Retinopathy - Testing Proportional Odds Assumption

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```
library(catdata)
data(retinopathy)
retinopathy$SM <- as.factor(retinopathy$SM)
```

For the fitting of the partial proportional odds models the function ”vglm” from the ”VGAM”–package is used. First a simple proportional odds model is fitted with ”vglm”.

For the ”vglm”–function the response (RET) does not necessarily have to be ordered, SM has to be factorized.

```
library(VGAM)

## Warning:  Paket ’VGAM’ wurde unter R Version 4.2.3 erstellt

# retinopathy£RET <- as.ordered(retinopathy£RET)
# retinopathy£SM <- as.factor(retinopathy£SM)
```

The models differ in the option ”parallel” for the used family ”cumulative”.

```
pom <- vglm(RET ~ SM + DIAB + GH + BP, family = cumulative(parallel=TRUE),
            data = retinopathy)
```

```
ppom <- vglm(RET ~ SM + DIAB + GH + BP, family = cumulative(parallel=FALSE),
             data = retinopathy)
```

First the proportional odds assumption is tested. The deviances of the two models can be received by the following command.

```
deviance(pom)

## [1] 904.1423
```

```
deviance(ppom)

## [1] 892.451
```

The p–value for the proportional odds assuption is computed:

```
1 - pchisq(deviance(pom) - deviance(ppom), df=4)

## [1] 0.0198011
```

Coefficients and standard errors of both models are obtainen in the corresponding summaries.

Summary proportional odds model:

```
summary(pom)

##
## Call:
## vglm(formula = RET ~ SM + DIAB + GH + BP, family = cumulative(parallel = TRUE),
##     data = retinopathy)
##
## Coefficients:
##                Estimate Std. Error z value Pr(>|z|)
## (Intercept):1 12.30253    1.29002   9.537  < 2e-16 ***
## (Intercept):2 13.67328    1.31715  10.381  < 2e-16 ***
## SM1           -0.25487    0.19191  -1.328    0.184
## DIAB          -0.13976    0.01348 -10.368  < 2e-16 ***
## GH            -0.45970    0.07445  -6.175 6.63e-10 ***
## BP            -0.07239    0.01351  -5.357 8.48e-08 ***
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Names of linear predictors: logitlink(P[Y<=1]),
## logitlink(P[Y<=2])
##
## Residual deviance: 904.1423 on 1220 degrees of freedom
##
## Log-likelihood: -452.0711 on 1220 degrees of freedom
##
## Number of Fisher scoring iterations: 5
##
## Warning: Hauck-Donner effect detected in the following estimate(s):
## '(Intercept):1'
##
##
## Exponentiated coefficients:
##       SM1      DIAB        GH        BP
## 0.7750152 0.8695700 0.6314743 0.9301668
```

Summary partial proportional odds model:

```
summary(ppom)

##
## Call:
## vglm(formula = RET ~ SM + DIAB + GH + BP, family = cumulative(parallel = FALSE),
##     data = retinopathy)
##
## Coefficients:
##                Estimate Std. Error z value Pr(>|z|)
## (Intercept):1 11.69187    1.38996   8.412  < 2e-16 ***
## (Intercept):2 14.92801    1.72286   8.665  < 2e-16 ***
## SM1:1         -0.40497    0.20538  -1.972   0.0486 *
## SM1:2          0.08631    0.25402   0.340   0.7340
## DIAB:1        -0.12910    0.01452  -8.889  < 2e-16 ***
## DIAB:2        -0.16678    0.01800  -9.264  < 2e-16 ***
## GH:1          -0.43473    0.08012  -5.426 5.76e-08 ***
## GH:2          -0.53591    0.09797  -5.470 4.50e-08 ***
## BP:1          -0.06801    0.01470  -4.627 3.72e-06 ***
## BP:2          -0.07538    0.01701  -4.432 9.33e-06 ***
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Names of linear predictors: logitlink(P[Y<=1]),
## logitlink(P[Y<=2])
##
## Residual deviance: 892.451 on 1216 degrees of freedom
##
## Log-likelihood: -446.2255 on 1216 degrees of freedom
##
## Number of Fisher scoring iterations: 8
##
## Warning: Hauck-Donner effect detected in the following estimate(s):
## '(Intercept):2'
##
##
## Exponentiated coefficients:
##     SM1:1     SM1:2    DIAB:1    DIAB:2      GH:1      GH:2
## 0.6669994 1.0901491 0.8788883 0.8463843 0.6474407 0.5851393
##      BP:1      BP:2
## 0.9342494 0.9273865
```

Now the proportional odds assumption for all covariates is taken away step by step. Afterwards the corresponding proportional odds assumptions are tested.

Global effect for BP:

```
ppom2 <- vglm (RET ~ SM + DIAB + GH + BP,
family = cumulative (parallel = FALSE ~ SM + DIAB + GH), data = retinopathy)
deviance(ppom2)

## [1] 892.6677
```

```
1-pchisq(deviance(ppom2)-deviance(ppom), df=1)

## [1] 0.6415537
```

Global effect for GH:

```
ppom3 <- vglm (RET ~ SM + DIAB + GH + BP,
family = cumulative (parallel = FALSE ~ SM + DIAB), data = retinopathy)
deviance(ppom3)

## [1] 893.7745
```

```
1-pchisq(deviance(ppom3)-deviance(ppom2), df=1)

## [1] 0.2927828
```

Global effect for DIAB:

```
ppom4 <- vglm (RET ~ SM + DIAB + GH + BP,
family = cumulative (parallel = FALSE ~ SM), data = retinopathy)
deviance(ppom4)

## [1] 897.9748
```

```
1-pchisq(deviance(ppom4)-deviance(ppom3), df=1)

## [1] 0.04041857
```

Global effect for SM (equivalent to proportional odds model):

```
1-pchisq(deviance(pom)-deviance(ppom4), df=1)

## [1] 0.0130116
```