

Linear and logistic regression

Ciaran Evans

Last time: parameter estimation for linear regression

$$\begin{bmatrix} Y_1 \\ Y_2 \\ \vdots \\ Y_n \end{bmatrix} = \begin{bmatrix} 1 & X_{11} & X_{12} & \cdots & X_{1k} \\ 1 & X_{21} & X_{22} & \cdots & X_{2k} \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 1 & X_{n1} & X_{n2} & \cdots & X_{nk} \end{bmatrix} \begin{bmatrix} \beta_0 \\ \vdots \\ \beta_k \end{bmatrix} + \begin{bmatrix} \varepsilon_1 \\ \varepsilon_2 \\ \vdots \\ \varepsilon_n \end{bmatrix}$$

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \boldsymbol{\varepsilon}$$

$$SSE(\boldsymbol{\beta}) = (\mathbf{y} - \mathbf{X}\boldsymbol{\beta})^T(\mathbf{y} - \mathbf{X}\boldsymbol{\beta})$$

$$\frac{\partial}{\partial \boldsymbol{\beta}} SSE(\boldsymbol{\beta}) =$$

Parameter estimation for linear regression

$$\frac{\partial}{\partial \beta} SSE(\beta) = -2\mathbf{X}^T(\mathbf{y} - \mathbf{X}\beta) \stackrel{set}{=} \mathbf{0}$$

Warmup

Work on the warmup activity:

https://sta711-s26.github.io/class_activities/ca_02.html

Submit your work on Canvas.

Warmup

```
library(Stat2Data)
data("FirstYearGPA")

lm(GPA ~ HSGPA + SATM, data = FirstYearGPA) |> coef()

## (Intercept)          HSGPA          SATM
## 0.7579761649 0.5305150632 0.0007984613

y <- FirstYearGPA$GPA
X <- cbind(1, FirstYearGPA$HSGPA, FirstYearGPA$SATM)
solve(t(X) %*% X) %*% t(X) %*% y

## [,1]
## [1,] 0.7579761649
## [2,] 0.5305150632
## [3,] 0.0007984613
```

Regression assumptions

$$\text{GPA}_i = \beta_0 + \beta_1 \text{HSGPA}_i + \beta_2 \text{SATM}_i + \varepsilon_i$$

Question: What assumptions do we often make when fitting a linear regression model?

Regression assumptions

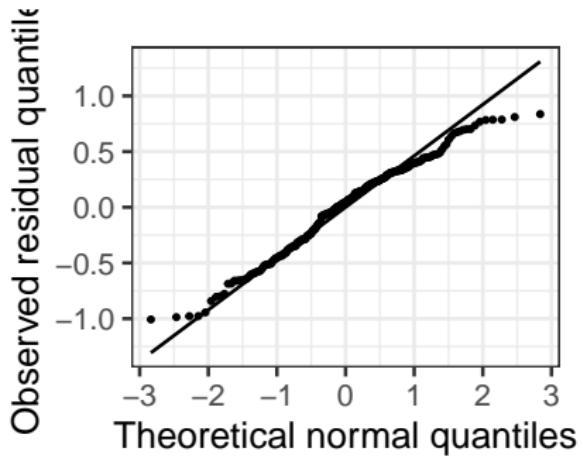
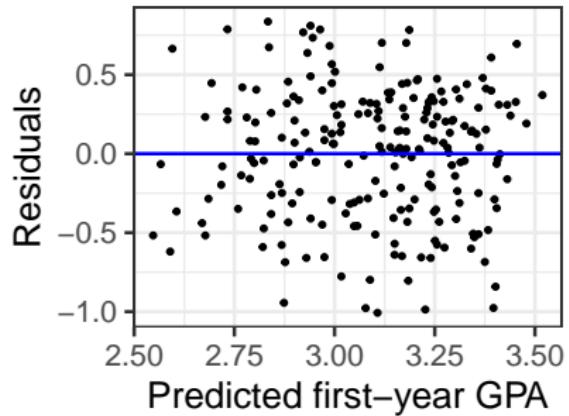
$$\text{GPA}_i = \beta_0 + \beta_1 \text{HSGPA}_i + \beta_2 \text{SATM}_i + \varepsilon_i$$

Some common assumptions:

- ▶ Shape
- ▶ Constant variance (variance of ε_i is the same for all observations)
- ▶ Normality (ε_i comes from a normal distribution)
- ▶ Independence

Question: How do we assess these assumptions?

Diagnostic plots



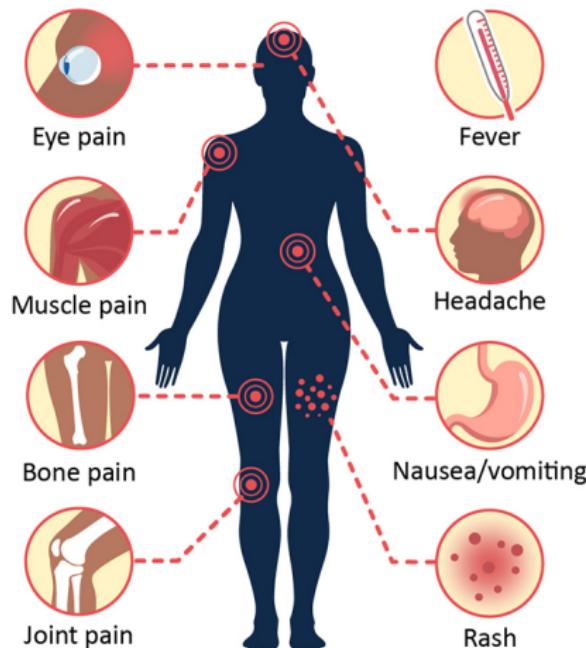
Question: Do the regression assumptions seem reasonable here?

Another motivating example: Dengue fever

Dengue fever: a mosquito-borne viral disease affecting 400 million people a year

Dengue Symptoms

Fever with any of the following



Motivating example: Dengue data

Data: Data on 5720 Vietnamese children, admitted to the hospital with possible dengue fever. Variables include:

- ▶ *Sex*: patient's sex (female or male)
- ▶ *Age*: patient's age (in years)
- ▶ *WBC*: white blood cell count
- ▶ *PLT*: platelet count
- ▶ other diagnostic variables...
- ▶ *Dengue*: whether the patient has dengue (0 = no, 1 = yes)

Research goal: Predict dengue status using diagnostic measurements

Fitting a model: initial attempt

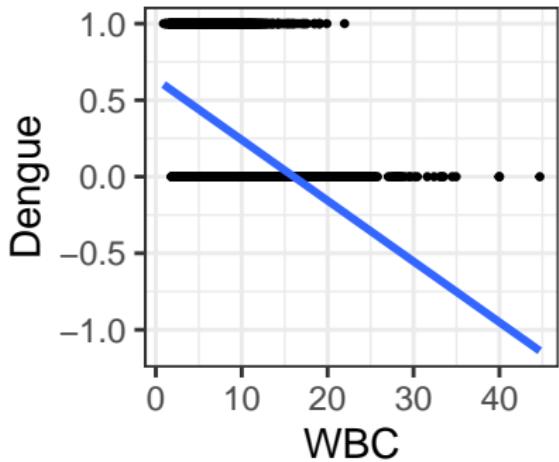
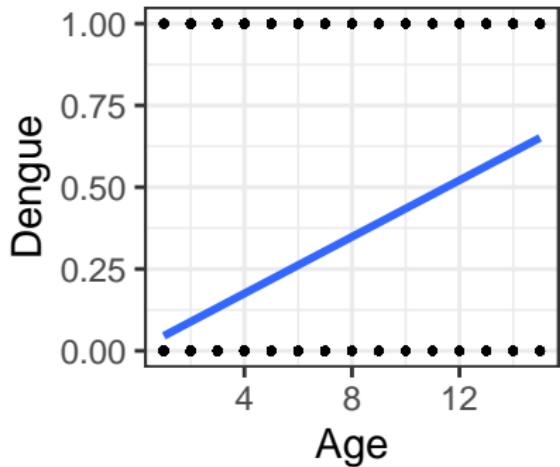
What if we try a linear regression model?

Y_i = dengue status of i th patient

$$Y_i = \beta_0 + \beta_1 WBC_i + \varepsilon_i \quad \varepsilon_i \stackrel{iid}{\sim} N(0, \sigma^2)$$

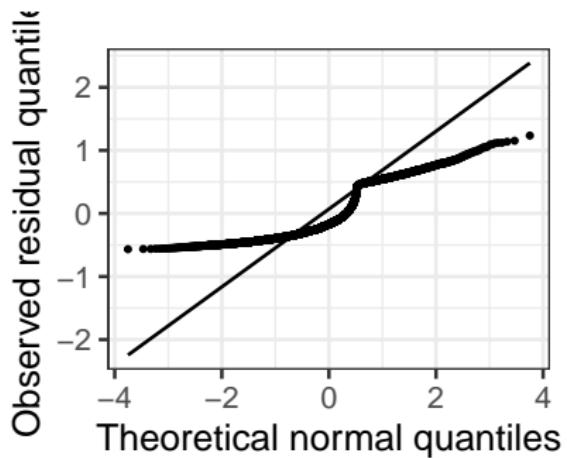
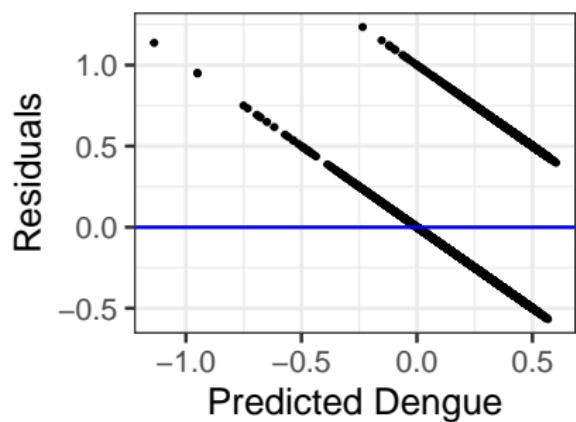
What are some potential issues with this linear regression model?

Don't fit linear regression with a binary response



Don't fit linear regression with a binary response

Diagnostic plots:



Second attempt

Let's rewrite the linear regression model:

Second attempt

$$Y_i | WBC_i \sim Bernoulli(p_i) \quad p_i = \mathbb{P}(Y_i = 1 | WBC_i)$$

$$p_i = \beta_0 + \beta_1 WBC_i$$

Are there still any potential issues with this approach?

Fixing the issue: logistic regression

$$Y_i | WBC_i \sim \text{Bernoulli}(p_i)$$

$$g(p_i) = \beta_0 + \beta_1 WBC_i$$

where $g : (0, 1) \rightarrow \mathbb{R}$ is unbounded.

Usual choice: $g(p_i) = \log \left(\frac{p_i}{1 - p_i} \right)$

Logistic regression model

$$Y_i | WBC_i \sim Bernoulli(p_i)$$

$$\log \left(\frac{p_i}{1 - p_i} \right) = \beta_0 + \beta_1 WBC_i$$

Why is there no noise term ε_i in the logistic regression model?

Discuss for 1–2 minutes with your neighbor, then we will discuss as a class.

Fitting the logistic regression model

$$Y_i | WBC_i \sim Bernoulli(p_i)$$

$$\log \left(\frac{p_i}{1 - p_i} \right) = \beta_0 + \beta_1 WBC_i$$

```
m1 <- glm(Dengue ~ WBC, data = dengue,  
            family = binomial)  
summary(m1)
```

Fitting the logistic regression model

$$Y_i | WBC_i \sim Bernoulli(p_i)$$

$$\log\left(\frac{p_i}{1 - p_i}\right) = \beta_0 + \beta_1 WBC_i$$

```
m1 <- glm(Dengue ~ WBC, data = dengue,
             family = binomial)
summary(m1)
```

```
##  
## Call:  
## glm(formula = Dengue ~ WBC, family = binomial, data = de  
##  
## Coefficients:  
##              Estimate Std. Error z value Pr(>|z|)  
## (Intercept)  1.73743   0.08499  20.44   <2e-16 ***  
## WBC        -0.36085   0.01243 -29.03   <2e-16 ***  
## ---
```

Making predictions

$$\log \left(\frac{\hat{p}_i}{1 - \hat{p}_i} \right) = 1.737 - 0.361 \ WBC_i$$

Work in groups of 2-3 on the following questions:

- ▶ What is the predicted odds of dengue for a patient with a WBC of 10?
- ▶ For a patient with a WBC of 10, is the predicted probability of dengue > 0.5 , < 0.5 , or $= 0.5$?
- ▶ What is the predicted *probability* of dengue for a patient with a WBC of 10?