1 / 38

### Logistic regression

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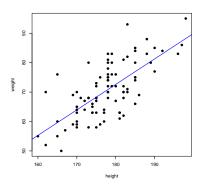
October 13, 2022

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#### Contents

- Introduction
- 2 Fitting the logistic model
- 3 Hypothesis testing
- Model building

#### Classical linear regression



#### Theoretical model:

$$v_i = \beta_0 + \beta_1 x_i + \varepsilon_i$$

Usual assumptions:

- $E(\varepsilon_i) = 0$ .
- $V(\varepsilon_i) = \sigma^2$  (constant variance).
- $Cov(\varepsilon_i, \varepsilon_j) = 0$  (independent observations).
- $\varepsilon_i \sim N(0, \sigma^2)$ .

#### Summarized:

$$Y_i|X_i \sim N(\beta_0 + \beta_1 X_i, \sigma^2)$$

Graffelman (UPC) Logistic regression October 13, 2022 3 / 38

#### Binary response

What if the response is a binary variable?

#### Examples:

- Explaining disease (0/1) on the basis of biomarkers.
- $\bullet$  Explaining admission (0/1) to a university or college using demographic variables and high school grades.
- Explaining low birth weight (0/1) on the basis of characteristics of the mother.
- ....

5 / 38

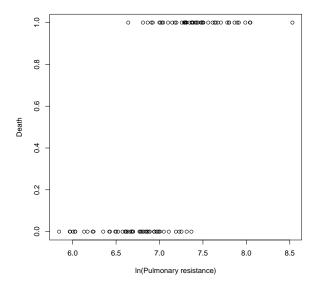
#### Example data set on Myocardial Infarction

| #   | Pulse | CI   | SI    | DBP   | PA    | VP    | PR   | Death |
|-----|-------|------|-------|-------|-------|-------|------|-------|
| 1   | 90    | 1.71 | 19.00 | 16.00 | 19.50 | 16.00 | 912  | 0     |
| 2   | 90    | 1.68 | 18.70 | 24.00 | 31.00 | 14.00 | 1476 | 1     |
| 3   | 120   | 1.40 | 11.70 | 23.00 | 29.00 | 8.00  | 1657 | 1     |
| 4   | 82    | 1.79 | 21.80 | 14.00 | 17.50 | 10.00 | 782  | 0     |
| 5   | 80    | 1.58 | 19.70 | 21.00 | 28.00 | 18.50 | 1418 | 1     |
| 6   | 80    | 1.13 | 14.10 | 18.00 | 23.50 | 9.00  | 1664 | 1     |
| 7   | 94    | 2.04 | 21.70 | 23.00 | 27.00 | 10.00 | 1059 | 0     |
| 8   | 80    | 1.19 | 14.90 | 16.00 | 21.00 | 16.50 | 1412 | 0     |
| 9   | 78    | 2.16 | 27.70 | 15.00 | 20.50 | 11.50 | 759  | 0     |
| 10  | 100   | 2.28 | 22.80 | 16.00 | 23.00 | 4.00  | 807  | 0     |
| 11  | 90    | 2.79 | 31.00 | 16.00 | 25.00 | 8.00  | 717  | 0     |
| 12  | 86    | 2.70 | 31.40 | 15.00 | 23.00 | 9.50  | 681  | 0     |
| 13  | 80    | 2.61 | 32.60 | 8.00  | 15.00 | 1.00  | 460  | 0     |
| 14  | 61    | 2.84 | 47.30 | 11.00 | 17.00 | 12.00 | 479  | 0     |
| 15  | 99    | 3.12 | 31.80 | 15.00 | 20.00 | 11.00 | 513  | 0     |
| 16  | 92    | 2.47 | 26.80 | 12.00 | 19.00 | 11.00 | 615  | 0     |
| 17  | 96    | 1.88 | 19.60 | 12.00 | 19.00 | 3.00  | 809  | 0     |
| 18  | 86    | 1.70 | 19.80 | 10.00 | 14.00 | 10.50 | 659  | 0     |
| 19  | 125   | 3.37 | 26.90 | 18.00 | 28.00 | 6.00  | 665  | 0     |
| 20  | 80    | 2.01 | 25.00 | 15.00 | 20.00 | 6.00  | 796  | 0     |
|     |       |      |       |       |       |       |      |       |
|     |       |      |       |       |       |       |      | •     |
| 101 | 112   | 1.54 | 13.80 | 25.00 | 31.00 | 8.00  | 1610 | i     |

CI = Cardiac index; SI = Systolic index; DBP = Diastolic blood pressure
PA = Pulmonary artery pressure; VP = Ventricular pressure; PR = Pulmonary resistance
Saporta, G. (2006) Probabilités, Analyse des Données et Statistique. Editions Technip, Paris.

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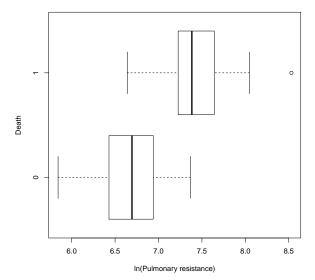
### Scatterplot



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6 / 38

# **Boxplot**

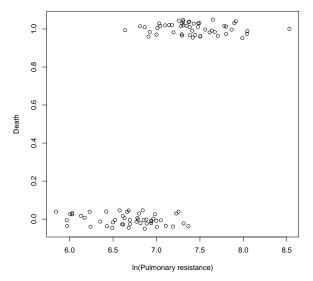


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7 / 38

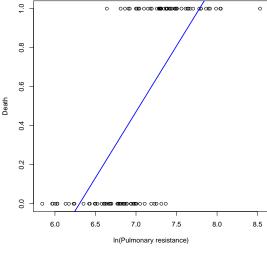
8 / 38

#### Scatterplot with jitter



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### Scatterplot with OLS regression line



Any problem?

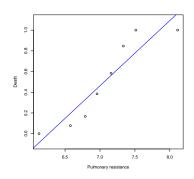
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### Categorized pulmonary resistance

| rango        |     | 0  | 1  | nronortion |
|--------------|-----|----|----|------------|
| range        | n   | U  | Т  | proportion |
| (5.79,6.46]  | 13  | 13 | 0  | 0.00       |
| (6.46, 6.69] | 13  | 12 | 1  | 80.0       |
| (6.69, 6.89] | 12  | 10 | 2  | 0.17       |
| (6.89, 7.03] | 13  | 8  | 5  | 0.38       |
| (7.03, 7.29] | 12  | 5  | 7  | 0.58       |
| (7.29, 7.38] | 13  | 2  | 11 | 0.85       |
| (7.38, 7.64] | 12  | 0  | 12 | 1.00       |
| (7.64, 8.58] | 13  | 0  | 13 | 1.00       |
| All          | 101 | 50 | 51 | 0.50       |

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#### **OLS** regression



```
> lm.out <- lm(pro~m)
> summarv(lm.out)
Call:
lm(formula = pro ~ m)
```

#### Residuals:

```
Min
              10
                  Median
                               30
                                       Max
-0.16296 -0.12971 -0.01517 0.10913 0.21427
```

#### Coefficients:

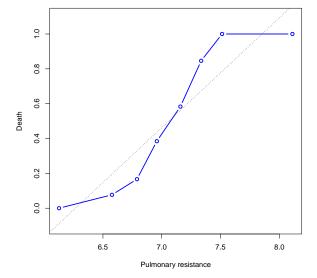
```
Estimate Std. Error t value Pr(>|t|)
(Intercept) -3.94996
                       0.70645 -5.591 0.001392 **
            0.63033
                       0.09959
                                 6.330 0.000727 ***
m
```

Residual standard error: 0.16 on 6 degrees of freedom Multiple R-squared: 0.8697, Adjusted R-squared: 0.848 F-statistic: 40.06 on 1 and 6 DF, p-value: 0.0007272

>

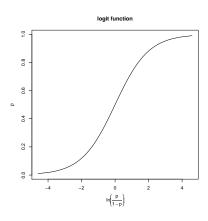
11 / 38

# Observed and fitted pattern



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#### The logit function



Logit (or logistic) function:

$$logit(\pi) = \ln\left(\frac{\pi}{1-\pi}\right)$$

Inverse of the logit function

$$logit^{-1}(\pi) = \frac{e^{\pi}}{e^{\pi} + 1}$$

Using  $\mathsf{logit}(\pi)$  as the response is the basis of logistic regression

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### The logistic regression model

$$\pi(x) = E(Y|x) = P(Y = 1|x)$$

Model: 
$$y = \pi(x) + \varepsilon$$
  $y|x \sim Bin(n = 1, \pi(x))$ 

$$\varepsilon = \left\{ \begin{array}{ll} 1 - \pi(x) & \text{if } y = 1 & \text{with prob.} & \pi(x) \\ -\pi(x) & \text{if } y = 0 & \text{with prob.} & 1 - \pi(x) \end{array} \right.$$

$$E\left(\varepsilon\right) = \left(1 - \pi(x)\right)\pi(x) - \pi(x)\left(1 - \pi(x)\right) = 0$$

$$V(\varepsilon) = \pi(x)(1 - \pi(x))$$

$$g(x) = \ln\left(\frac{\pi(x)}{1 - \pi(x)}\right) = \beta_0 + \beta_1 x$$

$$\pi(x) = \frac{e^{\beta_0 + \beta_1 x}}{e^{\beta_0 + \beta_1 x} + 1}$$

#### Note that

- $0 < \pi(x) < 1$
- $-\infty \le g(x) \le +\infty$

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#### Model and likelihood

$$L(\beta_0, \beta_1) = \prod_{i=1}^n \pi(x_i)^{y_i} [1 - \pi(x_i)]^{1 - y_i}$$

$$\ell(\beta_0, \beta_1) = \sum_{i=1}^n \{y_i \ln [\pi(x_i)] + (1 - y_i) \ln [1 - \pi(x_i)]\}$$

We maximize  $\ell(\beta_0, \beta_1)$  by numerical methods

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16 / 38

## Fitting a logistic model regression in R

```
model <- glm(Death~1PR, family = binomial(link = 'logit'), trace=FALSE)
summary(model)
Call:
glm(formula = death ~ 1PR. family = binomial(link = "logit"))
Deviance Residuals:
    Min
               10 Median
                                            Max
                                   30
-2 09196 -0 41945 0 01073 0 46258 2 36750
Coefficients:
           Estimate Std. Error z value Pr(>|z|)
(Intercept) -46.651
                         9.231 -5.054 4.33e-07
1PR
              6.613
                         1.307
                                 5.059 4.22e-07
(Dispersion parameter for binomial family taken to be 1)
   Null deviance: 140,006 on 100 degrees of freedom
Residual deviance: 64.529 on 99 degrees of freedom
ATC: 68.529
Number of Fisher Scoring iterations: 6
>
```

| Iteration | log-likelihood | Deviance |
|-----------|----------------|----------|
| 1         | -37.30         | 74.60    |
| 2         | -33.08         | 66.17    |
| 3         | -32.30         | 64.61    |
| 4         | -32.26         | 64.53    |
| 5         | -32.26         | 64.53    |
| 6         | -32.26         | 64.53    |

## Writing the fitted model

In OLS regression we used:

$$\hat{y}_i = b_0 + b_1 x_i$$

In logistic regression we have the fitted values:

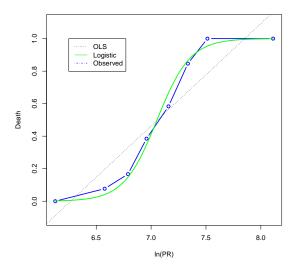
$$\hat{\pi}(x) = \frac{e^{-46.651 + 6.613Pul.Res}}{1 + e^{-46.651 + 6.613Pul.Res}}$$

or the estimated logit:

$$\hat{g}(x) = -46.651 + 6.613$$
Pul.Res

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### Plotting the fitted logistic model

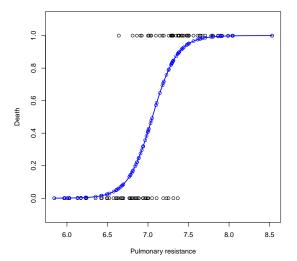


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Model building

20 / 38

# Plotting the fitted logistic model (usual representation)



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```
model <- glm(Death~1PR, family = binomial(link = 'logit'), trace=TRUE)
summary(model)
plot(1PR,Death,xlab="Pulmonary resistance",ylab="Death", ylim=c(-0.1,1.1))
curve(predict(model,data.frame(1PR=x),type="resp"),add=TRUE,col="blue",lwd=2)
points(1PR,fitted(model),pch=1,col="blue")</pre>
```

# Likelihood ratio test for comparing models (1/2)

We first compare the fitted model with a saturated model:

$$D = -2 \ln \left( \frac{\text{Likelihood fitted model}}{\text{Likelihood saturated model}} \right)$$

Hypothesis testing

- A saturated model is a model with as many data points as parameters.
- D is usually called the deviance, and is analogous to the sum-of-squares of the residuals.
- The likelihood of the saturated model is

$$\prod_{i=1}^{n} \pi(x_i)^{y_i} \left[1 - \pi(x_i)\right]^{1-y_i} = \prod_{i=1}^{n} y_i^{y_i} \left[1 - y_1\right]^{1-y_i} = 1$$

The deviance simplifies to

$$D = -2 \ln \text{(Likelihood fitted model)}$$

The null deviance is the deviance of a model containing only the intercept.

Graffelman (UPC) Logistic regression October 13, 2022 22 / 38

# Likelihood ratio test for comparing models (2/2)

 We wish to compare the model with and without the predictor (pulmonary resistance)

•

$$G = -2 \ln \left( \frac{\text{Likelihood without predictor}}{\text{Likelihood with predictor}} \right)$$

$$= -2 \left[ \ln \left( \text{Likelihood without predictor} \right) - \ln \left( \text{Likelihood with predictor} \right) \right]$$

$$= D(\text{without predictor}) - D(\text{with predictor})$$

• The reduction in deviance determines if the predictor is relevant.

Graffelman (UPC) Logistic regression October 13, 2022 23 / 38

October 13, 2022

24 / 38

# Assessing over all model fit (1/2)

> anova(model.test="Chisq")

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 $P\left(\chi_{(1)}^2 > 75.47\right) \approx 0$ 

# Assessing over all model fit (2/2)

- Some programs report McFadden's pseudo R<sup>2</sup> for assessing model fit.
- •

$$R_{\text{McFadden}}^2 = 1 - \frac{\text{Likelihood model considered}}{\text{Likelihood null model}}$$

- $0 \le R_{McFadden}^2 \le 1$
- For the example at hand

$$R_{McFadden}^2 = 1 - \frac{-32.26456}{-70.00291} = 0.539$$

• Interpretation different from  $R^2$  in standard linear regression

Graffelman (UPC) Logistic regression October 13, 2022 25 / 38

In logistic regression three procedures are in use to test predictors for significance

- Likelihood ratio test (LRT)
- Wald test

Introduction

Score test

The Wald test:  $H_0: \beta_i = 0$   $\beta_i \neq 0$ 

$$Z = rac{\hat{eta}_i}{\hat{SE}(\hat{eta}_i)} \sim N(0,1)$$
 under  $H_0$ 

Hypothesis testing

Wald confidence interval

$$CI(\beta_i) = \hat{\beta}_i \pm z_{1-\alpha/2} \hat{SE}(\hat{\beta}_i)$$

E.g. for Pulm. Res.

$$Z = \frac{6.613}{1.307} = 5.059$$
 p-value =  $2P(Z > 5.059) = 4.22e - 07$ 

$$CI(\beta_{PM}) = 6.613 \pm 1.96 \cdot 1.307 = (4.05, 9.18)$$

> confint(model)

Waiting for profiling to be done ... 2.5 % 97.5 %

(Intercept) -67.486679 -30.879875 1PR 4.380653 9.566105 >

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### Logistic regression with binary predictor

- $\bullet$   $\pi(x) = E(Y|x) = P(Y = 1|x)$
- The odds of Y = 1 with x = 1 is

$$\mathsf{odds} = \frac{\pi(1)}{1 - \pi(1)}$$

Hypothesis testing

- Note the logit is just the logarithm of the odds.
- The odds ratio is a widely used measure of association.

$$\mathsf{OR} = rac{\pi(1)/\left[1-\pi(1)
ight]}{\pi(0)/\left[1-\pi(0)
ight]}$$

• For the logistic model  $\pi(x) = \frac{e^{\beta_0 + \beta_1 x}}{\frac{e^{\beta_0 + \beta_1 x}}}{\frac{e^{\beta_0 + \beta_1 x}}{\frac{e^{\beta_0 + \beta_1 x}}}{\frac{e^{\beta_0 + \beta_1 x}}{\frac{e^{\beta_0 + \beta_1 x}}}{\frac{e^{\beta_0 + \beta_1 x}}{\frac{e^{\beta_0 + \beta_1 x}}{\frac{e^{\beta_0 + \beta_1 x}}}{\frac{e^{\beta_0 + \beta_1 x}}{\frac{e^{\beta_0 + \beta_1 x}}}{\frac{e^{\beta_0 + \beta$ 

•

$$\mathsf{OR} = \frac{\pi(1)/[1-\pi(1)]}{\pi(0)/[1-\pi(0)]} = \mathsf{e}^{\beta_1}$$

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### Example

$$CID = I_{CI < Me}$$

|     | Death |    |  |  |  |
|-----|-------|----|--|--|--|
| CID | 0     | 1  |  |  |  |
| 0   | 42    | 9  |  |  |  |
| 1   | 8     | 42 |  |  |  |

$$\mathsf{OR} = \frac{42 \times 42}{8 \times 9} = 24.5$$

#### Call:

glm(formula = Death ~ CId, family = binomial(link = "logit"), trace = TRUE)

#### Deviance Residuals:

Min 1Q Median Max -1.9145 -0.6231 0.5905 0.5905 1.8626

#### Coefficients:

Estimate Std. Error z value Pr(>|z|) (Intercept) -1.5404 0.3673 -4.194 2.74e-05 CIGTRUE 3.1987 0.5327 6.005 1.91e-09

Hypothesis testing

00000

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 140.006 on 100 degrees of freedom Residual deviance: 91.499 on 99 degrees of freedom AIC: 95.499

Number of Fisher Scoring iterations: 4

$$\mathsf{OR} = e^{3.1987} = 24.5$$

Graffelman (UPC) Logistic regression 28 / 38

$$CI(\beta_i) = \hat{\beta}_i \pm z_{1-\alpha/2} \hat{SE}(\hat{\beta}_i)$$

Hypothesis testing

$$CI(OR) = e^{\hat{eta}_i \pm z_{1-\alpha/2} \hat{SE}(\hat{eta}_i)}$$

For the data at hand:

$$CI(\beta_i) = (2.15, 4.24)$$

$$CI(OR) = (8.63, 69.59)$$

Graffelman (UPC) Logistic regression October 13, 2022 29 / 38

30 / 38

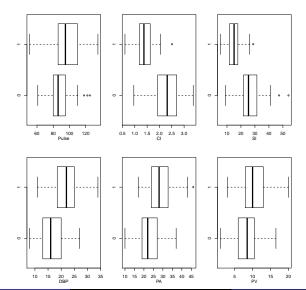
### Interpretation with continuous predictor

```
Call:
glm(formula = Death ~ Pulse, family = binomial(link = "logit").
   trace = TRUE)
Coefficients:
           Estimate Std. Error z value Pr(>|z|)
(Intercept) -2.73307 1.23132 -2.220 0.0264
            0.02991
                    0.01321
                                2.263
                                        0.0236
Pulse
(Dispersion parameter for binomial family taken to be 1)
   Null deviance: 140.01 on 100 degrees of freedom
Residual deviance: 134.45 on 99 degrees of freedom
ATC: 138.45
Number of Fisher Scoring iterations: 4
```

- Estimated logit  $\hat{g}(x) = -2.73307 + 0.02991$  Pulse
- The slope gives the change in the logit for a one-unit change in Pulse.
- With a one-unit change in Pulse, the odds for death is multiplied by  $e^{0.02991} = 1.03$
- ullet With a 10-unit change in Pulse, the odds for death is multiplied by  $e^{10 \times 0.02991} = 1.35$

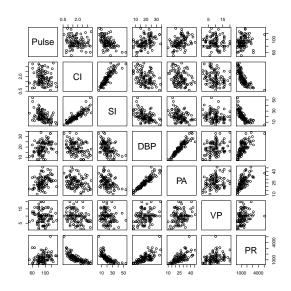
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### Boxplots for other predictors



Graffelman (UPC) Logistic regression October 13, 2022 31 / 38

### Relationships between predictors



Graffelman (UPC) Logistic regression October 13, 2022 32 / 38

33 / 38

### Multiple predictors

```
> summary(model)
Call:
glm(formula = Death ~ Pulse + CI + SI + DBP + PA + VP + 1PR,
    family = binomial(link = "logit"), trace = TRUE)
Deviance Residuals:
     Min
                      Median
-2.59039 -0.40158
                     0.02522
                             0.39452
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) 18.43452
                       52.39826
                                  0.352
                                           0.725
             0.04705
                        0.08874
                                  0.530
                                           0.596
Pulse
            -7.35661
                        6.15306
                                 -1.196
                                           0.232
                        0.39514
             0.10457
                                  0.265
                                           0.791
DBP
             0.05335
                        0.20022
                                  0.266
                                           0.790
PA
             0.25157
                        0.30728
                                  0.819
                                           0.413
             0.05218
                        0.07913
                                  0.659
                                           0.510
1PR
            -2.79126
                        7.29886 -0.382
                                           0.702
(Dispersion parameter for binomial family taken to be 1)
    Null deviance: 140.006 on 100 degrees of freedom
Residual deviance: 58.497 on 93 degrees of freedom
AIC: 74.497
Number of Fisher Scoring iterations: 7
>
But note that G = 140.006 - 58.497 = 81.509 and P\left(\chi_7^2 \ge 81.509\right) = 6.779506e - 15
```

October 13, 2022

34 / 38

#### After backward elimination

```
Call:
glm(formula = Death ~ CI + PA, family = binomial(link = "logit"),
    trace = TRUE)
Deviance Residuals:
                                   30
    Min
                10 Median
                                            Max
-2.22793 -0.39632
                    0.02777 0.44453 2.71096
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) 2.9331
                        1.7855 1.643
                                         0.1004
            -4 5491
                        0.9402 -4.838 1.31e-06
CT
PΛ
            0.2015
                        0.0622
                                 3.239
                                         0.0012
(Dispersion parameter for binomial family taken to be 1)
    Null deviance: 140.01 on 100 degrees of freedom
Residual deviance: 60.27 on 98 degrees of freedom
ATC: 66.27
Number of Fisher Scoring iterations: 6
>
                     G = 60.270 - 58.497 = 1.773 P\left(\chi_5^2 \ge 1.773\right) = 0.880
```

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Introduction

- In logistic regression, overdispersion sometimes occurs.
- Overdispersion refers to the fact that the variance exceeds the theoretical binomial variance.

Hypothesis testing

- With overdispersion, standard errors are typically too small.
- Overdispersion can be modelled with  $V(Y_i) = \phi E(Y_i)$ , where  $\phi$  is the overdispersion parameter
- $\phi$  can be estimated as  $\hat{\phi} = \frac{X^2}{df}$ .
- This can be done by quasi-binomial regression.

#### Example

```
model <- glm(Death~VP, family = binomial(link = 'logit'))
                                                                  model <- glm(Death~VP, family = quasibinomial(link = 'logit'))
> summary(model)
                                                                   > summary(model)
glm(formula = Death ~ VP, family = binomial(link = "logit"))
                                                                  glm(formula = Death ~ VP. family = quasibinomial(link = "logit"))
Deviance Residuals:
                                                                   Deviance Residuals:
             1Q Median
-1.6022 -1.1319 0.6562
                                                                                             1.1386
                                                                  -1.6022 -1.1319 0.6562
Coefficients:
                                                                   Coefficients:
            Estimate Std. Error z value Pr(>|z|)
                                                                   Estimate Std. Error t value Pr(>|t|)
(Intercept) -1.24190    0.52801 -2.352    0.0206 *
(Intercept) -1.24190
                        0.52391 -2.370 0.01777 *
             0.13340
                        0.05124 2.603 0.00923 **
                                                                                                    2.583
                                                                   VP
                                                                                0.13340
                                                                                           0.05164
                                                                                                             0.0113 *
---
(Dispersion parameter for binomial family taken to be 1)
                                                                   (Dispersion parameter for quasibinomial family taken to be 1.0156
    Null deviance: 140.01 on 100 degrees of freedom
                                                                       Null deviance: 140.01 on 100 degrees of freedom
Residual deviance: 132.48 on 99 degrees of freedom
                                                                   Residual deviance: 132.48 on 99 degrees of freedom
AIC: 136.48
                                                                   AIC: NA
Number of Fisher Scoring iterations: 4
                                                                   Number of Fisher Scoring iterations: 4
```

Graffelman (UPC) Logistic regression October 13, 2022 36 / 38

#### References

Hosmer, D. W., Lemeshow, S. & Sturdivant, R. X. (2013)
 Applied Logistic Regression. 3rd Edition. Wiley, New York.

Graffelman (UPC) Logistic regression October 13, 2022 37 / 38

38 / 38

Introduction

Low birth weight. In a study on low birth weight (LBW) of 189 babies, the following variables were registered: LOW (0 = > 2500 g; 1 = < 2500 g). AGE (of the mother), LWT (Weight of mother at last menstrual period). RACE (1 = White: 2 = Black: 3 = Other), SMOKE (Smoking status during pregnancy 0 = No: 1 = Yes), PTL (History of premature labor 0 = None; 1 = One; 2 = Two, etc.), HT (History of hypertension 0 = No; 1 = Yes), UI (Presence of Uuterine irritability 0 = No; 1 = Yes), FTV (Number of physician visits during the first trimester 0 None: 1 = One: 2 = Two etc.) and BWT (Recorded birth weight). The file lowbyt dat contains the data.

- Load the data in the R environment with the read.table instruction.
- Is LBW related to the smoking status of the mother? Make the corresponding two-way table and do a chi-square test to test for independence.
- Do a logistic regression of LBW on SMOKE, Report the estimated logit. Is there a significant association?
- Calculate the odds of LBW for smokers and non-smokers. Calculate the odds ratio (OR). Construct a 95% confidence interval for the OR.
- Investigate the effect of LWT on the risk of LBW. What relation do you expect? Does the data present evidence for the relation you expected? What's the effect of LWT on the odds of a LBW child? Is that effect significant?
- Calculate the predicted probabilities of LBW according to the last model, and plot the logistic regression curve
- Is smoking still relevant if we control for the effect of LWT? Calculate the adjusted OR of the effect of smoking. Give a 95% confidence interval for the adjusted OR and compare this with the unadjusted OR.
- Investigate the effect of RACE on the odds of a LBW child. Take care to use indicator variables for its categories. Is RACE a relevant predictor of LBW?
- Build a model with all available predictors in the database. If possible, try to simplify the model, and suggest what you would think that is a good model for the data.