Likelihood and Deviance

Recap

Definition: The *likelihood* L(Model) = P(Data|Model) of a model is the probability of the observed data, given that we assume a certain model and certain values for the parameters that define that model.

Coin example: flip a coin 5 times, with $\pi_i = P(Heads)$

- lacktriangle Model: $Y_i \sim Bernoulli(\pi_i)$, and $\widehat{\pi}_i = 0.9$
- **♣** Data: $y_1, \ldots, y_5 = T, T, T, T, H$
- ullet Likelihood: $L(\widehat{\pi}_i) = P(y_1, \dots y_5 | \pi_i = 0.9) = 0.00009$

Recap

Maximum likelihood estimation: pick the parameter estimate that maximizes the likelihood.

Coin example: flip a coin 5 times, with $\pi_i = P(Heads)$

- Observed data: T, T, T, T, H
- lacktriangle Likelihood: $L(\widehat{\pi}_i) = (1-\widehat{\pi}_i)^4(\widehat{\pi}_i)$
- Choose $\widehat{\pi}_i$ to maximize $L(\widehat{\pi}_i)$

Logistic regression

$$Y_i \sim Bernoulli(\pi_i) \ \ \logigg(rac{\pi_i}{1-\pi_i}igg) = eta_0 + eta_1 X_i.$$

Or in other words,

$$\pi_i = rac{\exp\{eta_0 + eta_1 X_i\}}{1 + \exp\{eta_0 + eta_1 X_i\}}$$

- lacktriangle To fit this model, we need to obtain estimates \widehat{eta}_0 and \widehat{eta}_1
- Let's start by exploring the likelihood with this model

Logistic regression likelihood

$$Y_i \sim Bernoulli(\pi_i) \;\; \pi_i = rac{\exp\{eta_0 + eta_1 X_i\}}{1 + \exp\{eta_0 + eta_1 X_i\}}$$

Data: $(X_1,Y_1),\ldots,(X_n,Y_n)$

Likelihood:

Logistic regression log likelihood

$$\log L(eta_0, eta_1) = \sum_{i=1}^n \left(Y_i \log(\pi_i) + (1-Y_i) \log(1-\pi_i)
ight)$$

Logistic regression log likelihood

$$egin{align} \log L(eta_0,eta_1) &= \sum_{i=1}^n Y_i \logigg(rac{e^{eta_0+eta_1 X_i}}{1+e^{eta_0+eta_1 X_i}}igg) + \ &\sum_{i=1}^n (1-Y_i) \logigg(1-rac{e^{eta_0+eta_1 X_i}}{1+e^{eta_0+eta_1 X_i}}igg) \end{aligned}$$

- lacktriangle Because we have two parameters, eta_0 and eta_1 , the situation is more difficult
- The math to find MLEs $\widehat{\beta}_0$ and $\widehat{\beta}_1$ is more complex than we will cover
- lacktriangledown R calculates $\widehat{\beta}_0$ and $\widehat{\beta}_1$ for us

Data: Grad application data

- admit: accepted to grad school? (0 = no, 1 = yes)
- gre: GRE score
- gpa: undergrad GPA
- rank: prestige of undergrad institution

Let's fit a logistic regression model with GPA as the predictor.

Data: Grad application data

- admit: accepted to grad school? (0 = no, 1 = yes)
- gre: GRE score
- gpa: undergrad GPA
- rank: prestige of undergrad institution

Let's fit a logistic regression model with GPA as the predictor.

```
glm(admit ~ gpa, family = binomial, data = grad_app)
```

```
glm(admit ~ gpa, family = binomial, data = grad_app)
##
## Call: glm(formula = admit ~ gpa, family = binomial, dat
##
## Coefficients:
## (Intercept)
                   gpa
## -4.358 1.051
##
## Degrees of Freedom: 399 Total (i.e. Null); 398 Residual
## Null Deviance: 500
## Residual Deviance: 487 AIC: 491
```

What are $\widehat{\beta}_0$ and $\widehat{\beta}_1$?

```
## Degrees of Freedom: 399 Total (i.e. Null); 398 Residual
## Null Deviance: 500
## Residual Deviance: 487 AIC: 491
```

For linear regression, the bottom part of the output usually contains things like R^2 and R^2_{adj} -- measures of how well the model fits the data.

What quantity have we been exploring that allows us to evaluate how well the model fits the data?

```
## Degrees of Freedom: 399 Total (i.e. Null); 398 Residual
## Null Deviance: 500
## Residual Deviance: 487 AIC: 491
```

For linear regression, the bottom part of the output usually contains things like R^2 and R^2_{adj} -- measures of how well the model fits the data.

Does R report the likelihood of the fitted model?

Deviance

R reports the *deviance*, rather than the likelihood.

Deviance:

Deviance

Deviance $= -2 \log L = 487$

```
## Degrees of Freedom: 399 Total (i.e. Null); 398 Residual
## Null Deviance: 500
## Residual Deviance: 487 AIC: 491
...
```

Class activity

https://sta214-f22.github.io/class_activities/ca_lecture_7.html

Class activity: deviance

```
glm(admit ~ gre, family = binomial, data = grad_app)

...
## Degrees of Freedom: 399 Total (i.e. Null); 398 Residual
## Null Deviance: 500
## Residual Deviance: 486.1 AIC: 490.1
...
```

What is the deviance of my fitted model?

Class activity: deviance

```
glm(admit ~ gre, family = binomial, data = grad_app)

...
## Degrees of Freedom: 399 Total (i.e. Null); 398 Residual
## Null Deviance: 500
## Residual Deviance: 486.1 AIC: 490.1
...
```

Which predictor (GRE or GPA) gives a model with a better fit?

Class activity: deviance

```
glm(admit ~ gre, family = binomial, data = grad_app)

...
## Degrees of Freedom: 399 Total (i.e. Null); 398 Residual
## Null Deviance: 500
## Residual Deviance: 486.1 AIC: 490.1
...
```

Which predictor (GRE or GPA) gives a model with a better fit?

GRE has a slightly smaller deviance (486.1 vs. 487), so GRE gives a slightly better fit.

Class activity: hypotheses

$$Y_i \sim Bernoulli(\pi_i) \ \ \logigg(rac{\pi_i}{1-\pi_i}igg) = eta_0 + eta_1 ext{GRE}_i.$$

We want to know if there is actually a relationship between GRE score and grad school admission.

How can I express this as null and alternative hypotheses about one or more model parameters?

Comparing deviances

```
##

Null deviance: 499.98 on 399 degrees of freedom

## Residual deviance: 486.06 on 398 degrees of freedom

...
```

499.98 = deviance for intercept-only model

$$\log\left(\frac{\pi_i}{1-\pi_i}\right) = \beta_0$$

486.06 = deviance for full model

$$\log \left(\frac{\pi_i}{1 - \pi_i} \right) = \beta_0 + \beta_1 \text{GRE}_i$$

drop-in-deviance:

Comparing deviances

 $\operatorname{drop-in-deviance}: G = \operatorname{deviance}$ for reduced model - deviance for full model = 13.92

Full model:
$$\log \left(\frac{\pi_i}{1-\pi_i} \right) = \beta_0 + \beta_1 \mathrm{GRE}_i$$

Reduced model:
$$\log \left(\frac{\pi_i}{1 - \pi_i} \right) = \beta_0$$

Why is G always ≥ 0 ?

Comparing deviances

 $\operatorname{drop-in-deviance}: G = \operatorname{deviance}$ for reduced model - deviance for full model = 13.92

Full model:
$$\log \left(\frac{\pi_i}{1-\pi_i} \right) = \beta_0 + \beta_1 \mathrm{GRE}_i$$

Reduced model:
$$\log \left(\frac{\pi_i}{1 - \pi_i} \right) = \beta_0$$

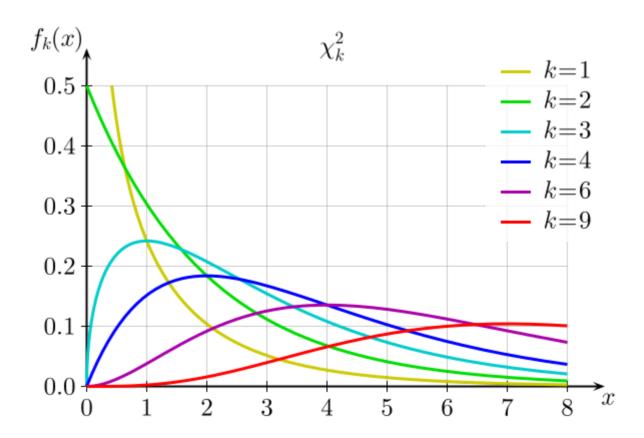
$$H_0: \beta_1 = 0 \quad H_A: \beta_1 \neq 0$$

If H_0 is true, how unusual is G=13.92?

χ^2 distribution

Under H_0 , $G \sim \chi^2_{df_{ ext{reduced}} - df_{ ext{full}}}$

 χ^2_k distribution: parameterized by degrees of freedom k



Computing a p-value

$$\log\left(rac{\pi_i}{1-\pi_i}
ight) = eta_0 + eta_1 \mathrm{GRE}_i$$

$$H_0: \beta_1 = 0 \quad H_A: \beta_1 \neq 0$$

G= deviance for reduced model - deviance for full model = 13.92 $\sim \chi_1^2$

```
pchisq(13.92, df = 1, lower.tail=FALSE)
```

[1] 0.0001907579

Concept check

Our p-value is 0.0002. What is the most appropriate conclusion? Go to https://pollev.com/ciaranevans637 to respond.

- (A) We reject the null hypothesis, since p < 0.05.
- (B) We fail to reject the null hypothesis, since p < 0.05.
- (C) The data provide strong evidence of a relationship between GRE score and the probability of admission to graduate school.
- (D) The data do not provide strong evidence of a relationship between GRE score and the probability of admission to graduate school.

Likelihood ratio test for nested models