Retinopathy - Sequential Logit Models

February 8, 2012

```
> library(catdata)
> data(retinopathy)
> attach(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))
> deviance(seqm1)

[1] 891
```

No category–specific effect for DIAB:

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

[1] 891
```

Testing the removed effect:

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

[1] 0.878
```

No category–specific effect for GH:

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

[1] 891
```

Testing the removed effect:

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

[1] 0.872
```

No category–specific effect for BP:

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

[1] 892
```

Testing the removed effect:

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

[1] 0.476
```

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

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

[1] 898
```

Testing the removed effect:

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

[1] 0.0166
```

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))

Pearson Residuals:
                    Min     1Q Median    3Q Max
logit(P[Y=1|Y>=1])  -4 -7e-01  3e-01 6e-01   3
logit(P[Y=2|Y>=2]) -14 -2e-05 -6e-06 2e-05   3

Coefficients:
              Value Std. Error t value
(Intercept):1 11.13       1.17      10
(Intercept):2 10.92       1.21       9
SM:1          -0.38       0.20      -2
SM:2           0.49       0.31       2
DIAB          -0.13       0.01     -10
GH            -0.42       0.07      -6
BP            -0.06       0.01      -5
```

```
Number of linear predictors:  2

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

Dispersion Parameter for sratio family:   1

Residual Deviance: 892 on 1219 degrees of freedom

Log-likelihood: -446 on 1219 degrees of freedom

Number of Iterations: 6
```

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] 0.0622
```

p–value SM2:

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

[1] 0.117
```

p–value DIAB:

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

[1] 0
```

p-value GH:

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

[1] 2.76e-10
```

p–value BP:

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

[1] 3.33e-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
0.686 1.634 0.880 0.654 0.940

> detach(retinopathy)
```