Count data: Poisson Models

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Counts

Count data

Count data:
Poisson
Models

Jan van den
Broek

Counts

The Poisson
distribution

Poisson
likelihood

evidence

Profile
log-likelihood
interval

Model
checking

Modeling risks:
population size

Modeling
rates: periods

	City			
Age	City 1	City 2	City 3	City 4
40-54	11	13	4	5
55-59	11	6	8	7
60-64	11	15	7	10
65-69	10	10	11	14
70-74	11	12	9	8
>75	10	2	12	7

The number of lung cancer cases in 4 Danish cities between 1968 and 1971.

The Poisson distribution

Call the count variable Y and the observed outcome y.

So the first of the 24 counts can be represented by Y_1 and its observation by y_1. For the ith count this is Y_i with observation y_i.

The **Poisson** probability of observing y_i for the ith count is then

$$P(Y_i = y_i) = \frac{e^{-\mu}\mu^{y_i}}{y_i!}$$

The parameter μ is the population mean of the counts. This means that if we had a large population of counts the mean of all these count would be μ.

Poisson distribution

Count data:
Poisson
Models

Jan van den
Broek

Counts

The Poisson
distribution

Poisson
likelihood

evidence

Profile
log-likelihood
interval

Model
checking

Modeling risks:
population size

Modeling
rates: periods

The variance of all these count would also be μ.

So, with a poisson distribution the mean and the variance are the same.

There seems to be some logic in that: if counts have a small mean, the variance can not be large since counts can not be smaller than zero.

For counts with a large mean say 200, some relatively small values or large values for the counts might occur and thus the variance can be large.

One can now use the poisson distribution to calculate the probability of the outcomes.

If for instance the population mean is known to be 10 then the probability of observing no cases is $e^{-10} = 4.5 \times 10^{-5}$ and that of observing 5 cases is $\frac{e^{-10}10^5}{5!} = 0.04$

So, for every of the 24 observations one can write down the probability of observing that observation.

Poisson likelihood

The product of these probabilities is the likelihood which depends on the population mean μ, so

$$L(\mu) = \frac{e^{-\mu}\mu^{y_1}}{y_1!} \cdot \frac{e^{-\mu}\mu^{y_2}}{y_2!} \cdot \ldots \cdot \frac{e^{-\mu}\mu^{y_{24}}}{y_{24}!}.$$

and the log-likelihood is

$$l(\mu) = \sum_{i=1}^{24} \left[-\mu + y_i \ln(\mu) - \ln(y_i!) \right]$$

That value for μ that maximises the log-likelihood and thus the likelihood is taken as an estimate for μ the **maximum likelihood estimate** m which in this case is the mean of the 24 counts.

Likelihood

Count data: Poisson Models

Jan van den Broek

Counts

The Poisson distribution

Poisson likelihood

evidence

Profile log-likelihood interval

Model checking

Modeling risks: population size

Modeling rates: periods

A measure for the peakedness of the log-likelihood is the second derivative at it's maximum : $l''(m)$.

For a flat function the second derivative is small, for a peaked function it is large. The amount of information is found by calculating the negative of the second derivative:

$$Information = -l''(m)$$

From this the standard error can be calculated:

$$standard\ error = \sqrt{\frac{1}{Information}}$$

evidence

Evidence

Count data:
Poisson
Models

Jan van den
Broek

Counts

The Poisson
distribution

Poisson
likelihood

evidence

Profile
log-likelihood
interval

Model
checking

Modeling risks:
population size

Modeling
rates: periods

Now the fact that the observations com from 4 different cities needs to be modelled.

A linear model for the 4 city groups is
$\beta_0 + \beta_1 city2 + \beta_2 city3 + \beta_3 city4$, were $city2$ is a indicator variable having value zero except for city 2. $city3$ and $city4$ only have one's for city 3 and city 4.

This is just a linear model for the one way anova case using indicator variables.

Evidence

Count data:
Poisson
Models

Jan van den
Broek

Counts

The Poisson
distribution

Poisson
likelihood

evidence

Profile
log-likelihood
interval

Model
checking

Modeling risks:
population size

Modeling
rates: periods

This linear model is used not for the population mean but for the logarithm of the population mean.

$$\ln(\mu) = \beta_0 + \beta_1 city2 + \beta_2 city3 + \beta_3 city4$$

One can also write the model as $\mu = e^{\beta_0 + \beta_1 city2 + \beta_2 city3 + \beta_3 city4}$ and plug this in the likelihood. The first derivatives w.r.t. the β's give the maximum likelihood estimates b_0, b_1, b_2 and b_3.

Evidence

Count data:
Poisson
Models

Jan van den
Broek

Counts

The Poisson
distribution

Poisson
likelihood

evidence

Profile
log-likelihood
interval

Model
checking

Modeling risks:
population size

Modeling
rates: periods

the interpretation of these b's can be seen as follows.

$$\ln(m) = b_0 + b_1 city2 + b_2 city3 + b_3 city4$$

For city 1 all the indicator variables are zero so the model for city 1 is $\ln(m_1) = b_0$. So e^{b_0} is the estimated mean count for city 1. For city 4 for instance only the indicator for city 4 is one so the model for city 4 is: $\ln(m_4) = b_0 + b_3$. Subtracting gives $ln(m_4) - ln(m_1) = \ln\left(\frac{m_4}{m_1}\right) = b_0 + b_3 - b_0 = b_3$.

Thus e^{b_3} shows how much larger m_4 is as compared to m_1. It is a **ratio**. This means that b_3 is the **log-ratio** comparing the mean of city 4 with that of city 1.

In order to see whether or not the cities differ in the mean number of cases one can fit a model with cities in it (Model 1) and one without the cities (Model 0)and then compare these models.

Model 0: The model is $\ln(\mu) = \beta_0$ or $\mu = e^{\beta_0}$

This model for μ is used in the log-likelihood. The derivative w.r.t. β_0 gives the maximum likelihood estimator b_0 for β_0, the second derivative gives the standard error.

The maximum of the log-likelihood, l_0, is obtained by plugging in the value the above maximum likelihood estimate. So take for μ in the log-likelihood e^{b_0} the fitted value for μ.

The maximum for the likelihood then is $L_0 = e^{l_0}$. L_0 gives the probability of the data if the estimated model 0 generated the data.

Evidence

Count data:
Poisson
Models

Jan van den
Broek

Counts

The Poisson
distribution

Poisson
likelihood

evidence

Profile
log-likelihood
interval

Model
checking

Modeling risks:
population size

Modeling
rates: periods

Model 1: The model is
$\ln(\mu) = \beta_0 + \beta_1 city2 + \beta_2 city3 + \beta_3 city4$ or
$\mu = e^{\beta_0 + \beta_1 city2 + \beta_2 city3 + \beta_3 city4}$. Plug in this value for μ in the log-likelihood.

The first derivatives w.r.t the β's gives the maximum likelihood estimators for the β's and the second derivatives gives the standard errors for these estimates.

The maximum of the log-likelihood, l_1, is obtained by plugging in the maximum likelihood estimates so by plugging in the fitted values. The maximum for the likelihood then is $L_1 = e^{l_1}$. L_1 gives the probability of the data if the estimated model 1 generated the data.

Count data:
Poisson
Models

Jan van den
Broek

Counts

The Poisson
distribution

Poisson
likelihood

evidence

Profile
log-likelihood
interval

Model
checking

Modeling risks:
population size

Modeling
rates: periods

Evidence

If L_1 is larger than L_0 then the observed data is more likely using model 1, this model makes the data more probable. In that case under model 1, one better understands why the data is observed as it is. Thus one calculates the likelihood ratio: $\frac{L_1}{L_0}$.

One can use **Akaike's information criterion (AIC)**:

$AIC = -2 \cdot (\text{ log-likelihood }) + 2 \cdot (\text{ number of parameters in the model }) = -2 \cdot l + 2 \cdot p$ were p is the number of parameters in the model.

That model is best that has the lowest AIC as compared to the others.

If the difference in AIC between models is small then the model with the smallest number of parameters is chosen (Occam's Razor) AIC is a measure of how good the model fits to the data as compared to the other models that are fitted.

Evidence

Count data:
Poisson
Models

Jan van den
Broek

Counts

The Poisson
distribution

Poisson
likelihood

evidence

Profile
log-likelihood
interval

Model
checking

Modeling risks:
population size

Modeling
rates: periods

One can calculate the likelihood ratio statistic :
$2 \cdot \ln\left(\frac{L_1}{L_0}\right) = 2(l_1 - l_0)$. This statistic has approximately a
chi-squared distribution with df degrees of freedom where df is
the difference of the number of parameters between the models.
The AIC values and the likelihood ratio test are in the output
below. City can be left out of the model.

```
## Single term deletions
##
## Model:
## cases ~ factor(city)
##               Df Deviance    AIC    LRT Pr(>Chi)
## <none>            25.621 130.01
## factor(city)  3   27.704 126.09 2.0833   0.5553
```

Profile log-likelihood interval

Profile log-likelihood interval

A way to look at the (log-)likelihood as a function of one parameter, e.g. a log-ratio β_1 (i.e. the parameter for city 2), is to focus on this parameter by holding it constant.

Then for each such a constant value of this parameter the log likelihood is maximized over all other parameters.

For every value of the fixed parameter, a maximum value for the log-likelihood is obtained.

To plot such a (log-)likelihood just put the different values of the parameter (β_1) on the horizontal axis and the value of the maximized (log-)likelihood on the vertical axis.

This (log-)likelihood is called **the profile (log-)likelihood**.

Count data:
Poisson
Models

Jan van den
Broek

Counts

The Poisson
distribution

Poisson
likelihood

evidence

Profile
log-likelihood
interval

Model
checking

Modeling risks:
population size

Modeling
rates: periods

Profile log-likelihood interval

This profile likelihood is used to determine confidence intervals that are based on the likelihood ratio test.

The likelihood ratio test statistic was $2 \cdot \ln\left(\frac{L_1}{L_0}\right) = 2(l_1 - l_0)$. l_1 is the maximum value of the log-likelihood if the alternative hypothesis is true.

It is the maximum value when the log likelihood is maximized over all the parameters in the model.

This maximum value can be denoted as l_1 or more specific $l(b_0, b_1, b_2, b_3)$.

Profile log-likelihood interval

l_0 is the maximum value of the log-likelihood if the null-hypothesis is true, that is it is the maximum value for the log-likelihood for a specific value for β_1.

This maximum value of the log-likelihood can be denoted as $l_0 = l(b_0, \beta_1 = 0, b_2, b_3)$ and can thus be seen as the maximum value of the log-likelihood under the null-hypothesis. To test other values then 0 the profile log likelihood $l_0 = l(b_0, \beta_1, b_2, b_3)$ can be used.

The likelihood ratio test statistic has approximately a chi-squared distribution with one degree of freedom.

So the likelihood ratio test with a significance level of 0.05 rejects the null-hypothesis if the likelihood ratio test statistic $(2(l(b_0, b_1, b_2, b_3) - l(b_0, \beta_1, b_2, b_3)))$ is larger then $\chi^2_{0.95}$ which is in the case of 1 degree of freedom equal to 3.84.

For all those values for β_1 for which the likelihood ratio test statistic is smaller than 3.84, the conclusion is that the null-hypothesis is not rejected.

This is an interpretation of a 95% confidence interval: all those values for the parameter of interest that, when put in the null-hypothesis would lead to not rejecting the null-hypothesis.

So look for which values for the likelihood ratio test one does not reject the null-hypothesis or equivalent for which values of the profile log-likelihood ($l(b_0, \beta_1, b_2, b_3, b_4)$) the null hypothesis is not rejected.

This determines the confidence interval.

Also a direct likelihood interpretation is possible: Als those values for the parameter for which the likelihood ratio w.r.t the maximum likelihood estimate is no larger then 7 (see logistic regression)

Count data:
Poisson
Models

Jan van den
Broek

Counts

The Poisson
distribution

Poisson
likelihood

evidence

Profile
log-likelihood
interval

Model
checking

Modeling risks:
population size

Modeling
rates: periods

Model checking

Model checking

Count data:
Poisson
Models

Jan van den
Broek

Counts

The Poisson
distribution

Poisson
likelihood

evidence

Profile
log-likelihood
interval

Model
checking

Modeling risks:
population size

Modeling
rates: periods

Every observation has its own fitted value . This fitted value for individual count i can be calculated by using $m_i = e^{b_0 + b_1 city2 + b_2 city3 + b_3 city4}$ and plugging in the values for the city indicators for that individual count.

The contribution for this observation to the maximum value of the likelihood is: $\frac{e^{-m_i} m_i^{y_i}}{y_i!}$.

In order to see how far the fitted value for this individual count is from the observation of this individual count one could calculate the likelihood contribution when the fitted value is replaced by the observation: $\frac{e^{-y_i} y_i^{y_i}}{y_i!}$.

Model checking

The contribution for this individual count to the deviance is

$$D(y_i) = 2 \cdot \left[\ln \left(\frac{e^{-y_i} y_i^{y_i}}{y_i!} \right) - \ln \left(\frac{e^{-m_i} m_i^{y_i}}{y_i!} \right) \right]$$

.

If this number is large then this individual count contributes a large number to the deviance and, if there are more of these counts, to a bad fit.

If this number is small then this individual count contributes a small value to the deviance implying the model fits this individuals count observation.

Note that the sum of all these individual contributions is the deviance for the model used here.

Model checking

Count data:
Poisson
Models

Jan van den
Broek

Counts

The Poisson
distribution

Poisson
likelihood

evidence

Profile
log-likelihood
interval

Model
checking

Modeling risks:
population size

Modeling
rates: periods

The deviance residuals are defined as the square root from the individual deviance contributions multiplied with a plus or a minus sign depending on whether or not the observation are larger or smaller then the fitted values:

$$res_{dev} = sign(y_i - m_i) \cdot \sqrt{D(y_i)}$$

A large residual means that this individual contributes a large individual deviance, thus contributing to a bad fit. Or, to put it differently: a large deviance residual means that the difference between the fitted value and the observation in terms of log-likelihoods is large for this individual.

One can now make a plot of the deviance residuals and the fitted values. One can then check whether or not there are large residuals

Modeling risks: population size

Modeling risks: population size

In the lung cancer research every city has a certain population size in every age group, but this size was considered to be very large as compared to the number of cases. The population sizes of the age groups were:

	City			
Age	City 1	City 2	City 3	City 4
40-54	3059	2879	3142	2520
55-59	800	1083	1050	878
60-64	710	923	895	839
65-69	581	834	702	631
70-74	509	634	535	539
>75	605	782	659	619

Modeling risks: population size

Count data:
Poisson
Models

Jan van den
Broek

Counts

The Poisson
distribution

Poisson
likelihood

evidence

Profile
log-likelihood
interval

Model
checking

Modeling risks:
population size

Modeling
rates: periods

Instead of assuming that the population sizes are large enough, one better tries to get them in the model.

One way to do that is to model the mean number of cases per individual in the population that is model $\frac{\mu}{population\ size}$.

So now a risk is modelled: the mean number of cases per individual.

The model then becomes
$\ln\left(\frac{\mu}{population\ size}\right) = \beta_0 + \beta_1 age + \beta_2 city2 + \cdots$ in the short notation mentioned above.

This is the same as
$\ln(\mu) = \beta_0 + \ln(population\ size) + \beta_1 age + \beta_2 city2 + \cdots$.

That is *ln(population size)* is in the model without a
β-parameter.

To put it differently the β for the variable *ln(population size)* is
taken to be one.

On calls a variable like this an **offset** variable.

Putting this in the model might be important if the population
sizes differ a lot among the different groups.

Count data:
Poisson
Models

Jan van den
Broek

Counts

The Poisson
distribution

Poisson
likelihood

evidence

Profile
log-likelihood
interval

Model
checking

Modeling risks:
population size

Modeling
rates: periods

Modeling rates: periods

Modeling rates: periods

Count data:
Poisson
Models

Jan van den
Broek

Counts

The Poisson
distribution

Poisson
likelihood

evidence

Profile
log-likelihood
interval

Model
checking

Modeling risks:
population size

Modeling
rates: periods

A common feature of count data is a period of observation over which these counts occur.

In the urinary track disease example for each patient the number of urinary track episodes was determined. Besides this the follow-up time for each patient was recorded. An individual with a long follow-up time might have more chance of showing the event of interest as compared to a patient with a shorter follow-up time.

Using *ln(followuptime)* as an **offset** in the model means that the mean number of events per time unit is modeled, which is a rate:

$\ln(\mu) = \beta_0 + \ln(followup) + \cdots$ or

$\ln(\frac{\mu}{followup}) = \beta_0 + \cdots$

Modeling rates: periods

Count data:
Poisson
Models

Jan van den
Broek

Counts

The Poisson
distribution

Poisson
likelihood

evidence

Profile
log-likelihood
interval

Model
checking

Modeling risks:
population size

Modeling
rates: periods

Sometimes the data can be more aggregated.

Suppose that in a research one is interested in the age effect on the number of deaths due to a certain cause. Suppose further that age is a factor with say 5 levels. In the first age group there were 3 subjects of which one died. The first subject was observed 3 weeks, the second for 5 weeks and the third for 7 weeks. The there are 15 person-weeks observed. This is an example of what is called **person-time**. Person-time shows how long several person were at risk.

The death rate then is $\frac{1}{15} = 0.067$ per person-week. Because this is the number of new cases per person-time this is also called the incidence rate.