Model Based Statistics in Biology.

Part V. The Generalized Linear Model.

Chapter 17.1 Poisson Regression

ReCap. Part I (Chapters 1,2,3,4), Part II (Ch 5, 6, 7)
ReCap Part III (Ch 9, 10, 11), Part IV (Ch 12, 13, 14)
17 Poisson Response Variables
17.1 Poisson Regression
17.2 Single Categorical Explanatory Variable (Log-linear Model)
17.3 Single Categorical Explanatory Variable (Sensitivity Analysis)
17.4 Two or More Categorical Explanatory Variables
17.5 Poisson ANCOVA
17.6 Model Revision

on chalk board

Ch17.xls

Find example with heterogeneous errors to show quasi? Show with spline (bowl) then without. Spline misleads

ReCap Part I (Chapters 1,2,3,4) Quantitative reasoning
ReCap Part II (Chapters 5,6,7) Hypothesis testing and estimation
ReCap (Ch 9, 10,11) The General Linear Model with a single explanatory variable.
ReCap (Ch 12,13,14) GLM with more than one explanatory variable
ReCap (Ch 15) GLM review
ReCap (Ch 16) The generalized linear model.
ReCap (Ch 17)
Many of the analyses undertaken in biology are concerned with frequencies.

Frequencies are also analyzed by the General*ized* Linear Model, which compares observed to expected (model) values.

We use the Analysis of Deviance to calculate the improvement in fit, the Likelihood ratio, and the likelihood ratio statistic.

Today: Poisson Regression.

Wrap-up. .

The example today demonstrated Poisson regression. The response variable has a variance that increases with the mean. The explanatory variable is numeric. The link between the response and explanatory variable is logarithmic, hence the analysis considers percent change in the response variable with change in the explanatory variable.

Poisson Regression.
Example: Death by Horsekick

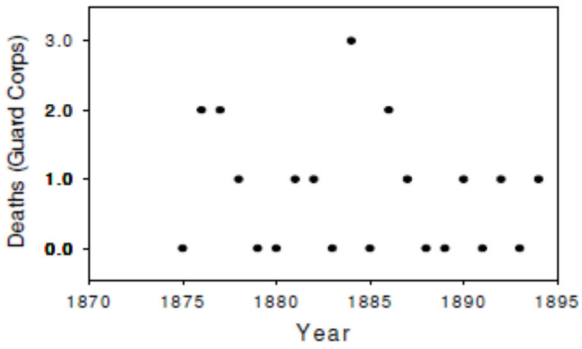
The classic example of Poisson data is the number of deaths by horse kick, for each of 16 corps in the Prussian army, from 1875 to 1894. The data were assembled and published by Ladislaus Bortkiewicz in his book, *The Law of Small Numbers* (1898). Bortkiewicz was an economist and statistician who taught at Berlin University (1901–1931). Bortkiewicz showed that the horsekick data fit a Poisson distribution, which was introduced 1837 by Siméon Poisson in *Récherches sur la Probabilité des Jugements en Matière Criminelle et en Matière Civile.*

The unit of analysis is a single army corps in a single year. The number of deaths per year in a single corps ranged from 0 to 3. The deaths occurred because most of the soldiers knew nothing about horses. They were conscripts from cities and did not know about why one does not stand behind a horse. The data are Poisson counts because we do not know the number of trials (kicks) that resulted in death.

With this data we ask: Was there any trend in the number of deaths?
Poisson regression as a special case of the generalized linear model.

1. Construct Model

Verbal model.
Does number of deaths by horsekick in Guard corps show a trend from 1875 to 1894?



Graphical model
If asked to draw a line on the graph, many people might draw a slight downward trend. How strong is the evidence for such a trend?

1. Construct Model

Response variable: Deaths/year
Explanatory variable: a numeric variable, Year.
Choice of error structure. The data consist of counts in definable units, a single army corps over a year. This points at one of several probability models for discrete variables. One such is the Poisson distribution for rare and random events. Another is the negative binomial distribution for clustered or contagious events, such as disease cases. We will start with the Poisson distribution. Then we will use a residual fit plot to check this choice.

1. Construct Model

Write the formal model using GzLM notation.

Deaths = η + ε

$\eta = \beta_o + \beta_{Yr}\, Yr$ This is called the linear predictor

ε This is the raw (unstandardized) residual.
For model checking, we will use a standardized residual.

This model shows an identity link between the response variable and the linear predictor. With this model β_{Yr} is the change in number of deaths per year. Looking at the data, this will mean fractional deaths per years. Alternatively, we can quantify the change as % per year.

The model is now written:

Deaths = e^{η} + ε

β_{Yr} now quantifies change as %/year rather than numbers/year.

This model estimates multiplicative effects on the data scale (counts).

The model snows a log link of the response variable to the linear predictor η.

Which link?

We can use either of these two links with the Poison distribution, depending on whether we want to look at additive changes in the response variable, or percent change. With count data we usually work with multiplicative changes. We report changes as percentages rather than as change in fractional number of units.

The log link is the canonical link for the Poisson distribution because it is additive on the scale given by the link. Canonical links have desirable statistical properties compared to alternatives. For Poisson error, the estimation routine does not always converge to an estimate when using the identity link.

Rewrite the formal model in standard 3 part format.

Distribution	$Deaths \sim Poisson(\lambda)$	λ is the mean count
Link	$Deaths = e^{\eta}$	This is the log link
Linear predictor	$\eta = \beta_o + \beta_{Yr}\, Yr$	

2. Execute analysis.
Place data in model format:
Column labeled Count,
with response variable # of deaths in each year.
Column labeled Year, the explanatory variable

Here is the SAS input file - >

The numbers are for Guard Corp.
In the next section of this chapter we will compare death rates among different corps.

```
Data Horsekick;
 Input Year 1-4 Deaths 7
 Duty $ 10 Corps $ 12-16;
cards;
1875  0  A guard
1876  2  A guard
1877  2  A guard
1878  1  A guard
1879  0  A guard
1880  0  A guard
1881  1  A guard
1882  1  A guard
1883  0  A guard
1884  3  A guard
1885  0  A guard
1886  2  A guard
1887  1  A guard
1888  0  A guard
1889  0  A guard
1890  1  A guard
1891  0  A guard
1892  1  A guard
1893  0  A guard
1894  1  A guard
```

2. Execute analysis.
We use the model statement to code the model in our statistical package

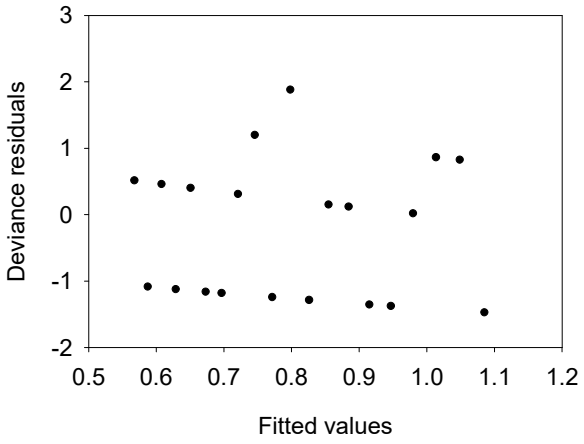
$$Deaths = e^{\beta_o + \beta_{Yr} Yr}$$

```
Proc Genmod;
  Model Deaths = Year/
  Link=log dist=poisson type1 type3;
  Obstats;
PROC PLOT data=; plot res*pred/vref=0;
```
SAS

```
PoissonMod <- glm(formula = Deaths ~ Year,
  family = poisson(link = log), data = Horsekick)
anova(PoissonMod)
```
R

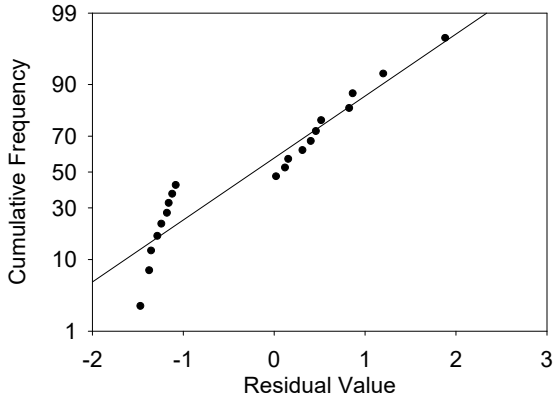
3. Evaluate model

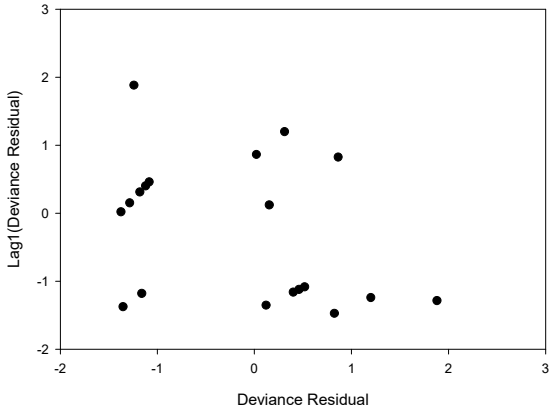
A1. Straight line assumption .
While there is pattern in the residuals, the pattern is not a curve (no bowls or arches). So the straight line assumption on a log scale is acceptable.



A2. Distributional assumptions.
Homogeneity. Judged acceptable

Normal. The zero observations, stacked on the left side of the plot show deviation from the normal line. The stack centers on the normal line, and so the deviations are judged not serious.





Independent. We know the temporal sequence of the observations so we check this assumption. Assumption judged acceptable – no trends up or down across the entire graph.

4. What is the evidence?

For the Generalized Linear Model we calculate the change in deviance ΔDev due to a term in the model, rather than the Sum of Squares for each term in the model. With 20 observations, we have 19 df after fitting the intercept β_o and 18 df after fitting the rate of change parameter β_{Yr}.

The goodness of fit of the data to the full (null) model is $Dev = 22.0500$
The fit of the data to the reduced model is $Dev = 21.4387$
The improvement due to the regression term is $\Delta Dev = 0.61$

Here are the df and deviance calculations, aligned with the model.

	Deaths	=	$\exp(\beta_o + \beta_{Yr} Yr)$	+	ϵ
residual df	19	=	1	+	18
Deviance	22.05	=	0.61	+	21.4387
Δ*Deviance*			0.61		

4. What is the evidence?

The results are displayed in an analysis of deviance (ANODEV) table.

Source	df	*Deviance* = G^2	ΔDev	Pr > ChiSq
Intercept	1	22.0500		
Year	1	21.4387	0.61	0.4343

Reduced model $\beta_o + \beta_{Year}$ hence: $Deaths = e^{(\beta_o + \beta_{Year} \cdot Year)} \neq constant$

Full model β_o hence: $Deaths = e^{(\beta_o)} = constant$

$$LR = \frac{L(\beta_o\ ,\ \beta_{Year}|Data)}{L(\beta_o\ |Data)} \qquad LR = e^{0.61/2} = 1.36$$

There is no evidence of change in death rate (%/year) in this data.

5. Analytic Mode.

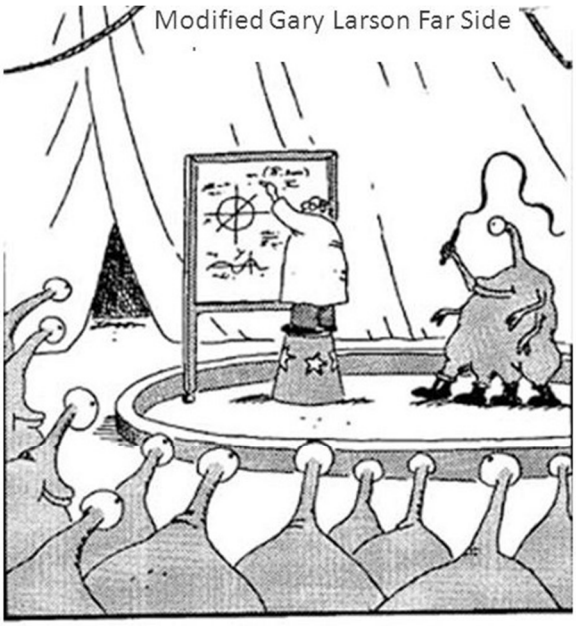
Our measure of evidence, the likelihood ratio, can be used in any of several analytic modes.

"Bayesian"? No. We have no prior information to set up a defensible prior probability.

Frequentist? No. The measurement protocols are definitely not repeatable.

Decision theoretic? No. We have no criteria for setting Type I error.

Evidentialist? Yes. We can infer from the data to a model validated by model checking.



Abducted by an alien circus company, Professor Tversky is forced to present p-values as evidence in center ring.

Tversky, A., & Kahneman, D. (1971). Belief in the law of small numbers. Psychological Bulletin, 76, 105-110.

This is an observational study with many sources of uncontrolled variability. We will avoid using probabilities (p-values) as evidence. .

Tversky and Kahnemann (1971) noted that p-values on data with uncontrolled variability tend to support belief in what they called the "law of small numbers," the judgmental bias that occurs when it is assumed that the characteristics of a population can be estimated from a small number of observations or data points.

10. Science conclusion. Analysis of parameters of biological interest.
The parameter describing rate of change from year to year was small in magnitude $\hat{\beta}_{Year} = -0.0341$ %/year. The estimate was no more likely than not, $\beta_{Year} = 0$. The rate parameter provides no additional information beyond the mean number of deaths over 20 years. Mean(Deaths/year) = 16 deaths / 20 years = 0.8 deaths/year Deaths are not decimal numbers so alternatively, we re-express the mean as an average time per event, 1.25 years/death.