# Retinopathy - Testing Proportional Odds Assumption

## February 8, 2012

```
> library(catdata)
> data(retinopathy)
> attach(retinopathy)
```

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)
> RET <- as.ordered(RET)
> SM <- as.factor(SM)
```

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

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

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

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

```
> deviance(pom)
```

```
[1] 904
```

```
> deviance(ppom)
```

```
[1] 892
```

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

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

```
[1] 0.0198
```

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))

Pearson Residuals:
              Min    1Q Median  3Q Max
logit(P[Y<=1])  -5 -0.42    0.3 0.6   3
logit(P[Y<=2])  -8  0.09    0.2 0.3   2

Coefficients:
              Value Std. Error t value
(Intercept):1 12.30       1.29      10
(Intercept):2 13.67       1.32      10
SM1           -0.25       0.19      -1
DIAB          -0.14       0.01     -10
GH            -0.46       0.07      -6
BP            -0.07       0.01      -5


Number of linear predictors:  2

Names of linear predictors: logit(P[Y<=1]), logit(P[Y<=2])

Dispersion Parameter for cumulative family:   1

Residual Deviance: 904 on 1220 degrees of freedom

Log-likelihood: -452 on 1220 degrees of freedom

Number of Iterations: 5
```

Summary partial proportional odds model:

```
> summary(ppom)

Call:
vglm(formula = RET ~ SM + DIAB + GH + BP, family = cumulative(parallel = FALSE))

Pearson Residuals:
               Min    1Q Median  3Q Max
logit(P[Y<=1])  -5 -0.43    0.3 0.6   3
logit(P[Y<=2]) -10  0.08    0.2 0.4   3

Coefficients:
              Value Std. Error t value
(Intercept):1 11.69       1.39     8.4
(Intercept):2 14.93       1.72     8.7
SM1:1         -0.40       0.21    -2.0
SM1:2          0.09       0.25     0.3
DIAB:1        -0.13       0.01    -8.9
```

```
DIAB:2        -0.17      0.02    -9.3
GH:1          -0.43      0.08    -5.4
GH:2          -0.54      0.10    -5.5
BP:1          -0.07      0.01    -4.6
BP:2          -0.08      0.02    -4.4


Number of linear predictors:  2

Names of linear predictors: logit(P[Y<=1]), logit(P[Y<=2])

Dispersion Parameter for cumulative family:    1

Residual Deviance: 892 on 1216 degrees of freedom

Log-likelihood: -446 on 1216 degrees of freedom

Number of Iterations: 6
```

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))
> deviance(ppom2)

[1] 893

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

[1] 0.642
```

Global effect for GH:

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

[1] 894

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

[1] 0.293
```

Global effect for DIAB:

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

[1] 898
```

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

```
[1] 0.0404
```

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

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

```
[1] 0.013
```

```
> detach(retinopathy)
```