

Retinopathy - Sequential Logit Models

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```
> 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 ~
> 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 ~
> 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 ~  
> 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)
```