Encephalitis - Loglinear Poisson Model and Normal Distribution Model

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First of all, the encephalitis data are loaded:

```r
> library(catdata)
> data(encephalitis)
> attach(encephalitis)
```

Some variables are renamed and recoded before fitting the model.

```r
> BAV <- country
> BAV[BAV==2] <- 0
> TIME <- year
```

The number of infections (count) is modeled in dependence on country and TIME. A Loglinear Poisson Model is fitted.

```r
> enc1 <- glm(count ~ TIME + I(TIME^2) + BAV + TIME*BAV, family = poisson)
> summary(enc1)
```

```
Call:
glm(formula = count ~ TIME + I(TIME^2) + BAV + TIME * BAV, family = poisson)

Deviance Residuals:
       Min          1Q       Median          3Q          Max
-1.7747     -0.4820      0.0403      0.5141      1.2125

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -0.255532   0.518309  -0.493 0.622005
TIME         0.513148   0.127845   4.014 5.97e-05 ***
I(TIME^2)    -0.030485   0.007871  -3.873 0.000108 ***
BAV         -1.587333   0.584286  -2.717 0.006594 **
TIME:BAV     0.211396   0.059441   3.556 0.000376 ***

---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 77.434  on 25 degrees of freedom
Residual deviance: 12.855  on 21 degrees of freedom
```
AIC: 105.74

Number of Fisher Scoring iterations: 4

For comparison the linear Normal Model with the identity link is fitted.

```r
> enc2 <- glm(count ~ TIME+I(TIME^2)+BAV+TIME*BAV, family = gaussian("identity"))
> summary(enc2)
```

Call:
```
glm(formula = count ~ TIME + I(TIME^2) + BAV + TIME * BAV, family = gaussian("identity"))
```

Deviance Residuals:
```
Min 1Q Median 3Q Max
-4.1325 -1.4000 -0.0303 1.4372 4.2604
```

Coefficients:
```
                           Estimate Std. Error t value Pr(>|t|)
(Intercept)              0.39710     1.69760  0.234  0.817312
TIME                     1.15424     0.47280  2.441  0.023577 *
I(TIME^2)                -0.06554     0.03027 -2.166  0.042002 *
BAV                     -4.41444     1.79700 -2.457  0.022816 *
TIME:BAV                 0.85309     0.20713  4.119  0.000489 ***
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

(Dispersion parameter for gaussian family taken to be 4.847447)

```
Null deviance: 399.54 on 25 degrees of freedom  
Residual deviance: 101.80 on 21 degrees of freedom  
AIC: 121.27
```

Number of Fisher Scoring iterations: 2

Fit of loglinear Normal Model. That means a normal model with log-link.

```r
> enc3 <- glm(count ~ TIME+I(TIME^2)+BAV+TIME*BAV, family= gaussian("log"), +                     start=enc2$coef)
> summary(enc3)
```

Call:
```
glm(formula = count ~ TIME + I(TIME^2) + BAV + TIME * BAV, family = gaussian("log"),
     start = enc2$coef)
```

Deviance Residuals:
```
Min 1Q Median 3Q Max
-5.3340 -0.8481 0.0009 1.1639 3.9298
```

Coefficients:
```
                           Estimate Std. Error t value Pr(>|t|)
(Intercept)               -0.223708    0.592457 -0.378  0.70952
```
TIME        0.499564  0.134163  3.724   0.00126 **
I(TIME^2)  -0.029337  0.007919  -3.704  0.00131 **
BAV        -1.478283  0.621729  -2.378   0.02700 *
TIME:BAV   0.198575  0.062320   3.186   0.00444 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 3.701177)

Null deviance: 399.538 on 25 degrees of freedom
Residual deviance: 77.724 on 21 degrees of freedom
AIC: 114.26

Number of Fisher Scoring iterations: 4