

Logistic Regression

The ASTA team

Contents

1	Introduction to logistic regression	1
1.1	Binary response	1
1.2	A linear model	2
2	Simple logistic regression	2
2.1	Logistic model	2
2.2	Logistic transformation	2
2.3	Odds-ratio	3
2.4	Simple logistic regression	3
2.5	Example: Credit card data	3
2.6	Example: Fitting the model	4
2.7	Test of no effect	4
2.8	Confidence interval for odds ratio	5
2.9	Plot of model predictions against actual data	6
3	Multiple logistic regression	6
3.1	Several numeric predictors	6
3.2	Example	6
3.3	Global test of no effects	7
3.4	Example	7
3.5	Test of influence of a given predictor	8
3.6	Model selection by stepwise selection	8
3.7	Prediction and classification	9

1 Introduction to logistic regression

1.1 Binary response

- We consider a binary response y with outcome 1 or 0. This might be a code indicating whether a person is able or unable to perform a given task.
- Furthermore, we are given an explanatory variable x , which is numeric, e.g. age.
- We shall study models for

$$P(y = 1 | x)$$

i.e. the probability that a person of age x is able to complete the task.

- We shall see methods for determining whether or not age actually influences the probability, i.e. is y independent of x ?

1.2 A linear model

$$P(y = 1 | x) = \alpha + \beta x$$

is simple, but often inappropriate. If β is positive and x sufficiently large, then the probability exceeds 1.

2 Simple logistic regression

2.1 Logistic model

Instead we consider the **odds** that the person is able to complete the task

$$\text{Odds}(y = 1 | x) = \frac{P(y = 1 | x)}{P(y = 0 | x)} = \frac{P(y = 1 | x)}{1 - P(y = 1 | x)}$$

which can have any positive value.

The **logistic model** is defined as:

$$\text{logit}(P(y = 1 | x)) = \log(\text{Odds}(y = 1 | x)) = \alpha + \beta x$$

The function $\text{logit}(p) = \log(\frac{p}{1-p})$ - i.e. **log of odds** - is termed **the logistic transformation**.

Remark that log odds can be any number, where zero corresponds to $P(y = 1 | x) = 0.5$. Solving $\alpha + \beta x = 0$ shows that at age $x_0 = -\alpha/\beta$ you have fifty-fifty chance of solving the task.

2.2 Logistic transformation

- The function `logit()` (remember to load `mosaic` first) can be used to calculate the logistic transformation:

```
p <- seq(0.1, 0.9, by = 0.2)
```

```
p
```

```
## [1] 0.1 0.3 0.5 0.7 0.9
```

```
l <- logit(p)
```

```
l
```

```
## [1] -2.1972246 -0.8472979 0.0000000 0.8472979 2.1972246
```

- The inverse logistic transformation `ilogit()` applied to the transformed values can recover the original probabilities:

```
ilogit(l)
```

```
## [1] 0.1 0.3 0.5 0.7 0.9
```

2.3 Odds-ratio

Interpretation of β :

What happens to odds, if we increase age by 1 year?

Consider the so-called **odds-ratio**:

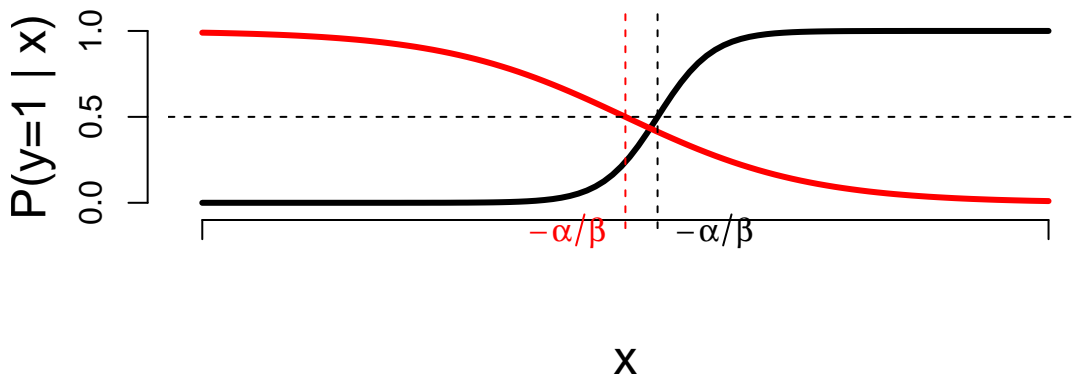
$$\frac{\text{Odds}(y = 1 | x + 1)}{\text{Odds}(y = 1 | x)} = \frac{\exp(\alpha + \beta(x + 1))}{\exp(\alpha + \beta x)} = \exp(\beta)$$

where we see, that $\exp(\beta)$ equals the odds for age $x + 1$ relative to odds at age x .

This means that when age increase by 1 year, then the relative change in odds is given by $100(\exp(\beta) - 1)\%$.

2.4 Simple logistic regression

Logistic curves



Examples of logistic curves. The black curve has a positive β -value ($=10$), whereas the red has a negative β ($=-3$).

In addition we note that:

- Increasing the absolute value of β yields a steeper curve.
- When $P(y = 1 | x) = \frac{1}{2}$ then logit is zero, i.e. $\alpha + \beta x = 0$.

This means that at age $x = -\frac{\alpha}{\beta}$ you have 50% chance to perform the task.

2.5 Example: Credit card data

We shall investigate if income is a good predictor of whether or not you have a credit card.

- Data structure: For each level of income, we let n denote the number of persons with that income, and credit how many of these that carries a credit card.

```
creInc <- read.csv("https://asta.math.aau.dk/datasets?file=income-credit.csv")
```

```
head(creInc)
```

```
##   Income  n credit
## 1     12  1     0
## 2     13  1     0
## 3     14  8     2
## 4     15 14     2
## 5     16  9     0
## 6     17  8     2
```

2.6 Example: Fitting the model

```
modelFit <- glm(cbind(credit,n-credit) ~ Income, data = creInc, family = binomial)
```

- `cbind` gives a matrix with two column vectors: `credit` and `n-credit`, where the latter is the vector counting the number of persons without a credit card.
- The response has the form `cbind(credit,n-credit)`.
- We need to use the function `glm` (generalized linear model).
- The argument `family=binomial` tells the function that the data has binomial variation. Leaving out this argument will lead R to believe that data follows a normal distribution - as with `lm`.
- The function `coef` extracts the coefficients (estimates of parameters) from the model summary:

```
coef(summary(modelFit))
```

```
##           Estimate Std. Error  z value    Pr(>|z|)
## (Intercept) -3.5179469 0.71033573 -4.952513 7.326117e-07
## Income      0.1054089 0.02615743  4.029788 5.582714e-05
```

2.7 Test of no effect

```
coef(summary(modelFit))
```

```
##           Estimate Std. Error  z value    Pr(>|z|)
## (Intercept) -3.5179469 0.71033573 -4.952513 7.326117e-07
## Income      0.1054089 0.02615743  4.029788 5.582714e-05
```

Our model for dependence of odds of having a credit card related to income(x) is

$$\text{logit}(x) = \alpha + \beta x$$

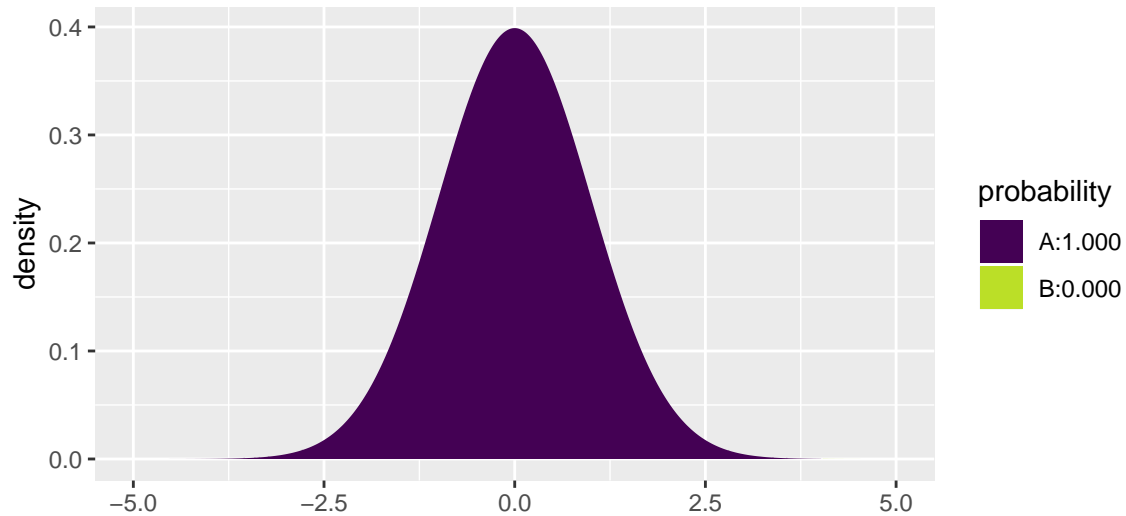
The hypothesis of no relation between income and ability to obtain a credit card corresponds to

$$H_0: \beta = 0$$

with the alternative $\beta \neq 0$. Inspecting the summary reveals that $\hat{\beta} = 0.1054$ is more than 4 standard errors away from zero.

With a z-score equal to 4.03 we get the tail probability

```
ptail <- 2*(1-pdist("norm",4.03,xlim=c(-5,5)))
```



```
ptail
```

```
## [1] 5.577685e-05
```

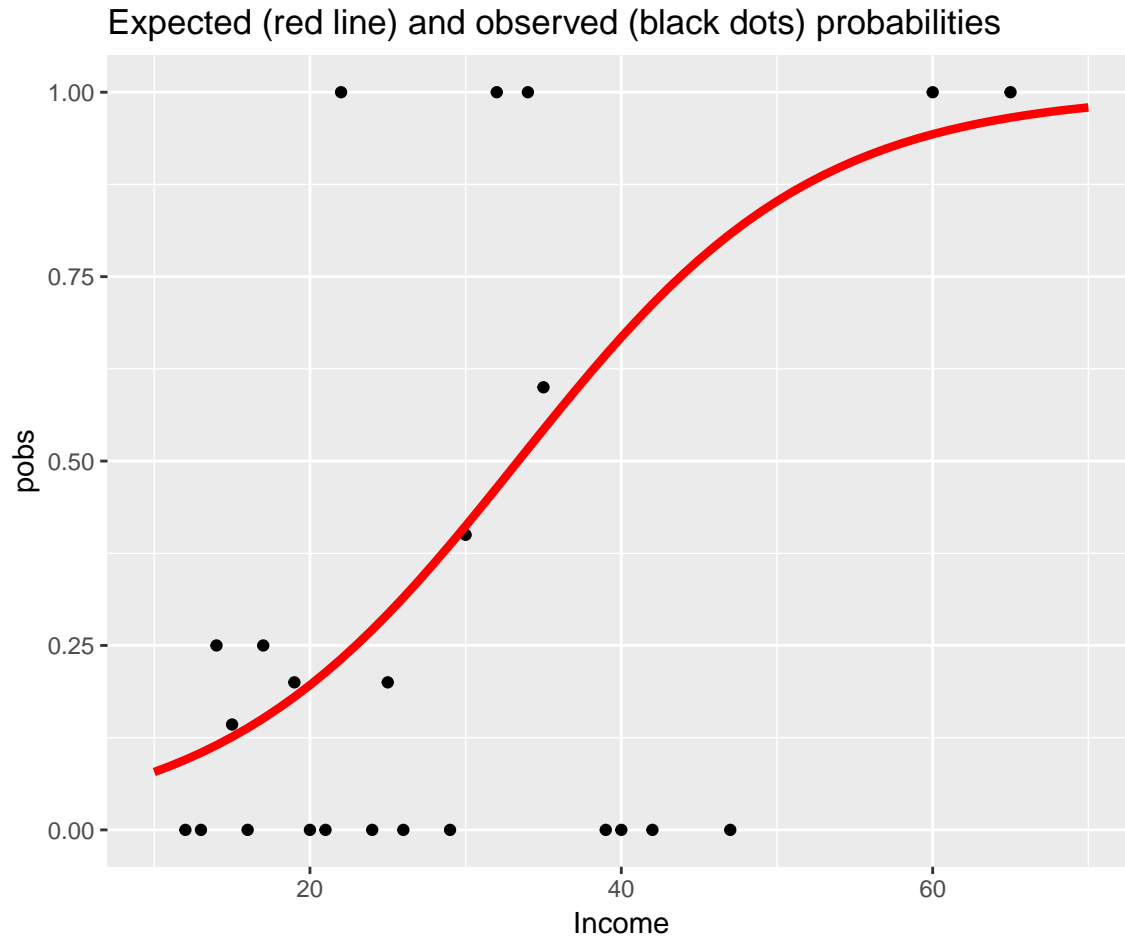
Which is very significant - as reflected by the p-value.

2.8 Confidence interval for odds ratio

From the summary:

- $\hat{\beta} = 0.10541$ and hence $\exp(\hat{\beta}) - 1 = 0.11$. If income increases by 1000 euro, then odds increases by 11%.
- Standard error on $\hat{\beta}$ is 0.02616 and hence a 95% confidence interval for log-odds ratio is $\hat{\beta} \pm 1.96 \times 0.02616 = (0.054; 0, 157)$.
- Corresponding interval for odds ratio: $\exp((0.054; 0, 157)) = (1.056; 1.170)$, i.e. the increase in odds is - with confidence 95% - between 5.6% and 17%.

2.9 Plot of model predictions against actual data



- Tendency is fairly clear and very significant.
- Due to low sample size at some income levels, the deviations are quite large.

3 Multiple logistic regression

3.1 Several numeric predictors

We generalize the model to the case, where we have k predictors x_1, x_2, \dots, x_k . Where some might be dummies for a factor.

$$\text{logit}(P(y = 1 | x_1, x_2, \dots, x_k)) = \alpha + \beta_1 x_1 + \dots + \beta_k x_k$$

Interpretation of β -values is unaltered: If we fix x_2, \dots, x_k and increase x_1 by one unit, then the relative change in odds is given by $\exp(\beta_1) - 1$.

3.2 Example

Wisconsin Breast Cancer Database covers 683 observations of 10 variables in relation to examining tumors in the breast.

- Nine clinical variables with a score between 0 and 10.
- The binary variable `Class` with levels `benign/malignant`.
- By default R orders the levels lexicographically and chooses the first level as reference ($y = 0$). Hence `benign` is reference, and we model odds of `malignant`.

We shall work with only 4 of the predictors, where two of these have been discretized.

```
BC <- read.table("https://asta.math.aau.dk/datasets?file=BC0.dat",header=TRUE)
head(BC)
```

```
##   nuclei cromatin Size.low Size.medium Shape.low      Class
## 1      1         3     TRUE      FALSE      TRUE     benign
## 2     10         3    FALSE      TRUE      FALSE     benign
## 3      2         3     TRUE      FALSE      TRUE     benign
## 4      4         3    FALSE      FALSE     FALSE     benign
## 5      1         3     TRUE      FALSE      TRUE     benign
## 6     10         9    FALSE      FALSE     FALSE malignant
```

3.3 Global test of no effects

First we fit the model `mainEffects` with main effect of all predictors - remember the notation \sim . for all predictors. Then we fit the model `noEffects` with no predictors.

```
mainEffects <- glm(Class~., data=BC, family=binomial)
noEffects <- glm(Class~1, data=BC, family=binomial)
```

First we want to test, whether there is any effect of the predictors, i.e the nul hypothesis

$$H_0: \beta_1 = \beta_2 = \beta_3 = \beta_4 = \beta_5 = 0$$

3.4 Example

Similarly to `lm` we can use the function `anova` to compare `mainEffects` and `noEffects`. Only difference is that we need to tell the function that the test is a chi-square test and not an F-test.

```
anova(noEffects, mainEffects, test="Chisq")
```

```
## Analysis of Deviance Table
##
## Model 1: Class ~ 1
## Model 2: Class ~ nuclei + cromatin + Size.low + Size.medium + Shape.low
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1         682      884.35
## 2         677      135.06  5   749.29 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

`mainEffects` is a much better model.

The test statistic is the Deviance (749.29), which should be small.

It is evaluated in a chi-square with 5 (the number of parameters equal to zero under the nul hypothesis) degrees of freedom.

The 95%-critical value for the $\chi^2(5)$ distribution is 11.07 and the p-value is in practice zero.

3.5 Test of influence of a given predictor

```
round(coef(summary(mainEffects)),4)
```

##	Estimate	Std. Error	z value	Pr(> z)
## (Intercept)	-0.7090	0.8570	-0.8274	0.4080
## nuclei	0.4403	0.0823	5.3484	0.0000
## cromatin	0.5058	0.1444	3.5026	0.0005
## Size.lowTRUE	-3.6154	0.8081	-4.4740	0.0000
## Size.mediumTRUE	-2.3773	0.7188	-3.3074	0.0009
## Shape.lowTRUE	-2.1490	0.6054	-3.5496	0.0004

For each predictor p can we test the hypothesis:

$$H_0 : \beta_p = 0$$

- Looking at the z-values, there is a clear effect of all 5 predictors. Which of course is also supported by the p-values.
- Is it relevant to include interactions?

3.6 Model selection by stepwise selection

We extend the model to BIG including interactions. And then perform a so-called **stepwise selection**:

```
BIG <- glm(Class~.^2, data=BC, family=binomial)
final <- step(BIG, k=log(dim(BC)[1]), trace=0)
round(coef(summary(final)), 4)
```

##	Estimate	Std. Error	z value	Pr(> z)
## (Intercept)	0.0337	0.9025	0.0373	0.9702
## nuclei	0.3015	0.0837	3.6038	0.0003
## cromatin	0.4456	0.1441	3.0930	0.0020
## Size.lowTRUE	-5.4213	1.1359	-4.7729	0.0000
## Size.mediumTRUE	-2.2948	0.6895	-3.3282	0.0009
## Shape.lowTRUE	-2.2488	0.6485	-3.4676	0.0005
## nuclei:Size.lowTRUE	0.5690	0.2356	2.4149	0.0157

- **step**: Stepwise removal of “insignificant” predictors from BIG (our model including all interactions).
- Choice of $k=\log(\dim(BC)[1])$ corresponds to the so-called BIC (Bayesian Information Criterion), which we shall not treat in detail. Just note that when k increases, we gradually obtain a simpler model, i.e. the number of predictors decrease.
- If `trace=1`, you will see all steps in the iterative process.
- We end up with a model including one interaction.

3.7 Prediction and classification

```
BC$pred <- round(predict(final,type="response"),3)
```

- We add the column `pred` to our dataframe `BC`.
- `pred` is the final model's estimate of the probability of malignant.

```
head(BC[,c("Class", "pred")])
```

```
##      Class  pred
## 1    benign 0.004
## 2    benign 0.890
## 3    benign 0.010
## 4    benign 0.929
## 5    benign 0.004
## 6 malignant 0.999
```

Not good for patients 2 and 4.

We may classify by `round(BC$pred)`:

- 0 to denote benign
- 1 to denote malignant

```
tally(~ Class + round(pred), data = BC)
```

```
##           round(pred)
## Class           0    1
##  benign       432  12
##  malignant     11 228
```

23 patients are misclassified.

```
sort(BC$pred[BC$Class=="malignant"])[1:5]
```

```
## [1] 0.084 0.092 0.107 0.123 0.179
```

There is a malignant woman with a predicted probability of malignancy, which is only 8.4%.

If we assign all women with predicted probability of malignancy above 5% to further investigation, then we catch all malignant.

```
tally(~ Class + I(pred>.05), data = BC)
```

```
##           I(pred > 0.05)
## Class      TRUE FALSE
##  benign      39   405
##  malignant  239     0
```

The expense is that the number of false positive increases from 12 to 39.

```
tally(~ Class + I(pred>.1), data = BC)
```

```
##           I(pred > 0.1)
## Class      TRUE FALSE
##  benign      26   418
##  malignant  237     2
```

- If we instead set the alarm to 10%, then the number of false positives decreases from 39 to 26.
- But at the expense of 2 false negative.