

Teratology - Alternative Binary Models

February 1, 2012

First the teratology data are loaded. The data set exists in two different versions, "teratology" shows the aggregated count data whereas "teratology2" includes the original data.

```
> library(catdata)
> data(teratology)
> data(teratology2)
```

For the first two models, the simple independence model and the quasi-likelihood model, the aggregated data are needed.

```
> attach(teratology)
```

The simple and naive independence model is fitted by the following command.

```
> mLogit <- glm(cbind(D,L) ~ as.factor(Grp), family=binomial())
> summary(mLogit)
```

Call:

```
glm(formula = cbind(D, L) ~ as.factor(Grp), family = binomial())
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-4.4295	-0.9750	-0.0285	1.4024	2.7826

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.1440	0.1292	8.855	< 2e-16 ***
as.factor(Grp)2	-3.3225	0.3308	-10.043	< 2e-16 ***
as.factor(Grp)3	-4.4762	0.7311	-6.122	9.22e-10 ***
as.factor(Grp)4	-4.1297	0.4762	-8.672	< 2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 509.43 on 57 degrees of freedom
Residual deviance: 173.45 on 54 degrees of freedom
AIC: 252.92

Number of Fisher Scoring iterations: 5

Now the quasi-likelihood model is fitted. The coefficients are the same as in the independence model before, only the standard errors have to be multiplied by $\sqrt{\hat{\phi}}$.

```
> mQuasi <- glm(cbind(D,L) ~ as.factor(Grp), family=quasibinomial(link="logit"))
> summary(mQuasi)
```

Call:

```
glm(formula = cbind(D, L) ~ as.factor(Grp), family = quasibinomial(link = "logit"))
```

Deviance Residuals:

	Min	1Q	Median	3Q	Max
	-4.4295	-0.9750	-0.0285	1.4024	2.7826

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	1.1440	0.2187	5.231	2.81e-06 ***
as.factor(Grp)2	-3.3225	0.5600	-5.933	2.18e-07 ***
as.factor(Grp)3	-4.4762	1.2375	-3.617	0.000656 ***
as.factor(Grp)4	-4.1297	0.8061	-5.123	4.14e-06 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for quasibinomial family taken to be 2.864945)

Null deviance: 509.43 on 57 degrees of freedom
 Residual deviance: 173.45 on 54 degrees of freedom
 AIC: NA

Number of Fisher Scoring iterations: 5

The next model to be fitted is a GEE with independence correlation structure. For that purpose the library "gee" is loaded.

```
> library(gee)
```

Now we use the original data set "teratology2".

```
> detach(teratology)
> attach(teratology2)
```

The GEE is fitted by the following command. The coefficients are again equal to those from the independence model, the standard errors for the independence models can be found in the column "Naive S.E.". The new standard errors from the GEE are those in the column "Robust S.E.".

```
> mGee <- gee(y ~ as.factor(Grp), id=Rat, family=binomial)
```

	(Intercept)	as.factor(Grp)G2	as.factor(Grp)G3
	1.143981	-3.322513	-4.476184
as.factor(Grp)G4	-4.129663		

```
> summary(mGee)
```

```
GEE:  GENERALIZED LINEAR MODELS FOR DEPENDENT DATA  
gee S-function, version 4.13 modified 98/01/27 (1998)
```

```
Model:
```

```
Link:                               Logit  
Variance to Mean Relation: Binomial  
Correlation Structure:      Independent
```

```
Call:
```

```
gee(formula = y ~ as.factor(Grp), id = Rat, family = binomial)
```

```
Summary of Residuals:
```

	Min	1Q	Median	3Q	Max
	-0.75840979	-0.10169492	-0.03448276	0.24159021	0.96551724

```
Coefficients:
```

	Estimate	Naive S.E.	Naive z
(Intercept)	1.143981	0.1296195	8.825688
as.factor(Grp)G2	-3.322513	0.3319396	-10.009393
as.factor(Grp)G3	-4.476185	0.7335486	-6.102098
as.factor(Grp)G4	-4.129663	0.4778032	-8.643020

	Robust S.E.	Robust z
(Intercept)	0.2758667	4.146861
as.factor(Grp)G2	0.4400582	-7.550168
as.factor(Grp)G3	0.6104577	-7.332507
as.factor(Grp)G4	0.5763810	-7.164814

```
Estimated Scale Parameter: 1.006633
```

```
Number of Iterations: 1
```

```
Working Correlation
```

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]
[1,]	1	0	0	0	0	0	0	0	0	0
[2,]	0	1	0	0	0	0	0	0	0	0
[3,]	0	0	1	0	0	0	0	0	0	0
[4,]	0	0	0	1	0	0	0	0	0	0
[5,]	0	0	0	0	1	0	0	0	0	0
[6,]	0	0	0	0	0	1	0	0	0	0
[7,]	0	0	0	0	0	0	1	0	0	0
[8,]	0	0	0	0	0	0	0	1	0	0
[9,]	0	0	0	0	0	0	0	0	1	0
[10,]	0	0	0	0	0	0	0	0	0	1
[11,]	0	0	0	0	0	0	0	0	0	0
[12,]	0	0	0	0	0	0	0	0	0	0
[13,]	0	0	0	0	0	0	0	0	0	0
[14,]	0	0	0	0	0	0	0	0	0	0
[15,]	0	0	0	0	0	0	0	0	0	0

```

[16,] 0 0 0 0 0 0 0 0 0 0
[17,] 0 0 0 0 0 0 0 0 0 0
      [,11] [,12] [,13] [,14] [,15] [,16] [,17]
[1,] 0 0 0 0 0 0 0
[2,] 0 0 0 0 0 0 0
[3,] 0 0 0 0 0 0 0
[4,] 0 0 0 0 0 0 0
[5,] 0 0 0 0 0 0 0
[6,] 0 0 0 0 0 0 0
[7,] 0 0 0 0 0 0 0
[8,] 0 0 0 0 0 0 0
[9,] 0 0 0 0 0 0 0
[10,] 0 0 0 0 0 0 0
[11,] 1 0 0 0 0 0 0
[12,] 0 1 0 0 0 0 0
[13,] 0 0 1 0 0 0 0
[14,] 0 0 0 1 0 0 0
[15,] 0 0 0 0 1 0 0
[16,] 0 0 0 0 0 1 0
[17,] 0 0 0 0 0 0 1

```

For the following beta-binomial model the library "VGAM" with its function "vglm" and the data set "teratology" is needed.

```
> library(VGAM)
```

```
> detach(teratology2)
```

```
> attach(teratology)
```

Furthermore we construct the Variable N as sum of all fetuses in one litter. We will use N to make a subset with $N > 1$ for the beta-binomial model.

```
> N <- D + L
```

Now the beta-binomial model is fitted.

```
> mBetaBin <- vglm(cbind(D,L) ~ as.factor(Grp), family=betabinomial, subset=N>1)
> summary(mBetaBin)
```

Call:

```
vglm(formula = cbind(D, L) ~ as.factor(Grp), family = betabinomial,
      subset = N > 1)
```

Pearson Residuals:

	Min	1Q	Median	3Q	Max
logit(mu)	-2.6590	-0.66871	-0.17322	0.90076	1.4024
logit(rho)	-1.4941	-0.96860	0.21215	0.69365	3.9075

Coefficients:

	Value	Std. Error	t value
(Intercept):1	1.3451	0.24439	5.5040

```
(Intercept):2  -1.1401    0.32344 -3.5250
as.factor(Grp)2 -3.0868    0.52088 -5.9262
as.factor(Grp)3 -3.8647    0.86337 -4.4763
as.factor(Grp)4 -3.9197    0.68382 -5.7320
```

Number of linear predictors: 2

Names of linear predictors: logit(mu), logit(rho)

Dispersion Parameter for betabinomial family: 1

Log-likelihood: -93.29728 on 109 degrees of freedom

Number of Iterations: 7

For the following two mixed models again the original data are required.

```
> detach(teratology)
> attach(teratology2)
```

With the function "glmmPQL" from the "MASS"-library a mixed model is fitted by penalized quasi-likelihood, the mixed model contains random intercepts but no random slopes.

```
> mMixPql<- glmmPQL(y ~ as.factor(Grp), random=~1 | Rat, family=binomial)
> summary(mMixPql)
```

Linear mixed-effects model fit by maximum likelihood

```
Data: NULL
      AIC BIC logLik
      NA  NA     NA
```

Random effects:

```
Formula: ~1 | Rat
      (Intercept)  Residual
StdDev:    1.455986  0.8006729
```

Variance function:

```
Structure: fixed weights
Formula: ~invwt
```

Fixed effects: y ~ as.factor(Grp)

	Value	Std.Error	DF	t-value	p-value
(Intercept)	1.687058	0.3057620	549	5.517553	0
as.factor(Grp)G2	-4.130280	0.6141687	54	-6.724993	0
as.factor(Grp)G3	-5.274063	0.9808235	54	-5.377178	0
as.factor(Grp)G4	-5.109542	0.7474739	54	-6.835747	0

Correlation:

```
      (Intr) a.(G)G2 a.(G)G3
as.factor(Grp)G2 -0.498
as.factor(Grp)G3 -0.312  0.155
as.factor(Grp)G4 -0.409  0.204  0.128
```

Standardized Within-Group Residuals:

Min	Q1	Med	Q3	Max
-3.5217300	-0.3475892	-0.1548062	0.2821502	5.1647080

Number of Observations: 607

Number of Groups: 58

In order to fit a mixed model by maximum likelihood we load the library "glmmML".

```
> library(glmmML)
```

For a mixed model to be fitted by Gauss-Hermite quadrature we need the function "glmmML" with the option "method='ghq'", the favoured number of quadrature points is determined by the option "n.points".

```
> mGaussH <- glmmML(y ~ as.factor(Grp), cluster=Rat, method = "ghq", n.points = 14, boot = TRUE)
> summary(mGaussH)
```

```
Call: glmmML(formula = y ~ as.factor(Grp), cluster = Rat, method = "ghq", n.points = 14, boot = TRUE)
```

	coef	se(coef)	z	Pr(> z)
(Intercept)	1.802	0.3623	4.976	6.50e-07
as.factor(Grp)G2	-4.515	0.7360	-6.134	8.58e-10
as.factor(Grp)G3	-5.855	1.1899	-4.921	8.63e-07
as.factor(Grp)G4	-5.594	0.9191	-6.087	1.15e-09

Scale parameter in mixing distribution: 1.533 gaussian
Std. Error: 0.2878

LR p-value for H₀: sigma = 0: 2.7e-15

Residual deviance: 435.6 on 602 degrees of freedom AIC: 445.6

Again we change the data set, for the discrete mixture model "teratology" is required.

```
> detach(teratology2)
> attach(teratology)
```

For discrete mixture models the library "flexmix" with its functions "flexmix" and "stepFlexmix" can be used.

```
> library(flexmix)
```

In "stepFlexmix" the procedure is run several times, the maximum likelihood solution is returned. The favoured number of iterations can be specified by the option "nrep". The number of components is determined by the option "k".

Due to random processes the results of different runs of "stepFlexmix" will differ slightly.

```

> detach(package:nlme)
> library(stats4)

> mDiscmix <-stepFlexmix(cbind(D,L) ~ 1, k = 2, nrep=5,
+                        model = FLXMRglmfix(family = "binomial", fixed = ~as.factor(Grp)))

2 : * * * * *

> summary(mDiscmix)

Call:
stepFlexmix(cbind(D, L) ~ 1, model = FLXMRglmfix(family = "binomial",
fixed = ~as.factor(Grp)), k = 2, nrep = 5)

      prior size post>0 ratio
Comp.1  0.7   43      53 0.811
Comp.2  0.3   15      53 0.283

'log Lik.' -92.89085 (df=6)
AIC: 197.7817   BIC: 210.1444

> parameters(mDiscmix)

              Comp.1      Comp.2
coef.as.factor(Grp)2 -4.310975 -4.3109746
coef.as.factor(Grp)3 -5.510396 -5.5103961
coef.as.factor(Grp)4 -5.083411 -5.0834110
coef.(Intercept)      2.461489 -0.2095442

```