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Exercise Sheet 7 Generalized Linear Models

Discussion of the tutorial exercises on December 5 and 8, 2022

Preparations Download the data set credit.dat from Moodle. The data set describes 1000 consumer loans of a German bank. The response variable of interest is kredit and it is given in dichotomous form: 1 indicates that the loan was repayed properly, 0 indicates the opposite. We consider the covariates laufzeit, moral, laufkont, alter, and beruf. A detailed description of the data set can be found at https://data.ub.uni-muenchen.de/23/1/DETAILS.html.

Problem 1 (*)

- a) We are working with the aggregated data, i.e., aggregate the data first to obtain binomial data instead of binary data. For this, you have to define a new variable no_kredit=1-kredit. Then, characterize the scale (quantitative, ordinal, nominal, dichotomous) of each of the 5 selected variables of the data set. Transform all nominal and ordinal covariates into factor variables in R using the function as.factor.
- b) Perform an explorative data analysis (EDA). For this, do the following two steps.
 - i) How many debtors repay their loan? Use the function table on the original data.
 - ii) Determine the influence of each covariate on the response. Use the function cat_plot for categorical covariates and the function gam for quantitative covariates. An example is given in the example from the lecture. Do you need to transform quantitative covariates or merge categories of categorical covariates?
- c) Fit a logistic regression model to the data using the transformations or merging you decided on in b).
 - $glm(cbind(kredit,no_kredit) \sim ...$, family=binomial(link = "logit")) Using the step function with direction="forward", decide if some covariates are not important. We call the resulting model my.glm.step.main.
- d) Perform partial deviance tests for all the nested models using the R-function anova(my.glm.step.main, test="Chisq") and explain the outcome with $\alpha = 0.05$. What is the null hypothesis and the rejection rule for this test? Decide if you want to remove another covariate from the model.
- e) Perform a residual deviance test at the $\alpha = 0.05$ level (without using a pre-defined R-function). Explain the outcome. What is the null hypothesis and the rejection rule for the residual deviance test?

f) Investigate the pairwise interaction effects of the covariates. For this, make interaction plots for all possible interactions. Using the R function step, sequentially add interaction effects by

model.inter = step(my.glm.step.main, .^ 2, direction="forward).

Compare with your interaction plots if the selection makes sense.

For interaction plots between a quantitative and a categorical covariate, use interact_plot. For interaction plots between two categorical covariates, use cat_plot. To obtain an interaction plot between two quantitative covariates, first group them using cut(alter, breaks = quantile(alter, probs =c(0, 0.2, 0.4, 0.6, 0.8, 1), na.rm = T)).

Problem 2 (Additional) Consider the complementary log-log regression model

$$Y_i | \boldsymbol{X}_i = \boldsymbol{x}_i \sim Bernoulli(p(\boldsymbol{x}_i))$$
 independent $p(\boldsymbol{x}_i) = 1 - \exp\left(-\exp(\boldsymbol{x}_i^T \boldsymbol{\beta})\right), \quad i = 1, \dots, n,$

where $\boldsymbol{x}_i^T \boldsymbol{\beta} = \beta_0 + \beta_1 x_i$.

- a) Determine the log-likelihood function ℓ of this model.
- b) Determine the scaled score equation $s(\beta) = s(\beta_0, \beta_1) = (\frac{\partial \ell}{\partial \beta_0} \frac{\partial \ell}{\partial \beta_1})^T$.
- c) Determine the scaled Hessian matrix $H(\beta)$ of the log-likelihood,

$$m{H}(m{eta}) = egin{pmatrix} rac{\partial^2 \ell}{\partial^2 eta_0} & rac{\partial^2 \ell}{\partial eta_0 \partial eta_1} \ rac{\partial^2 \ell}{\partial eta_1 \partial eta_0} & rac{\partial^2 \ell}{\partial^2 eta_1} \end{pmatrix}$$

d) Determine the deviance of this model.