_2 = 1) = p_2$, $\mathbb{P}(y_3 = 0) = 1 - p_3$
  - Likelihood: $\ell = (1 - p_1) \times p_2 \times (1 - p_3)$
- logit(p) or $\log(\text{odds})$ is linearly associated with the predictors.
  - odds = $p/(1 - p)$

Maximize the likelihood ℓ.

Example: graduate school admission.

A simulated graduate school admission data. As we all know, stronger candidates have higher probability of getting in.

- admit
  - 1: admitted; 0: rejected.
- rank
  - 1: from good undergraduate schools; 0: from not as good undergraduate schools.
- gre
- gpa

In [2]:

```
df <- read.csv("https://stats.idre.ucla.edu/stat/data/binary.csv
")
df$rank <- ceiling(df$rank/2) - 1
head(df)
```

A data.frame: 6 × 4

admit	gre	gpa	rank
<int>	<int>	<dbl>	<dbl>
0	380	3.61	1
1	660	3.67	1
1	800	4.00	0
1	640	3.19	1
0	520	2.93	1
1	760	3.00	0

If we only look at rank.

Investigate the association between admit and rank in terms of odds ratio.

In [3]:

```
table(df[,c("rank", "admit")])[c(2,1),c(2,1)]
```

```
    admit
rank   1   0
   1  40 148
   0  87 125
```

In [4]:

```
OR <- 40*125/(87*148); OR
```

0.388319353836595

Interpretation?

In [5]:

```
fit1 <- glm(admit~rank,
            family = binomial(link = "logit"),
            data = df)
summary(fit1)
```

```
Call:
glm(formula = admit ~ rank, family = binomial(link =
"logit"),
    data = df)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.0279  -1.0279  -0.6917   1.3347   1.7593

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -0.3624     0.1396  -2.596  0.00944 **
rank         -0.9459     0.2264  -4.178 2.94e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.'
0.1 ' ' 1

(Dispersion parameter for binomial family taken to b
e 1)

    Null deviance: 499.98  on 399  degrees of freedo
m
Residual deviance: 481.66  on 398  degrees of freedo
m
AIC: 485.66

Number of Fisher Scoring iterations: 4
```

In [6]:

```
exp(fit1$coefficients)
OR
```

(Intercept)
0.696000000000002
rank
0.388319353836889

0.388319353836595

Why does $\exp(\beta_1) = \mathrm{OR}$***?***

The model is

$$\log(\frac{p_i}{1-p_i}) = \beta_0 + \beta_1 \times rank_i$$

where p_i is the probability of admission of the i^{th} applicant.

Note that we use a linear predictor to model the probability. So it is called a generalized linear model.

Confidence interval

The CI is not symmetrical. It is symmetrical on the log scale.

In [7]:

```
exp(confint(fit1))
```

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

A matrix: 2 × 2 of type dbl

	2.5 %	97.5 %
(Intercept)	0.5279583	0.9134167
rank	0.2473729	0.6017864

Prediction

In [8]:

```
# type = "response" gives the fitted probability
nd <- data.frame(rank = c(0,1))
predict(fit1, type = "response", newdata = nd)
```

1
0.410377358490567
2
0.212765957446936

On average, the probability of admission for rank 0 is 0.41 and 0.21 for rank 1.

In [9]:

```
# type = "link" give the fitted linear predictor
predict(fit1, type = "link", newdata = nd)
```

1
-0.362405618647715
2
-1.30833281964942

Recall that $\log(\frac{p_i}{1-p_i}) = \beta_0 + \beta_1 \times rank_i$

In [10]:

```
log(0.212765957446936/(1-0.212765957446936))
log(0.410377358490567/(1-0.410377358490567))
```

-1.30833281964942

-0.362405618647713

If we only look at GPA.

GPA is continuous, therefore we can no longer make the 2x2 table to get the odds ratio.

Regression!

In [11]:

```
fit2 <- glm(admit~gpa,
            family = binomial(),
            data = df)
summary(fit2)
# the link function for binomial family is logit by default - ca
nonical link
```

```
Call:
glm(formula = admit ~ gpa, family = binomial(), data
= df)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.1131  -0.8874  -0.7566   1.3305   1.9824

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -4.3576     1.0353  -4.209 2.57e-05 ***
gpa           1.0511     0.2989   3.517 0.000437 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’
0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to b
e 1)

    Null deviance: 499.98  on 399  degrees of freedo
m
Residual deviance: 486.97  on 398  degrees of freedo
m
AIC: 490.97

Number of Fisher Scoring iterations: 4
```

In [12]:

```
fit2$coefficients
```

(Intercept)

-4.35758730334778

gpa

1.05110872619157

In [13]:

```
exp(fit2$coefficients)
```

(Intercept)
0.0128092552447367
gpa
2.86082122777123

In [14]:

```
predict(fit2, newdata=data.frame(gpa=4), type="response")
```

1: 0.461786564607921

In [15]:

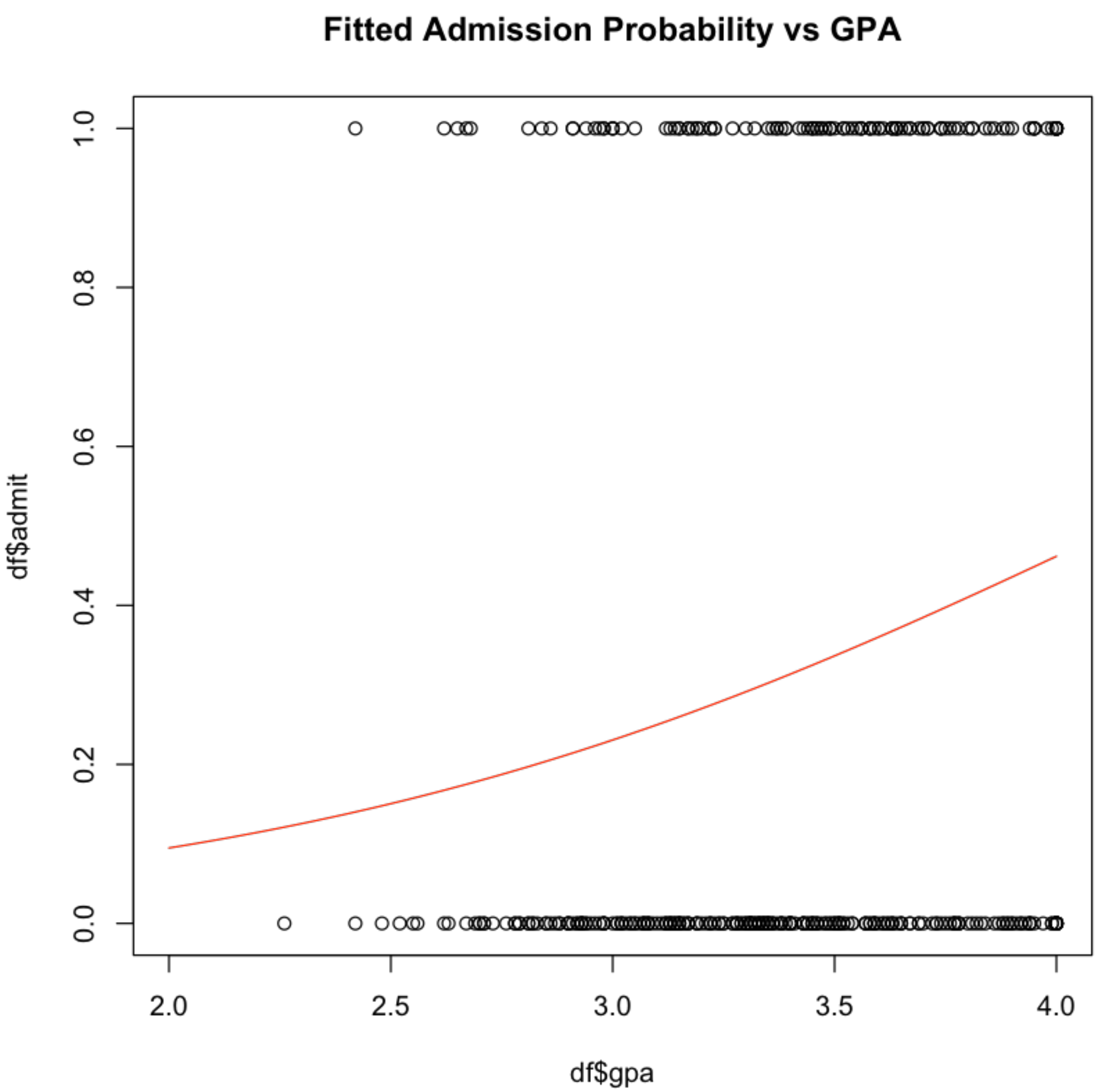
```
exp(-4.35758730334778+1.05110872619157*4)/(1+exp(-4.357587303347
78+1.05110872619157*4))
```

0.461786564607916

In [16]:

```
lb <- 2
ub <- 4
plot(x = df$gpa, y = df$admit,
     main = "Fitted Admission Probability vs GPA", xlim = c(lb,u
b))
fitted.admit <- predict(fit2,
                        newdata = data.frame(gpa = seq(lb,ub,0.0
1)),
                        type = "response")
lines(sort(x = seq(lb,ub,0.01)), y = sort(fitted.admit), col = "
red")

# The relationship should be a S-shaped curve.
# We are not seeing the curve because the range of GPA is too sm
all.
```



If we look at all variables in the dataset.

In [17]:

```
fit3 <- glm(admit~., family = binomial(), data = df)
summary(fit3)
```

```
Call:
glm(formula = admit ~ ., family = binomial(), data =
df)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.4290  -0.8902  -0.6552   1.1937   2.1122

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept) -4.679673   1.100498  -4.252 2.12e-05 **
*
gre          0.002280   0.001085   2.101  0.03568 *
gpa          0.864058   0.327562   2.638  0.00834 **
rank        -0.938317   0.232946  -4.028 5.62e-05 **
*
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’
0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to b
e 1)

    Null deviance: 499.98  on 399  degrees of freedo
m
Residual deviance: 463.37  on 396  degrees of freedo
m
AIC: 471.37

Number of Fisher Scoring iterations: 3
```

Compare two models, one being a reduced version of the other (variable selection).

Note that even though we are using the anova( ) function, we are not performing analysis of variance. Instead, we are performing analysis of deviance.

- Residual deviance is $-2 \log \text{likelihood}$.
  - Because residuals in linear regression does not make sense anymore.
- Therefore the difference in deviances translates to the ratio of likelihoods.
- Likelihood ratio test - which is a χ^2 test.

In [18]:

```
# print is not necessary in R or Rstudio.
print(anova(fit2, fit3, test = "LRT"))
# LRT -> likelihood ratio test
# test = "Chisq" is equivalent here.
```

```
Analysis of Deviance Table

Model 1: admit ~ gpa
Model 2: admit ~ gre + gpa + rank
  Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
1       398     486.97
2       396     463.37  2   23.594 7.526e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.'
0.1 ' ' 1
```

Reject the reduced model.

Test whether the model is significant - goodness of fit test

- Basically compare the model with the null model (intercept only model).

In [19]:

```r
print(anova(fit1, test = "Chisq"))
```

```
Analysis of Deviance Table

Model: binomial, link: logit

Response: admit

Terms added sequentially (first to last)


     Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
NULL                   399     499.98
rank  1   18.313       398     481.66 1.874e-05 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’
0.1 ‘ ’ 1
```

11.2 Poisson Regression

- Used to model count data
  - Poisson distribution is commonly used to model counts.
  - $Y \sim Poisson(\lambda)$, then the mean and variance of Y are both λ.
  - PDF: $\mathbb{P}(Y = y|\lambda) = \frac{e^{-\lambda}\lambda^y}{y!}$
- Specifically, use Poisson distributions to model the count and use regression to model the rate parameter λ.
- Find the parameters that maximize the probability of observing the actual data.
  - Again, MLE.

Example: Ship damage data

- incidents
  - Number of damage incidents during service
- service
  - Aggregate months of service
- type
  - 5 types of ships, A-E
- year
  - Year of construction

In [20]:

```
library(MASS)
ds <- ships
ds <- ds[ds$service>0, ]
head(ds)
```

A data.frame: 6 × 5

type	year	period	service	incidents
<fct>	<int>	<int>	<int>	<int>
A	60	60	127	0
A	60	75	63	0
A	65	60	1095	3
A	65	75	1095	4
A	70	60	1512	6
A	70	75	3353	18

If we only look at number of incidents vs. ship type

In [21]:

```
fit4 <- glm(incidents~type,
            family = poisson(link = "log"),
            data = ds)
summary(fit4)
```

```
Call:
glm(formula = incidents ~ type, family = poisson(lin
k = "log"),
    data = ds)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-4.6716  -2.2039  -0.5921   0.8632   4.0113

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)   1.7918     0.1543  11.612  < 2e-16 ***
typeB         1.7957     0.1666  10.777  < 2e-16 ***
typeC        -1.2528     0.3273  -3.827  0.00013 ***
typeD        -0.9045     0.2875  -3.146  0.00165 **
typeE        -0.1178     0.2346  -0.502  0.61570
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’
0.1 ‘ ’ 1

(Dispersion parameter for poisson family taken to be
1)

    Null deviance: 614.54  on 33  degrees of freedom
Residual deviance: 170.71  on 29  degrees of freedom
AIC: 278.58

Number of Fisher Scoring iterations: 6
```

In [22]:

```
summary(fit4)$coefficients
```

A matrix: 5 × 4 of type dbl

	Estimate	Std. Error	z value	Pr(>|z|)
(Intercept)	1.7917595	0.1543033	11.611929	3.584389e-31
typeB	1.7957199	0.1666196	10.777362	4.403311e-27
typeC	-1.2527630	0.3273268	-3.827254	1.295807e-04
typeD	-0.9044563	0.2874596	-3.146377	1.653066e-03
typeE	-0.1177830	0.2346477	-0.501957	6.156978e-01

In [23]:

```
exp(confint(fit4))
```

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

A matrix: 5 × 2 of type dbl

	2.5 %	97.5 %
(Intercept)	4.3635322	8.0019099
typeB	4.3975819	8.4645779
typeC	0.1438568	0.5253836
typeD	0.2243790	0.6978918
typeE	0.5573675	1.4040665

Interpretation?

Does the result mean that Type B is more prone to damage than Type A?

Consider the duration of service in the incidents-type relationship.

In [24]:

```r
# The canonical link for poisson regression is log, so omitted.
fit5 <- glm(incidents~type+offset(log(service)),
            family = poisson(), data = ds)
summary(fit5)
```

```
Call:
glm(formula = incidents ~ type + offset(log(service)
), family = poisson(),
    data = ds)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-5.3041  -0.9926  -0.4034   0.7209   3.6616

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -5.4202     0.1543 -35.127  < 2e-16 ***
typeB        -0.8837     0.1666  -5.304 1.13e-07 ***
typeC        -0.8260     0.3273  -2.524   0.0116 *
typeD        -0.1459     0.2875  -0.507   0.6118
typeE         0.3429     0.2346   1.461   0.1439
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’
0.1 ‘ ’ 1

(Dispersion parameter for poisson family taken to be
1)

    Null deviance: 146.328  on 33  degrees of freedo
m
Residual deviance:  90.889  on 29  degrees of freedo
m
AIC: 198.76

Number of Fisher Scoring iterations: 5
```

Further include the year of construction in the model.

In [25]:

```
fit6 <- glm(incidents~type+as.factor(year)+offset(log(service)),
family = poisson(), data = ds)
```

Further include period in the relationship

In [26]:

```
fit7 <- glm(incidents~type+as.factor(year)+as.factor(period)+off
set(log(service)), family = poisson(), data = ds)
```

Model comparison (variable selection)

In [27]:

```
# anova() allows for comparison of many models at the same time.
print(anova(fit5, fit6, fit7, test = "LRT"))
```

```
Analysis of Deviance Table

Model 1: incidents ~ type + offset(log(service))
Model 2: incidents ~ type + as.factor(year) + offset
(log(service))
Model 3: incidents ~ type + as.factor(year) + as.fac
tor(period) + offset(log(service))
  Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
1        29     90.889
2        26     49.355  3   41.534 5.038e-09 ***
3        25     38.695  1   10.660  0.001095 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’
0.1 ‘ ’ 1
```