GOLM INTO. doex

GzLM GzLMM Generalized Linear Mixed Models Generalized Linear Models

Special session

2:00 PM Tuesday 24 Oct 2017

Learning Goals

Analysis of Deviance
 Likelihood ratio tests from any probability model

2 Probability models for count data

**Binomial** 

Poisson

--- > Overdispersed Poisson

--- > Negative Binomial

3 Link Functions

"Canonical Link" (the default)

Science founded links

BF H? 1 Tabl 7-4-2

Poisson-

D224

30-9:30 Mun

nifet Olufemi solutions to DAY

Sutter April Bluston The Bunton

ODE.V	The analysis of of deviance is used for any error structure
	normal as well as others

Calculate the p-value for the G statistic



					2					
We have a	already seen ana	alysis of devian	ce for norm	al error mod	el			Elev H(%) Ele	ev(km)	
	http://www.mur						850	0.59	0.26	
		0,				7 1 -	3000	0.37	0.91	
	Regression (Fly	y heterozygosity	/)	Ch 5 page 9	)	8	4600	0.41	1.4	
	•	rage(H) =	0.351429				6200	0.4	1.89	
							8000	0.31	2.44	
	Exp	(H) 0.5796	+	-0.12706 I	Elevation		8600	0.18	2.62	
	1 11					1	10000	0.2	3.05	
		Hnull			Halternative	- e				
	Elevation H	average(H)	residuals	res^2	Exp(H)	residuals _	res^2			
	0.26 0	.59								
	0.91 0	.37		1			100			
	1.4 0	.41								
A	1.89	0.4								
	2.44 0	.31								
	2.62 0	.18								
	3.05	0.2						Im	provement ir	n fit
¥								-		0
	Sum		SS total =			SS res =			= 5	SS regre
7										
1										
*7	The improvement									
	The improvement	ent was due to o	one additior	nal paramete	r (1 df)					
				(-)						
	The likelihood r	•	Stotal)^(-n.			7				
	Calculate the lil	kelihood ratio		LR =						
			<b>D</b> )							
	The test statisti		-K)			7				
	Calculate the G	statistic				_				
	We use the cur	mulative chisqua	are distribu	tion to obtain	the p-value					
		CHISQ.DIST(3.		0.05	•					

MODEV

The analysis of of deviance is used for any error structure normal as well as others

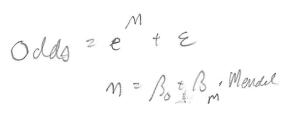
The analysis of deviance for a binomial distribjiton is shown in chapter 16.2 http://www.mun.ca/biology/schneider/b4605/LNotes/Pt5/Ch16\_2.pdf

See pages 4 & 5 for calculation of the G statistic

For the Mendel pea data G =

We use the cumulative chisquare distribution to obtain the p-value 1 - CHISQ.DIST(3.84,1,2) 0.05

Calculate the p-value for the G statistic



L(M, Mm (Data)

2 Probability models for count data

**Binomial** 

Poissor --- > Overdispersed Poisson

--- > Negative Binomial

For examples see Ch 16.1

http://www.mun.ca/biology/schneider/b4605/LNotes/Pt5/Ch16\_1.pdf

## 3 Link Functions "Canonical Link" (the default) Science founded links

We start with the identity link, which is the canonical link for normal errors.

Here is the model for the analysis of the limpet data

$$VO_2 = \beta o + \beta_{sal}$$
  $SAL + \beta_{sp} SP + \beta sal*Sp SAL*Sp + \epsilon$ 

We rewrite this as

 $VO_2 = v + \varepsilon$ 

where

where 
$$VO_2 = V + \varepsilon$$
  
 $V = \beta o + \beta_{sal}$  SAL +  $\beta_{sp}$  SP +  $\beta$ sal\*Sp SAL\*Sp  
 $VO_2 = e + \varepsilon$ 

For a logarithmic line we have

$$VO_2 = e^{v} + \varepsilon$$

There is a canonical for each distribution.

Distribution Link

identity normal

Poisson Log

**Binomial** (log Odds) logit

Negative Binomi: log

Gamma inverse

In some cases it makes sense to use a different link.

For example, we would prefer using the identity (or perhaps log) link for the Gamma distribution The identity (additive effects) and log link (multiplicative effects) are more interpretable.

To gain experience with the GzLM try working the eCh 17.2

Poisson Error

Ch 18.3

Binomiall Error

In each case the data set is small. And the R-code is provided.