

Building Logistic Regression Models

Fit and Sparse Data

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Section 1

- 1 Model Fit
- 2 Linearity of Predictors
- 3 Effects of Sparse Data

- ① Goodness of fit test (Chapter 3). Using G^2 and X^2 generally limited to “non-sparse” contingency tables.
 - A *goodness of fit* can be used only in the number of predictor levels is fixed and relatively small to the overall sample size
 - Only appropriate for grouped binary data with most ($\geq 80\%$) of fitted cell counts being “large” (e.g., $\hat{\mu}_i > 5$)
 - For continuous predictors or many predictors with small fitted values, distributions of X^2 and G^2 are not well approximated by χ^2 . For better approximations, try grouping data before applying X^2 , G^2
 - Hosmer-Lemeshow test forms groups using ranges of $\hat{\pi}$ values
 - Or can try to group predictor values (if only 1 or 2 predictors)

- ② Check whether fit improves by adding other predictors or interactions between predictors
- ③ Residuals (Chapter 3)
 - Standardized Pearson residuals, `rstandard(model, type="pearson")`
 - Standardized Deviance residuals, `rstandard(model)`

Example (Berkeley Graduate Admissions)

Admissions data for 6 departments at UC Berkeley by gender

```
> ftable(UCBAdmissions,row.vars="Dept",  
+   col.vars=c("Gender","Admit"))
```

	Gender		Male		Female	
	Admit		Admitted	Rejected	Admitted	Rejected
Dept						
A			512	313	89	19
B			353	207	17	8
C			120	205	202	391
D			138	279	131	244
E			53	138	94	299
F			22	351	24	317

Example (continued)

- Admissions rates are higher for departments A and B but lower for C through D
- Odds ratio (of acceptance to rejection) for males vs females does not seem to be very different from 1 (except A)

```
> round(apply(UCBAdmissions,3,odds.ratio),2)
```

A	B	C	D	E	F
0.35	0.80	1.13	0.92	1.22	0.83

- Ignoring department, i.e. merging them, the odds ratio seems to favor male. That is because more males were applying to departments with higher acceptance rates and vice versa for females

```
> odds.ratio(UCBGbyA) # Marginal odds ratio
```

```
[1] 1.84108
```

Example (continued)

Fitting the model (to the correct format data), conditional odds ratio of acceptance with gender conditional on dept is $\exp(-0.999) = 0.9$ which is not significantly different from 1.

```
> UCB.logit=glm(cbind(Admit,Reject)~Gender+Dept,family=binomial)
> summary(UCB.logit)
```

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-2.62456	0.15773	-16.640	<2e-16 ***
GenderMale	-0.09987	0.08085	-1.235	0.217
DeptA	3.30648	0.16998	19.452	<2e-16 ***
DeptB	3.26308	0.17878	18.252	<2e-16 ***
DeptC	2.04388	0.16787	12.176	<2e-16 ***
DeptD	2.01187	0.16992	11.840	<2e-16 ***
DeptE	1.56717	0.18044	8.685	<2e-16 ***

```
Null deviance: 877.056 on 11 degrees of freedom
Residual deviance: 20.204 on 5 degrees of freedom
AIC: 103.14
```

Example (continued)

- Data is grouped so perform goodness of fit test (using G^2), which indicates a lack of fit

```
> 1-pchisq(UCB.logit$deviance,UCB.logit$df.residual)
[1] 0.001144078
```

- Standardized Pearson residuals, the first two observations corresponding to Dept A, don't seem to fit well

```
> round(rstandard(UCB.logit,type="pearson"),2)
      1      2      3      4      5      6      7      8      9
-4.03  4.03 -0.28  0.28  1.88 -1.88  0.14 -0.14  1.63
     10     11     12
-1.63 -0.30  0.30
```


Example (continued)

So we fit a model excluding Dept A and remove gender.

```
> UCBnoGA.logit=glm(cbind(Admit,Reject)~Dept,family=binomial,  
+ data=berk,subset=(Dept!="A"))  
> summary(UCBnoGA.logit)
```

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-2.6756	0.1524	-17.553	<2e-16 ***
DeptB	3.2185	0.1749	18.402	<2e-16 ***
DeptC	2.0600	0.1674	12.306	<2e-16 ***
DeptD	2.0108	0.1699	11.835	<2e-16 ***
DeptE	1.5861	0.1798	8.822	<2e-16 ***

```
Null deviance: 539.4581 on 9 degrees of freedom  
Residual deviance: 2.6815 on 5 degrees of freedom  
AIC: 69.916
```

Residuals are better, GoF has high p-value, and AIC much smaller. Dept A has its “own” separate model/interpretation.

Section 2

- 1 Model Fit
- 2 Linearity of Predictors
- 3 Effects of Sparse Data

Linearity of predictors

With (quantitative) predictors we need to check if an additive linear model is adequate or whether higher order polynomial terms and interactions are necessary.

Example

A nice example with two predictors where a quadratic form of the first predictor is (somewhat) useful, but no interaction, can be found at <https://freakonometrics.hypotheses.org/8210> and script at [freakonometrics.R](#)

Section 3

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Effects of Sparse Data

Sparse data are when certain combinations of variables have no actual data or “limited” information. This can lead to parameter estimates being infinite (in value), but most often in software you may see extremely large standard errors.

Example

Consider,

		S	F
X	1	8	2
	0	10	0

Fitting a simple logistic regression will yield the estimates odds ratio

$$e^{\hat{\beta}} = \frac{8 \times 0}{2 \times 10} = 0 \quad \Rightarrow \quad \hat{\beta} = \log(0) = -\infty$$

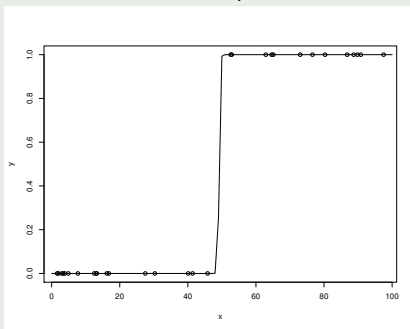
Effects of Sparse Data

Infinite estimates exist when predictor values (x values) where $y = 1$ can be *separated* from predictor values where $y = 0$. This extends to multidimensional predictor space.

Example

Simulate/generate data (with no values at $x = 50$) such that

$$y = \begin{cases} 0 & x < 50 \\ 1 & x > 50 \end{cases}$$



Example (continued)

```
> fit=glm(y~x,family=binomial)
```

Warning messages:

```
1: glm.fit: algorithm did not converge
```

```
2: glm.fit: fitted probabilities numerically 0 or 1 occurred
```

```
> summary(fit)
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-297.566	174094.706	-0.002	0.999
x	6.051	3542.717	0.002	0.999

Null deviance: 4.1054e+01 on 29 degrees of freedom

Residual deviance: 5.0225e-09 on 28 degrees of freedom

AIC: 4

Although $\hat{\beta} = 6.051$ the standard error is 3542.717.

We learned

- Model fit via GoF and Residuals
- Linearity of predictors
- Effects of sparse data on model fit