Project 2 - TMA4315

martin.o.berild@ntnu.no
10014

yaolin.ge@ntnu.no
10026

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Initially, we load the R-package `VGAM` to fit *Vector Generalized Linear and Addtive Models*, and `ggplot` as our plotting tool of choice.

```
library(VGAM)
library(ggplot2)
```

In this project, we will use multinomial regression on a dataset containing marital status, etnicity and age of individuals in New Zealand. The data is loaded in the code below, and the print display seven individuals.

```
attach(marital.nz)
head(marital.nz)
```

```
##   age ethnicity            mstatus
## 1  29  European             Single
## 2  55  European  Married/Partnered
## 3  44  European  Married/Partnered
## 4  53  European Divorced/Separated
## 5  45  European  Married/Partnered
## 7  30  European             Single
```

There are a total of four catagories for marital status `mstatus` and we will try to predict the probabilty of each based on the age. A multinomial regression model with a linear effect of `age` is fit to the data as

```
mod1 <- vglm(mstatus ~ age, multinomial)
summary(mod1)
```

```
##
## Call:
## vglm(formula = mstatus ~ age, family = multinomial)
##
## Pearson residuals:
##                         Min      1Q   Median       3Q    Max
## log(mu[,1]/mu[,4]) -11.75 -0.1441 -0.13965 -0.13372  5.706
## log(mu[,2]/mu[,4]) -13.53  0.2871  0.31147  0.40939  1.212
## log(mu[,3]/mu[,4]) -12.47 -0.2364 -0.09098 -0.02037 82.311
##
## Coefficients:
##                Estimate Std. Error z value Pr(>|z|)
## (Intercept):1  6.753157   0.515150   13.11   <2e-16 ***
## (Intercept):2  9.531824   0.482073   19.77   <2e-16 ***
## (Intercept):3 13.121214   0.513771   25.54   <2e-16 ***
## age:1         -0.099335   0.008043  -12.35   <2e-16 ***
## age:2         -0.102873   0.007100  -14.49   <2e-16 ***
## age:3         -0.252080   0.008955  -28.15   <2e-16 ***
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Names of linear predictors: log(mu[,1]/mu[,4]), log(mu[,2]/mu[,4]),
## log(mu[,3]/mu[,4])
##
## Residual deviance: 6822.79 on 18153 degrees of freedom
##
## Log-likelihood: -3411.395 on 18153 degrees of freedom
##
## Number of Fisher scoring iterations: 7
##
## Warning: Hauck-Donner effect detected in the following estimate(s):
## '(Intercept):2', 'age:3'
##
##
## Reference group is level  4  of the response
```

The `mstatus` is a categorical nominal response $Y \in \{1, 2, 3, 4\}$ modelled with the linear effect of a numerical covariate `age`. Given a catoregory r of the response, the probability of the subject having the rth `mstatus` is given by

$$\pi_r = P(Y = r), \;\; r = 1, 2, 3, 4.$$

The response is usually reformulated to a vector $\boldsymbol{y}$ of $c = 3$ dummy variables:

$$y_r = \begin{cases} 1, & Y = r \\ 0, & \text{otherwise} \end{cases} \qquad r = 1, 2, 3.$$

where the 4th category is a *refrence* category, i.e. $y_4 = 1 - y_1 - y_2 - y_3$. The multinomial distribution for m independent trials is given by

$$\begin{aligned} f(\boldsymbol{y}|\boldsymbol{\pi}) &= \frac{m!}{y_1! \cdot y_2! \cdot y_3! \cdot (1 - y_1 - y_2 - y_3)!} \pi_1^{y_1} \cdot \pi_2^{y_2} \cdot \pi_3^{y_3} \cdot (1 - \pi_1 - \pi_2 - \pi_3)^{1 - y_1 - y_2 - y_3} \\ &= \mathcal{M}(m, \boldsymbol{\pi}), \end{aligned}$$

where $\mathcal{M}(m, \boldsymbol{\beta})$ is the multinomial probability mass function with m trials and probabilities $\boldsymbol{\pi} = (\pi_1, \pi_2, \pi_3)$. Using the linear predictor $\eta_{i,r} = \boldsymbol{x}_i^T \boldsymbol{\beta}_r$ and considering the logit model we have the probabilities:

$$\pi_{i,r} = \frac{\exp(\boldsymbol{x}_i^T \boldsymbol{\beta}_r)}{\sum_{s=1}^{c+1} \exp(\boldsymbol{x}_i^T \boldsymbol{\beta}_s)}. \tag{1}$$

However, this model is non-identifiable as adding a constant to the linear predictor would yield the same probabilities. Therefore as mentioned previously, one of the categories is used as *reference* category s.t. $\boldsymbol{\beta}_r = \boldsymbol{\beta}_r - \boldsymbol{\beta}_{c+1}$, where $c + 1 = 4$ in this model. The resulting probabilities are found by

$$\pi_{i,r} = \frac{1}{1 + \sum_{s=1}^{c} \exp(\boldsymbol{x}_i^T \boldsymbol{\beta}_s)} \begin{cases} \exp(\boldsymbol{x}_i^T \boldsymbol{\beta}_r), & r = 1, 2, \ldots, c \\ 1, & \text{otherwise} \end{cases} . \tag{2}$$

An alternative representation is the logarithmic odds or relative risk between category r and the reference category $c + 1$ as

$$\log \frac{\pi_{i,r}}{\pi_{i,c+1}} = \boldsymbol{x}_i^T \boldsymbol{\beta}_r. \tag{3}$$

This logarithmic odds is also the output of a `predict()` call using the model object `mod1`, and is presented in the `Pearson residuals` in the `summary()` ouput above. Note that with this representation the a prositive effect β_r only implies that the odds of category r increase relative the reference category, and not that the probability of r increase by itself.

In general, the interpretation odd ratio is the magnitude of change in the odds between two categories r_1 and r_2 for a individual i by a unit change in the jth element of the covariate, $x_{i,j}$, as

$$\boldsymbol{x}_i^* = \boldsymbol{x}_i + (0, \dots, 1, \dots, 0)^T,$$

gives the odds ratio:

$$\frac{\pi^*_{i,r_1}/\pi^*_{i,r_2}}{\pi_{i,r_1}/\pi_{i,r_2}} = \frac{\exp[\boldsymbol{x}_i^{*T}(\boldsymbol{\beta}_{r_1} - \boldsymbol{\beta}_{r_2})]}{\exp[\boldsymbol{x}_i^{T}(\boldsymbol{\beta}_{r_1} - \boldsymbol{\beta}_{r_2})]} = \exp[(\boldsymbol{x}_i^* - \boldsymbol{x}_i)^T(\boldsymbol{\beta}_{r_1} - \boldsymbol{\beta}_{r_2})] = \exp(\boldsymbol{\beta}_{r_1,j} - \boldsymbol{\beta}_{r_2,j}).$$

A similar interpretation can be found for the odds between category r and the complementary of r (or simply not in the category r), and is formulized as

$$\frac{\pi_{i,r}}{1-\pi_{i,r}} = \frac{\exp(\boldsymbol{x}_i^T\boldsymbol{\beta}_r)}{1 + \sum_{s\in\mathcal{S}}\exp(\boldsymbol{x}_i^T\boldsymbol{\beta}_{\boldsymbol{s}})},$$

where $\mathcal{S} = \{s \in [1, c] \setminus r\}$ is the set containing all categories but r and the reference.

Observe that $\pi_r(\boldsymbol{x}) \propto \exp(\boldsymbol{x}^T\boldsymbol{\beta}_r)$ with the denominator being the a normalizing constant, and that the effects $\boldsymbol{\beta}_r$ includes a interecept $\beta_{0,r}$ and the effect of age $\beta_{\text{age},r}$ for category r. Therefore, as $x > 0$ the function $\pi(\boldsymbol{x})$ is a monotonic function only for a intercept $\beta_{0,r} = 0$, and otherwise it's slope is changing from decreasing to increase or oppositley depending on the sign of the effect of age.

We could also formulate the multinomial logistic regression as a latent utility model:

$$u_r = \eta_r + \epsilon_r,$$

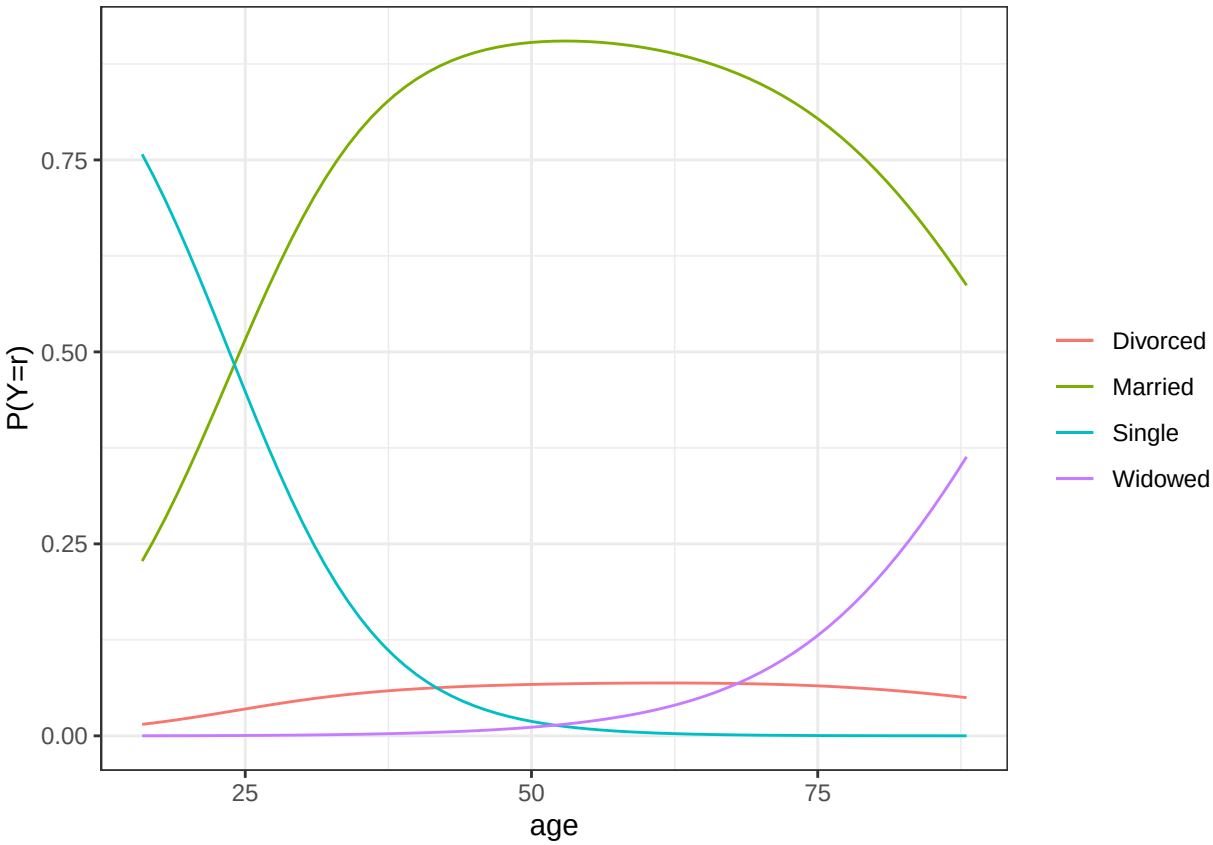
where u_r is the utility, η_r the linear predictor and ϵ_r some error of the rth category. Furthermore, we assume that the error follow a standard Gumbel distribution, $\epsilon \sim \text{Gumbel}(0, 1)$. The aim is to find the probabilities of choosing $Y = r$ for all r or find the probability that the rth utility, $u_{i,r}$ is larger than all other utilities for a given subject i. The differece between two identically distributed Gumbel distributions follows a logistic distibution and, thus, the probabilities π_r in the latent utility model is found similar previous formulation using Equation (1).

```
mod0 <- vglm(mstatus ~ 1, multinomial)
anova(mod0, mod1, test="LRT", type="I")
```

```
## Analysis of Deviance Table
##
## Model 1: mstatus ~ 1
## Model 2: mstatus ~ age
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1     18156     8423.7
## 2     18153     6822.8  3   1600.9 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

To obtain predictions of the probabilties of the belonging to the respective categories given a age between 16 and 88 can be found rewriting Equation (3) using Equation (2). The different probabilities can be visualized in the figure below, where the probabilities functions $\pi_r(x) = P(Y = r)$ is plotted against the covariate `age`, x.

```
ymp1 = predict(mod1,newdata = data.frame(age=seq(16,88)))
ymp1.df = as.data.frame(matrix(cbind(seq(16,88),exp(ymp1)*(1/(1 + rowSums(exp(ymp1)))),
                                     (1/(1 + rowSums(exp(ymp1))))),ncol=5,
                               dimnames = list(c(),c("age","pi1","pi2","pi3","pi4"))))
```



The number of `Single` is monotonically decreasing as the age gets higher, which is reasonable since people generally get `Married` or find a partner during their life. And since a individual can't go back to being single because of the `Divorced/Seperated` category, it can't start increasing again as age increases.

The probability of getting `Married` however is increasing until age is $\simeq 50$, where it starts to decrease. This could be explained by individual getting `Divorced` or `Seperated` after some time together, or that their partner dies resulting in being placed in the `Widowed` category.

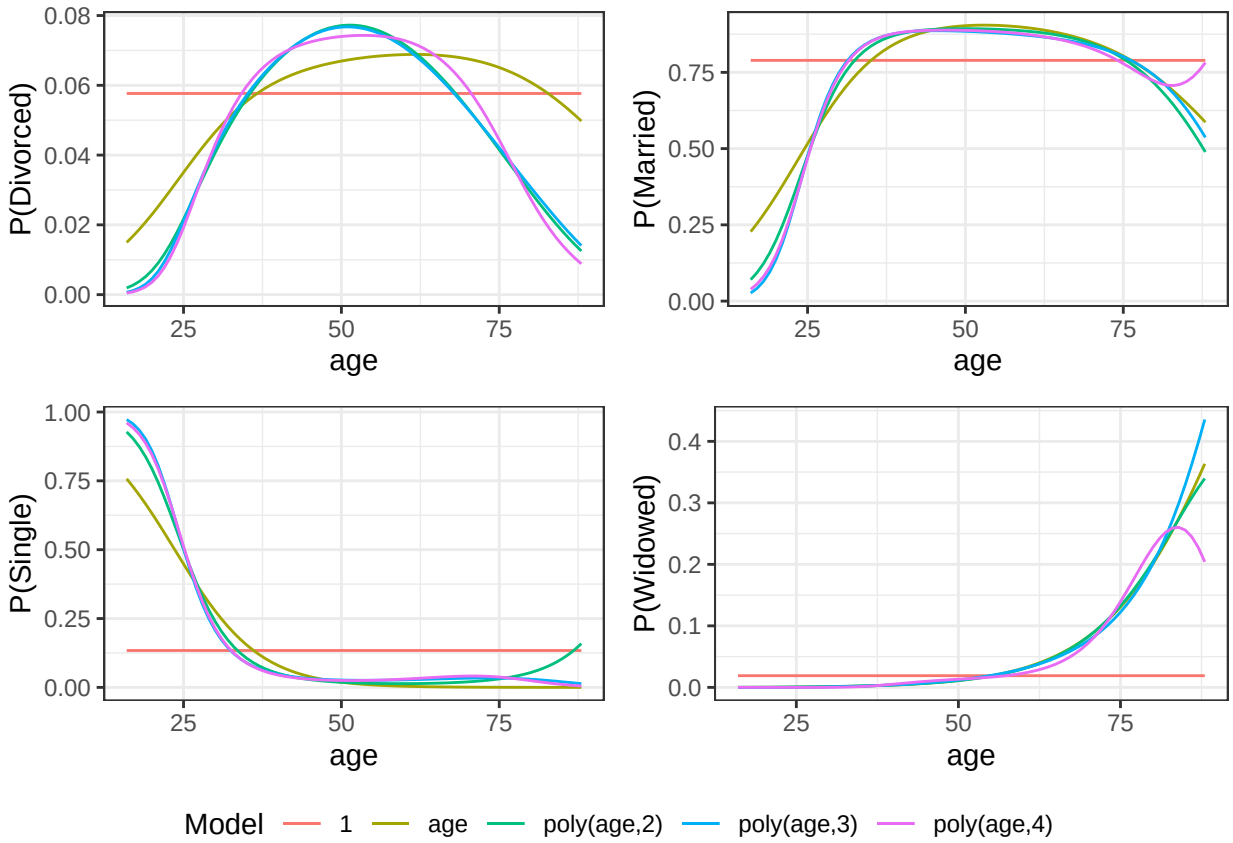
The `Divorced`category is close to horisontal but is slightly concave with a maximum around age 65, and lastly, the widow is monotonically increasing. Both of these functions have a reasonable behavior as the number of proportion of `Widowed` should go up because of the correlation between `age`and `mortality`.

Thus far we have only considered a linear effect of `age`; however, models that regard a linear effect of higher degrees of `age` might yield a better approximation. We will now fit different multinomial logit models with degrees of `age` up to four as covariates and, then, perform model selection based on the *Akaike information criterion* (AIC). In the code below the models are fit and the probabilities of `age` betwen 16 to 88 is predicted.

```
ymp0 = predict(mod0,newdata = data.frame(age=seq(16,88)))
ymp0.df = as.data.frame(matrix(cbind(seq(16,88),exp(ymp0)*(1/(1 + rowSums(exp(ymp0)))),
                                     (1/(1 + rowSums(exp(ymp0))))),ncol=5,
                               dimnames = list(c(),c("age","pi1","pi2","pi3","pi4"))))
mod2 <- vglm(mstatus ~ poly(age,2), multinomial)
ymp2 = predict(mod2,newdata = data.frame(age=seq(16,88)))
ymp2.df = as.data.frame(matrix(cbind(seq(16,88),exp(ymp2)*(1/(1 + rowSums(exp(ymp2)))),
                                     (1/(1 + rowSums(exp(ymp2))))),ncol=5,
                               dimnames = list(c(),c("age","pi1","pi2","pi3","pi4"))))
mod3 <- vglm(mstatus ~ poly(age,3), multinomial)
ymp3 = predict(mod3,newdata = data.frame(age=seq(16,88)))
ymp3.df = as.data.frame(matrix(cbind(seq(16,88),exp(ymp3)*(1/(1 + rowSums(exp(ymp3)))),
```

```
                                    (1/(1 + rowSums(exp(ymp3)))),ncol=5,
                                dimnames = list(c(),c("age","pi1","pi2","pi3","pi4"))))
mod4 <- vglm(mstatus ~ poly(age,4), multinomial)
ymp4 = predict(mod4,newdata = data.frame(age=seq(16,88)))
ymp4.df = as.data.frame(matrix(cbind(seq(16,88),exp(ymp4)*(1/(1 + rowSums(exp(ymp4)))),
                                    (1/(1 + rowSums(exp(ymp4)))),ncol=5,
                                dimnames = list(c(),c("age","pi1","pi2","pi3","pi4"))))
```

Using these predicted probabilities the figure below is constructed to visualized the dissimilarities between the models (presented in different colors). The associated categories is highlighted on the y-axis.



As previously mentioned the model selection will be based on minimizing the AIC which is calculated as

$$\text{AIC} = 2 \cdot k - 2 \cdot \ln(\hat{\text{L}}).$$

Here, k is the number of parameters in the model and $\hat{\text{L}}$ is the likelihood. The AIC then tries to asses the goodness-of-fit through the likelihood but also considers the complexity or number of parameters of the model as a penalty. For example in the model with a 4th degree polynomial of `age` we have $k = 3 \cdot 5$ parameters; 3 from the number of categories $c = 3$ using the $r = 4$ as reference, and 5 for the number of terms in a 4th degree polynomial. In R we can use the built in function `AIC()` to calculate the AIC for a `VGAM` object. The AIC values for the respective models is printed below.

```
AIC(mod0)
```

```
## [1] 8429.723
```

```
AIC(mod1)
```

```
## [1] 6834.79
```

```
AIC(mod2)
```

```
## [1] 6583.123
```

```
AIC(mod3)
```

```
## [1] 6555.048
```

```
AIC(mod4)
```

```
## [1] 6552.665
```

Here, we observe that the most complex model, a 4th degree polynomial of `age`, has the highest AIC score. Considering the predicted probabilities in the above figures, the best model seem to overfit the data as seen by the tails for high values of `age` in `Married` and `Widowed` turn alot compared to the other models. In other words, the model might perform bad on new unseen data.