

# TMA4315: Project 1

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## Problem 1

a)

Since the response variables  $y_i \sim \text{Bernoulli}(\pi_i)$ , where  $\pi_i = \Pr(y_i = 1 \mid \mathbf{x}_i)$ . The conditional mean is given by  $Ey_i = \pi_i$ , which is connected to the covariates via the following relationship:

$$\mathbf{x}_i^T \boldsymbol{\beta} =: \eta_i = \Phi^{-1}(\pi_i),$$

or equivalently:  $\pi_i = \Phi(\eta_i)$ . This results in the likelihood function

$$\begin{aligned} L(\boldsymbol{\beta}) &= \prod_{i=1}^n \pi_i^{y_i} (1 - \pi_i)^{1-y_i} \\ &= \prod_{i=1}^n \Phi(\eta_i)^{y_i} (1 - \Phi(\eta_i))^{1-y_i}. \end{aligned}$$

Thus, the log-likelihood becomes

$$l(\boldsymbol{\beta}) := \ln(L(\boldsymbol{\beta})) = \sum_{i=1}^n \underbrace{y_i \ln(\Phi(\eta_i)) + (1 - y_i) \ln(1 - \Phi(\eta_i))}_{=l_i(\boldsymbol{\beta})} = \sum_{i=1}^n l_i(\boldsymbol{\beta}).$$

To find the score function, we calculate

$$\begin{aligned} \frac{\partial l_i(\boldsymbol{\beta})}{\partial \boldsymbol{\beta}} &= \frac{y_i}{\Phi(\eta_i)} \frac{\partial \Phi(\eta_i)}{\partial \boldsymbol{\beta}} - \frac{1 - y_i}{1 - \Phi(\eta_i)} \frac{\partial \Phi(\eta_i)}{\partial \boldsymbol{\beta}} \\ &= \frac{y_i}{\Phi(\eta_i)} \phi(\eta_i) \mathbf{x}_i - \frac{1 - y_i}{1 - \Phi(\eta_i)} \phi(\eta_i) \mathbf{x}_i \\ &= \frac{y_i(1 - \Phi(\eta_i)) - (1 - y_i)\Phi(\eta_i)}{\Phi(\eta_i)(1 - \Phi(\eta_i))} \phi(\eta_i) \mathbf{x}_i \\ &= \frac{y_i - \Phi(\eta_i)}{\Phi(\eta_i)(1 - \Phi(\eta_i))} \phi(\eta_i) \mathbf{x}_i. \end{aligned}$$

Consequently, the score function is given by

$$\mathbf{s}(\boldsymbol{\beta}) = \sum_{i=1}^n \frac{y_i - \Phi(\eta_i)}{\Phi(\eta_i)(1 - \Phi(\eta_i))} \phi(\eta_i) \mathbf{x}_i = \mathbf{X}^T D \Sigma^{-1} (\mathbf{y} - \boldsymbol{\mu}),$$

where  $D = \text{diag}(\phi(\eta_i))$  and  $\Sigma = \text{diag}(\text{Var}(y_i)) = \text{diag}(\Phi(\eta_i)(1 - \Phi(\eta_i)))$ . Next, we find the expected Fisher information,  $F(\beta)$ . We find it by using the result

$$\begin{aligned} F(\beta) &= \text{Var}(\mathbf{s}(\beta)) = \text{Var}\left(\sum_{i=1}^n \frac{y_i - \Phi(\eta_i)}{\Phi(\eta_i)(1 - \Phi(\eta_i))} \phi(\eta_i) \mathbf{x}_i\right) \\ &= \sum_{i=1}^n \left[ \frac{\phi(\eta_i)}{\Phi(\eta_i)(1 - \Phi(\eta_i))} \right]^2 \text{Var}(y_i \mathbf{x}_i) = \sum_{i=1}^n \left[ \frac{\phi(\eta_i)}{\Phi(\eta_i)(1 - \Phi(\eta_i))} \right]^2 \mathbf{x}_i \text{Var}(y_i) \mathbf{x}_i^T \\ &= \sum_{i=1}^n \left[ \frac{\phi(\eta_i)}{\Phi(\eta_i)(1 - \Phi(\eta_i))} \right]^2 \pi_i(1 - \pi_i) \mathbf{x}_i \mathbf{x}_i^T = \sum_{i=1}^n \frac{\phi(\eta_i)^2}{\Phi(\eta_i)(1 - \Phi(\eta_i))} \mathbf{x}_i \mathbf{x}_i^T, \end{aligned}$$

Where in the third equality we have used that the  $y_i$ 's are independent. The expected Fisher information can also be verified to have this expression by the general relationship

$$F(\beta) = \sum_{i=1}^n \frac{h'(\eta_i)^2}{\text{Var}(y_i)} \mathbf{x}_i \mathbf{x}_i^T,$$

where  $h'(\eta_i) = \Phi'(\eta_i) = \phi(\eta_i)$  and  $\text{Var}(y_i) = \pi_i(1 - \pi_i) = \Phi(\eta_i)(1 - \Phi(\eta_i))$ .

**b)**

The expected Fisher information is given by

$$F(\beta) = \sum_{i=1}^n \frac{\phi(\eta_i)^2}{\Phi(\eta_i)(1 - \Phi(\eta_i))} \mathbf{x}_i \mathbf{x}_i^T = \mathbf{X}^T \mathbf{W} \mathbf{X},$$

where  $\mathbf{W} = \text{diag}\left(\frac{\phi(\eta_i)^2}{\Phi(\eta_i)(1 - \Phi(\eta_i))}\right)$ .

The Fisher scoring algorithm states that the next iterate is given by

$$\beta^{(t+1)} = \beta^{(t)} + F(\beta^{(t)})^{-1} \mathbf{s}(\beta^{(t)}).$$

We also need the deviance, which is defined as

$$D = 2(l_{\text{saturated}} - l(\hat{\beta})).$$

When we fit a parameter for each data point (which is the case for the saturated model), the result for the Bernoulli distribution is that  $\hat{\pi}_i = y_i$ . This means that the likelihood function of the saturated model is given by

$$L_{\text{saturated}} = \prod_{i=1}^n \hat{\pi}_i^{y_i} (1 - \hat{\pi}_i)^{1-y_i} = \prod_{i=1}^n y_i^{y_i} (1 + y_i)^{1-y_i} = 1,$$

Where we have used  $0^0 = 1$ . Consequently, the log-likelihood  $l_{\text{saturated}} = \ln(1) = 0$  and the deviance becomes  $-2l(\hat{\beta})$ . Next follows the Implementation of `myglm` in R:

```
Phi <- function(x) return (pnorm(x))
phi <- function(x) return (dnorm(x))

myglm <- function(formula, data, start = NULL){
```

```

# response variable
resp <- all.vars(formula)[1]
y <- as.matrix( data[resp] )

# model matrix
X <- model.matrix(formula, data)
n <- dim(X)[1]
p <- dim(X)[2]

# starting beta
if (is.null(start)){
  beta = rep(0, p)
}
else {
  beta = start
}

# Fisher scoring algorithm
max_iter <- 50
tol <- 1e-10
iter <- 0
rel.err <- Inf

F.inv = NULL
eta = NULL

while (rel.err > tol & iter < max_iter){
  # Calculate eta.
  eta <- X %*% beta

  # Calculate score.
  D <- diag(as.vector(phi(eta)), n, n)
  Sigma <- diag(as.vector(Phi(eta)*(1 - Phi(eta))), n, n)
  mu.vec <- as.vector(Phi(eta))
  score = t(X) %*% D %*% solve(Sigma) %*% (y - mu.vec)

  # Calculate Fisher information and its inverse.
  W <- diag(as.vector(phi(eta)^2 / (Phi(eta)*(1-Phi(eta)))), n, n)
  F <- t(X) %*% W %*% X
  F.inv <- solve(F)

  # Update beta.
  beta.new <- beta + F.inv %*% score

  iter <- iter + 1
  rel.err <- max(abs(beta.new - beta) / abs(beta.new))
  beta <- beta.new
}

# Calculating std.errors and deviance.

```

```

std.Error <- sqrt(diag(F.inv))
deviance = -2 * sum(y*log(pnorm(eta)) + (1 - y)*log(1 -pnorm(eta)))

return (list("coefficients" = data.frame(beta, std.Error),
        "deviance" = deviance,
        "vcov" = F.inv))
}

```

c)

Simulation of 1000 Bernoulli draws with a random probability.

```

# probability
x = runif(1000, 0, 1)
# draw n bernoulli with prob x
y <- rbinom(1000, 1, x)
df <- data.frame(y, x)
### fit using glm
model <- glm(y ~ x, family = binomial(link = "probit"), data = df)
# beta
model$coefficients

## (Intercept)          x
##   -1.590625    3.154880

# se for beta
summary(model)

##
## Call:
## glm(formula = y ~ x, family = binomial(link = "probit"), data = df)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -2.2847  -0.7795   0.3492   0.7610   2.2741
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -1.5906      0.1019  -15.61  <2e-16 ***
## x              3.1549      0.1802   17.51  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 1386.3  on 999  degrees of freedom
## Residual deviance: 1006.5  on 998  degrees of freedom
## AIC: 1010.5
##
## Number of Fisher Scoring iterations: 4

# vcov
vcov(model)

##              (Intercept)          x
## (Intercept)  0.01038231 -0.01643530

```

```
## x          -0.01643530  0.03246122
```

```
# deviance
```

```
model$deviance
```

```
## [1] 1006.469
```

```
### fit using myglm
```

```
mymodel <- myglm(y ~ x, data = df)
```

```
# beta
```

```
mymodel$coefficients
```

```
##              y std.Error
```

```
## (Intercept) -1.590628 0.1018983
```

```
## x           3.154886 0.1801788
```

```
# vcov
```

```
mymodel$vcov
```

```
##              (Intercept)          x
```

```
## (Intercept)  0.01038326 -0.01643695
```

```
## x           -0.01643695  0.03246440
```

```
# deviance
```

```
mymodel$deviance
```

```
## [1] 1006.469
```

## Problem 2

a)

```
#install.packages("ISwR")
```

```
library(ISwR) # Install the package if needed
```

```
data(juul)
```

```
juul$menarche <- juul$menarche - 1
```

```
juul.girl <- subset(juul, age>8 & age<20 & complete.cases(menarche))
```

```
mod.probit <- glm(menarche ~ age, family=binomial(link="probit"), data= juul.girl)
```

```
anova(mod.probit, test = "Chisq")
```

```
## Analysis of Deviance Table
```

```
##
```

```
## Model: binomial, link: probit
```

```
##
```

```
## Response: menarche
```

```
##
```

```
## Terms added sequentially (first to last)
```

```
##
```

```
##
```

```
##      Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
```

```
## NULL              518      719.39
```

```
## age    1          522      517      197.39 < 2.2e-16 ***
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The low p-value suggests that age has an effect on the response variable.

b)

Relating to the juul data set, we define for each observation/individual

$$y_i = \begin{cases} 0, & \text{if menarche has occurred.} \\ 1, & \text{if menarche has not occurred.} \end{cases}$$

and  $t_i$  as the age at the time of examination, which corresponds to **age** in the data set. Let  $T_i \sim \mathcal{N}(\mu, \sigma^2)$ , where  $T_i$  is the time until menarche occurs for the  $i$ 'th individual. Furthermore, let

$$\begin{aligned} \pi_i &:= P(y_i = 1) = P(T_i \leq t_i) \\ &= P\left(\frac{T_i - \mu}{\sigma} \leq \frac{t_i - \mu}{\sigma}\right) = \Phi\left(\frac{t_i - \mu}{\sigma}\right) \end{aligned}$$

This, in turn, gives

$$\Phi^{-1}(\pi_i) = -\frac{\mu}{\sigma} + \frac{1}{\sigma}t_i = \beta_0 + \beta_1 t_i,$$

where  $\beta_0 = -\mu/\sigma$  and  $\beta_1 = 1/\sigma$ .

Let  $\mu = \mu(\beta_0, \beta_1)$  and  $\sigma = \sigma(\beta_0, \beta_1)$ . If  $\hat{\beta}_0$  and  $\hat{\beta}_1$  denotes the MLEs of  $\beta_0$  and  $\beta_1$ , respectively, then  $\hat{\mu} = \mu(\hat{\beta}_0, \hat{\beta}_1)$  is the MLE of  $\mu$  and  $\hat{\sigma} = \sigma(\hat{\beta}_0, \hat{\beta}_1)$  of  $\sigma$ . It follows that

$$\sigma = \frac{1}{\beta_1}, \quad \mu = -\frac{\beta_0}{\beta_1},$$

Consequently, the MLEs are given as

$$\hat{\sigma}(\hat{\beta}_1) = \frac{1}{\hat{\beta}_1}, \quad \hat{\mu}(\hat{\beta}_0, \hat{\beta}_1) = -\frac{\hat{\beta}_0}{\hat{\beta}_1}.$$

The corresponding standard errors of these estimators can then be estimated using the delta method. A first order Taylor expansion of  $\hat{\mu}$  gives [Legge til mitt forslag under](#):

$$\hat{\mu} \approx \hat{\mu}(\mathbf{b}) + \nabla \hat{\mu}(\mathbf{b})(\hat{\beta} - \mathbf{b}),$$

where we have used the notation  $\hat{\beta} = (\hat{\beta}_0, \hat{\beta}_1)^T$  and exoanded around  $\hat{\beta} = \mathbf{b} = (b_0, b_1)^T$ . Next, we take the variance of this linear approximation, such that

$$\begin{aligned} \text{Var}(\hat{\mu}) &\approx \text{Var}\left(\nabla \hat{\mu}(\mathbf{b})^T \hat{\beta}\right) \\ &= \nabla \hat{\mu}(\mathbf{b})^T \text{Var}(\hat{\beta}) \nabla \hat{\mu}(\mathbf{b}). \end{aligned}$$

Since  $\nabla \hat{\mu} = (-1/\hat{\beta}_1, \hat{\beta}_0/\hat{\beta}_1^2)^T$ , we can calculate the standard error as in the code below

```
mod.probit <- glm(menarche ~ age, family = binomial(link = 'probit'), data = juul.girl)
b <- mod.probit$coefficients
grad.mu <- c(-1/b[2], b[1]/b[2]^2)
se.mu <- t(grad.mu) %*% vcov(mod.probit) %*% grad.mu
se.mu
```

```
##           [,1]
## [1,] 0.01404909
```

et annerledes svar her altså. Hva tenker du ?

$$\mu(\beta_0, \beta_1) \approx \hat{\mu} + \frac{\partial \mu}{\partial \beta_0}(\hat{\beta}_0, \hat{\beta}_1) (\beta_0 - \hat{\beta}_0) + \frac{\partial \mu}{\partial \beta_1}(\hat{\beta}_0, \hat{\beta}_1) (\beta_1 - \hat{\beta}_1),$$

so

$$\begin{aligned} \text{Var}(\mu) &\approx \left( \frac{\partial \mu}{\partial \beta_0} \right)^2 \text{Var}(\beta_0) + \left( \frac{\partial \mu}{\partial \beta_1} \right)^2 \text{Var}(\beta_1) + 2 \left( \frac{\partial \mu}{\partial \beta_0} \right) \left( \frac{\partial \mu}{\partial \beta_1} \right) \text{Cov}(\beta_0, \beta_1) \\ &= \left( -\frac{1}{\beta_1} \right)^2 \text{Var}(\beta_0) + \left( \frac{\beta_0}{\beta_1^2} \right)^2 \text{Var}(\beta_1) - \frac{2\beta_0}{\beta_1^3} \text{Cov}(\beta_0, \beta_1). \end{aligned}$$

A similar derivation for  $\sigma$  yields

$$\begin{aligned} \text{Var}(\sigma) &\approx \left( \frac{\partial \sigma}{\partial \beta_0} \right)^2 \text{Var}(\beta_0) + \left( \frac{\partial \sigma}{\partial \beta_1} \right)^2 \text{Var}(\beta_1) + 2 \left( \frac{\partial \sigma}{\partial \beta_0} \right) \left( \frac{\partial \sigma}{\partial \beta_1} \right) \text{Cov}(\beta_0, \beta_1) \\ &= \left( -\frac{1}{\beta_1^2} \right)^2 \text{Var}(\beta_1). \end{aligned}$$

Thus, the standard error of the MLE estimators are

$$\widehat{\text{SE}}(\hat{\sigma}) = \frac{1}{\hat{\beta}_1^2} \text{SE}(\hat{\beta}_1), \quad \widehat{\text{SE}}(\hat{\mu}) = \frac{1}{\hat{\beta}_1} \sqrt{\text{Var}(\hat{\beta}_0) + \left( \frac{\hat{\beta}_0}{\hat{\beta}_1} \right) \text{Var}(\hat{\beta}_1)},$$

where it was used (assumed?) that  $\text{Cov}(\beta_0, \beta_1) = 0$ . In R we find the  $\beta$ 's and their standard error using the summary-function.

```
mod.probit <- glm(menarche ~ age, family = binomial(link = 'probit'), data = juul.girl)
s <- summary(mod.probit)
df <- s$coefficients
df
```

```
##              Estimate Std. Error   z value    Pr(>|z|)
## (Intercept) -11.3703291 1.06345963 -10.69183 1.111563e-26
## age          0.8623271 0.08106225  10.63784 1.986860e-26
```

```
beta0 <- df[1,1]
beta1 <- df[1,2]
se0 <- df[2,1]
se1 <- df[2,2]
```

From the readout we get  $\hat{\beta}_0 = -11.3703291$  with a standard error of 0.8623271 and  $\hat{\beta}_1 = 1.0634596$  with a standard error of 0.0810622. Thus  $\hat{\mu} = 10.6918296$  and  $\hat{\sigma} = 0.9403272$ . Their standard errors are  $\widehat{\text{SE}}(\hat{\sigma}) = 0.0716765$  and  $\widehat{\text{SE}}(\hat{\mu}) = 0.7716134$ .

c)

```
mod.logit <- glm(menarche ~ age, family = binomial(link = 'logit'), data = juul.girl)
mod.logit$coefficients[2]
```

```
##      age
## 1.517289
```

To show find the distribution of the  $T_i$ 's, we start with the cumulative distribution:

$$\Pr(T_i \leq t_i) = \Pr(y_i = 1 \mid t_i) = \pi_i = \frac{1}{1 + e^{-\eta_i}}.$$

The pdf of  $T_i$  is then given as

$$\begin{aligned} f_{T_i}(t_i) &= \frac{d}{dt_i} \left( \frac{1}{1 + e^{-\eta_i}} \right) = \frac{\beta_1 e^{-\beta_0 - \beta_1 t_i}}{(1 + e^{-\beta_0 - \beta_1 t_i})^2} \\ &= \frac{e^{-(t_i - (-\beta_0/\beta_1))/(1/\beta_1)}}{1/\beta_1 (1 + e^{-(t_i - (-\beta_0/\beta_1))/(1/\beta_1)})^2} = \frac{e^{-(t_i - \mu)/s}}{s(1 + e^{-(t_i - \mu)/s})^2}. \end{aligned}$$

This is the logistic distribution, with parameters  $\mu = -\beta_0/\beta_1$  and  $s = 1/\beta_1$ , where we have used the parametrization from [Wikipedia](#). We compute estimates of the mean and variance from the estimates of  $\beta_0$  and  $\beta_1$  in the output above. An estimate of the mean is then given by  $E(T_i) = -\beta_0/\beta_1 \approx 13.1901147$  and an estimate of the variance is given by  $\text{Var}(T_i) = s^2\pi^2/3 = \pi^2/(3\beta_1^2) \approx 1.4290323$ .

d)

We now assume that the latent ages follow a log-normal distribution, i.e.

$$T_i \sim \text{Lognormal}(\mu, \sigma^2).$$

This is equivalent to stating that  $\ln T_i \sim \mathcal{N}(\mu, \sigma^2)$ . Now we can follow the same approach as in 2b):

$$\begin{aligned} \pi_i &:= \Pr(y_i = 1) = \Pr(T_i \leq t_i) = \Pr(\ln T_i \leq \ln t_i) \\ &= \Pr\left(\frac{\ln T_i - \mu}{\sigma} \leq \frac{\ln t_i - \mu}{\sigma}\right) = \Phi\left(\frac{\ln t_i - \mu}{\sigma}\right) \end{aligned}$$

This, in turn, gives

$$\Phi^{-1}(\pi_i) = -\frac{\mu}{\sigma} + \frac{1}{\sigma} \ln t_i = \beta_0 + \beta_1 \ln t_i,$$

where  $\beta_0 = -\mu/\sigma$  and  $\beta_1 = 1/\sigma$ . Consequently, we fit GLM with a probit link-function on  $\ln t_i$ :

```
mod.lognorm <- glm(menarche ~ log(age), family = binomial(link = "probit"), data = juul.girl)
summary(mod.lognorm)
```

```
##
## Call:
## glm(formula = menarche ~ log(age), family = binomial(link = "probit"),
##      data = juul.girl)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -2.28617  -0.11683   0.00315   0.10715   2.54738
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -29.060      2.704  -10.75  <2e-16 ***
## log(age)      11.287      1.049   10.76  <2e-16 ***
```



```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 719.39  on 518  degrees of freedom
## Residual deviance: 198.05  on 517  degrees of freedom
## AIC: 202.05
##
## Number of Fisher Scoring iterations: 8
```

Exactly as in 2b),