

Encephalitis - Loglinear Poisson Model and Normal Distribution Model

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First of all, the encephalitis data are loaded:

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

Some variables are renamed and recoded before fitting the model.

```
> 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.

```
> 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.

```
> 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.

```
> enc3 <- glm(count ~ TIME+I(TIME^2)+BAV+TIME*BAV, family = gaussian("log"),
+             start=enc1$coef)
> summary(enc3)
```

Call:

```
glm(formula = count ~ TIME + I(TIME^2) + BAV + TIME * BAV, family = gaussian("log"),
     start = enc1$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