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)
```

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)
```

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)
```