Retinopathy - Sequential Logit Models

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

For sequential models again the "vglm"–function from the "VGAM"–library is needed, but now family option "sratio" is required.

```
> library(VGAM)
```

Now several sequential logit models are fitted and compared by their corresponding deviances. The first model is the sequential logit model with all category–specific effects, so the option "parallel=FALSE" is used.

```
> seqm1 <- vglm(RET ~ SM + DIAB + GH + BP, family = sratio (link="logit",
+ parallel=FALSE), data = retinopathy)
> deviance(seqm1)

[1] 891.4193
```

No category–specific effect for DIAB:

```
> seqm2 <- vglm(RET ~ SM + DIAB + GH + BP, family = sratio (link="logit",
+ parallel=FALSE ~ SM + GH + BP), data = retinopathy)
> deviance(seqm2)

[1] 891.4428
```

Testing the removed effect:

```
> 1-pchisq(deviance(seqm2)-deviance(seqm1), df=1)

[1] 0.8781324
```

No category–specific effect for GH:

```
> seqm3 <- vglm(RET ~ SM + DIAB + GH + BP, family = sratio (link="logit",
+ parallel=FALSE ~ SM + BP), data = retinopathy)
> deviance(seqm3)

[1] 891.4689
```

Testing the removed effect:

```
> 1-pchisq(deviance(seqm3)-deviance(seqm2), df=1)
```

```
[1] 0.8716468
```

No category–specific effect for BP:

```
> seqm4 <- vglm(RET ~ SM + DIAB + GH + BP, family = sratio (link="logit",
+ parallel=FALSE ~ SM), data = retinopathy)
> deviance(seqm4)

[1] 891.9767
```

Testing the removed effect:

```
> 1-pchisq(deviance(seqm4)-deviance(seqm3), df=1)

[1] 0.4760739
```

No category–specific effect for GH (only global effects):

```
> seqm5 <- vglm(RET ~ SM + DIAB + GH + BP, family = sratio (link="logit",
+ parallel=TRUE), data = retinopathy)
> deviance(seqm5)

[1] 897.7104
```

Testing the removed effect:

```
> 1-pchisq(deviance(seqm5)-deviance(seqm4), df=1)

[1] 0.01664239
```

As the last test is significant, model "seqm4" is analyzed in detail.

```
> summary(seqm4)

Call:
vglm(formula = RET ~ SM + DIAB + GH + BP, family = sratio(link = "logit",
    parallel = FALSE ~ SM), data = retinopathy)

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept):1 11.12783    1.16861   9.522  < 2e-16 ***
(Intercept):2 10.91554    1.21342   8.996  < 2e-16 ***
SM:1          -0.37755    0.20248  -1.865   0.0622 .
SM:2           0.49077    0.31285   1.569   0.1167
DIAB          -0.12823    0.01229 -10.430  < 2e-16 ***
GH            -0.42480    0.06730  -6.312 2.76e-10 ***
BP            -0.06227    0.01220  -5.104 3.33e-07 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Names of linear predictors: logitlink(P[Y=1|Y>=1]), logitlink(P[Y=2|Y>=2])

Residual deviance: 891.9767 on 1219 degrees of freedom
```

```
Log-likelihood: -445.9884 on 1219 degrees of freedom

Number of Fisher scoring iterations: 6

Warning: Hauck-Donner effect detected in the following estimate(s):
'(Intercept):1'


Exponentiated coefficients:
     SM:1      SM:2      DIAB        GH        BP
0.6855376 1.6335785 0.8796526 0.6539010 0.9396286
```

The summary gives no p–values for the individual covariates, they have to be computed separately. For this purpose the t–values are copied from the summary. The quadratic t–values are the wald–statistics which can be used to produce the individual p–values.

p–value intercept1:

```
> 1 - pchisq(9.5223^2, df=1)

[1] 0
```

p–value intercept2:

```
> 1 - pchisq(8.9957^2, df=1)

[1] 0
```

p–value SM1:

```
> 1 - pchisq((-1.8646)^2, df=1)

[1] 0.06223749
```

p–value SM2:

```
> 1 - pchisq(1.5687^2, df=1)

[1] 0.1167179
```

p–value DIAB:

```
> 1 - pchisq((-10.4303)^2, df=1)

[1] 0
```

p-value GH:

```
> 1 - pchisq((-6.3116)^2, df=1)

[1] 2.761653e-10
```

p–value BP:

```
> 1 - pchisq((-5.1037)^2, df=1)

[1] 3.330761e-07
```

To receive the corresponding odds–ratios, the following command can be used.

```
> exp(coefficients(seqm4)[3:7])

     SM:1      SM:2      DIAB        GH        BP
0.6855376 1.6335785 0.8796526 0.6539010 0.9396286
```