

Retinopathy - Testing Proportional Odds Assumption

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```
> 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 assumption is computed:

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

```
[1] 0.0198
```

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))
```

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
> 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)

```