

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)
> # 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 assumption is computed:

```
> 1 - pchisq(deviance(pom) - deviance(ppom), df=4)
[1] 0.0198011
```

Coefficients and standard errors of both models are obtained 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)
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```

(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:

```

> ppm2 <- vglm (RET ~ SM + DIAB + GH + BP,
+ family = cumulative (parallel = FALSE ~ SM + DIAB + GH), data = retinopathy)
> deviance(ppm2)

```

```
[1] 892.6677
```

```
> 1-pchisq(deviance(ppm2)-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

```