

Winter Institute in Data Science and Big Data

Generalized Linear Models

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Overview

- ▶ Previously we have seen “closed form” estimators for quantities of interest, such as $\mathbf{b} = (\mathbf{X}'\mathbf{X})^{-1}\mathbf{X}'\mathbf{y}$.
- ▶ Moving to nonlinear models for categorical and limited support outcomes requires a more flexible process.
- ▶ **Maximum Likelihood Estimation** (Fisher 1922, 1925) is a classic method that finds the value of the estimator “most likely to have generated the observed data, assuming the model specification is correct.”
- ▶ There is both an abstract idea to absorb and a mechanical process to master.

More Background

- ▶ Suppose we care about some political phenomenon \mathbf{Y} , and determine that it has distribution $f()$.
- ▶ The stochastic component is:

$$\mathbf{Y} \sim f(\mu, \tau).$$

- ▶ The systematic component is:

$$\mu = g^{-1}(\mathbf{X}\boldsymbol{\beta})$$

- ▶ This setup is very general and covers all of the nonlinear regression models we will cover.
- ▶ You have seen the linear model in a similar form before:

$$\mathbf{Y}_i = \mathbf{X}_i\boldsymbol{\beta} + \boldsymbol{\epsilon}_i$$

$$\boldsymbol{\epsilon}_i = N(0, \sigma^2).$$

More Background

- But now we are going to think of it in this more general way, for example:

$$Y_i \sim N(\mu_i, \sigma^2)$$

$$\mu_i = \mathbf{X}_i \boldsymbol{\beta}.$$

- An even more general way specifies a **link function**:

$$g(\mathbf{Y}_i) = \mathbf{X}_i \boldsymbol{\beta} + \boldsymbol{\epsilon}_i$$

$$\mathbf{Y}_i = g^{-1}(\mathbf{X}_i \boldsymbol{\beta}) + \boldsymbol{\epsilon}_i$$

$$\mathbf{Y}_i = g^{-1}(\mu_i) + \boldsymbol{\epsilon}_i$$

- We typically write this in expected value terms:

$$\mathbb{E}[Y | \mathbf{X}, \boldsymbol{\beta}] = \mathbf{M}$$

The Likelihood Function

- Assume that:

$$x_1, x_1, \dots, x_n \sim \text{iid } f(x|\theta),$$

where θ is a parameter that is critical to the data generation process (DGP).

- Since these values are independent, the joint distribution of the observed data is just the product of their individual PDF/PMFs:

$$f(\mathbf{x}|\theta) = f(x_1|\theta)f(x_2|\theta) \cdots f(x_n|\theta) = \prod_{i=1}^n f(x_i|\theta).$$

- But once we observe the data \mathbf{x} is fixed.
- It is θ that is unknown, so rewrite the joint distribution function according to:

$$f(\mathbf{x}|\theta) = L(\theta|\mathbf{x}).$$

- Note that this is a purely *notational* change, nothing is different mathematically.

The Likelihood Function

- Fisher (1922) justifies this because at this point we know \mathbf{x} .

$$f(\mathbf{x}|\theta) \longrightarrow L(\theta|\mathbf{x}).$$

- A semi-Bayesian justification works as follows, we want to perform:

$$p(\mathbf{x}|\theta) = \frac{p(\mathbf{x})}{p(\theta)}p(\theta|\mathbf{x}).$$

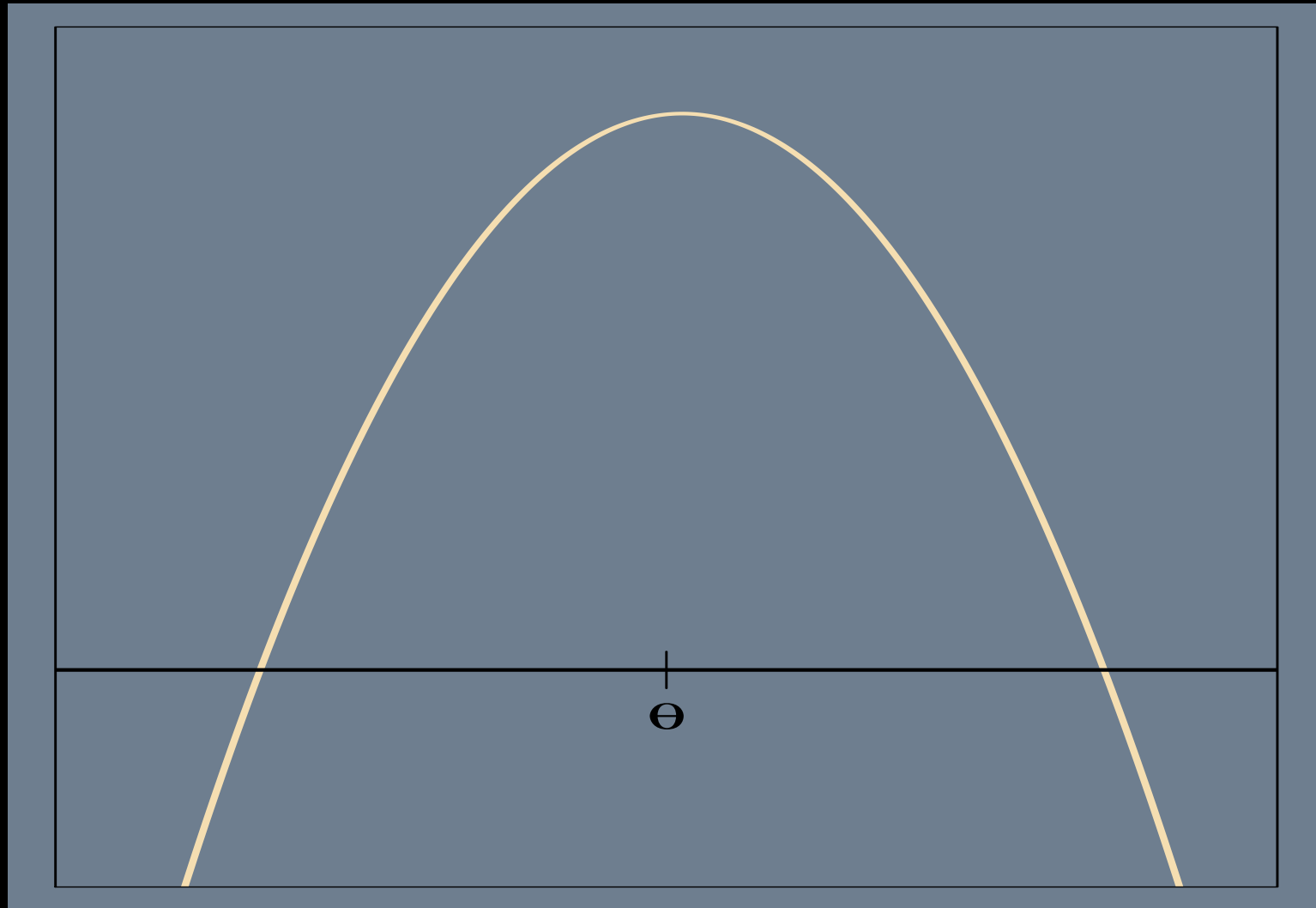
but $p(\mathbf{x}) = 1$ since the data has already occurred, and if we put a finite uniform prior on θ over its finite allowable range (support), then $p(\theta) = 1$.

- Therefore:

$$p(\mathbf{x}|\theta) = \frac{1}{1}p(\theta|\mathbf{x}) = p(\theta|\mathbf{x}).$$

- The only caveat here is the finiteness of the support of θ .

Generic Likelihood Function Illustration



Poisson MLE

- Start with the Poisson PMF for x_i :

$$p(X = x_i) = f(x_i|\theta) = \frac{e^{-\theta}\theta^{x_i}}{x_i!},$$

which requires the assumptions: non-concurrence of arrivals, the number of arrivals is proportion to the time of study, this rate is constant over the time, and there is no serial correlation of arrivals.

- The likelihood function is created from the joint distribution:

$$L(\theta|\mathbf{x}) = \prod_{i=1}^n \frac{e^{-\theta}\theta^{x_i}}{x_i!} = \frac{e^{-\theta}\theta^{x_1}}{x_1!} \frac{e^{-\theta}\theta^{x_2}}{x_2!} \cdots \frac{e^{-\theta}\theta^{x_n}}{x_n!} = e^{-n\theta}\theta^{\sum x_i} \left(\prod_{i=1}^n x_i! \right)^{-1}.$$

- Suppose we have the data: $\mathbf{x} = \{5, 1, 1, 1, 0, 0, 3, 2, 3, 4\}$, then the likelihood function is:

$$L(\theta|\mathbf{x}) = \frac{e^{-10\theta}\theta^{20}}{207360},$$

which is the probability of observing *this* exact sample.

Poisson MLE

- It is often easier to deal the logarithm of the MLE:

$$\log L(\theta|\mathbf{x}) = \ell(\theta|\mathbf{x}) = \log \left(e^{-n\theta} \theta^{\sum x_i} \left(\prod_{i=1}^n x_i! \right)^{-1} \right) = -n\theta + \sum_{i=1}^n x_i \log(\theta) - \log \left(\prod_{i=1}^n x_i! \right).$$

- For our small example this is:

$$\ell(\theta|\mathbf{x}) = -10\theta + 20 \log(\theta) - \underbrace{\log(207360)}_{12.242}.$$

- Importantly, for the family of functions that we will use the likelihood function and the log-likelihood function have the same mode (maximum of the function) for θ .
- They are both guaranteed to be concave to the x-axis.

Obtaining the Poisson MLE

- ▶ Freshman calculus: where is the maximum of the function? At the point when first derivative of the function equals zero.
- ▶ So take the first derivative, set it equal to zero, and solve.
- ▶ $\frac{d}{d\theta}\ell(\theta|\mathbf{x}) \equiv 0$ is called the **likelihood equation**.
- ▶ For the example:

$$\ell(\theta|\mathbf{x}) = -10\theta + 20\log(\theta) - \underbrace{\log(207360)}_{12.242}.$$

Taking the derivative, and setting equal to zero:

$$\frac{d}{d\theta}\ell(\theta|\mathbf{x}) = -10 + 20\theta^{-1} \equiv 0,$$

so that $20\theta^{-1} = 10$, and therefore $\hat{\theta} = 2$ (note the hat).

Obtaining the Poisson MLE

► More generally:

$$\begin{aligned}\ell(\theta|\mathbf{x}) &= -n\theta + \sum_{i=1}^n \log(\theta) - \log\left(\prod_{i=1}^n x_i!\right) \\ \frac{d}{d\theta}\ell(\theta|\mathbf{x}) &= -n + \frac{1}{\theta} \sum_{i=1}^n x_i \equiv 0 \\ \hat{\theta} &= \frac{1}{n} \sum_{i=1}^n x_i = \bar{\mathbf{x}}\end{aligned}$$

► It is *not* true that the MLE is always the data mean.

General Steps

► This process is import to us:

1. Identify the PMF or PDF.
2. Create the likelihood function from the joint distribution of the observed data.
3. Change to the log for convenience.
4. Take the first derivative with respect to the parameter of interest.
5. Set equal to zero.
6. Solve for the MLE.

Poisson Example in R

```
# POISSON LIKELIHOOD AND LOG-LIKELIHOOD FUNCTION
```

```
llhfunc<-function(X,p,do.log=TRUE) {  
  d <- rep(X,length(p))  
  q.vec <- rep(length(y.vals),length(p)); p.vec <- rep(p,q.vec)  
  print(q.vec)  
  d.mat <- matrix(dpois(d,p.vec,log=do.log),ncol=length(p))  
  print(d.mat)  
  if (do.log==TRUE) apply(d.mat,2,sum)  
  else apply(d.mat,2,prod)  
}
```

Poisson Example in R

```
# HERE'S A TEST FUNCTION
```

```
y.vals<-c(1,3,1,5,2,6,8,11,0,0)
```

```
llhfunc(y.vals,c(4,30))
```

```
[1] 10 10
```

```
      [,1]      [,2]
```

```
[1,] -2.6137 -26.599
```

```
[2,] -1.6329 -21.588
```

```
[3,] -2.6137 -26.599
```

```
[4,] -1.8560 -17.782
```

```
[5,] -1.9206 -23.891
```

```
[6,] -2.2615 -16.172
```

```
[7,] -3.5142 -13.395
```

```
[8,] -6.2531 -10.089
```

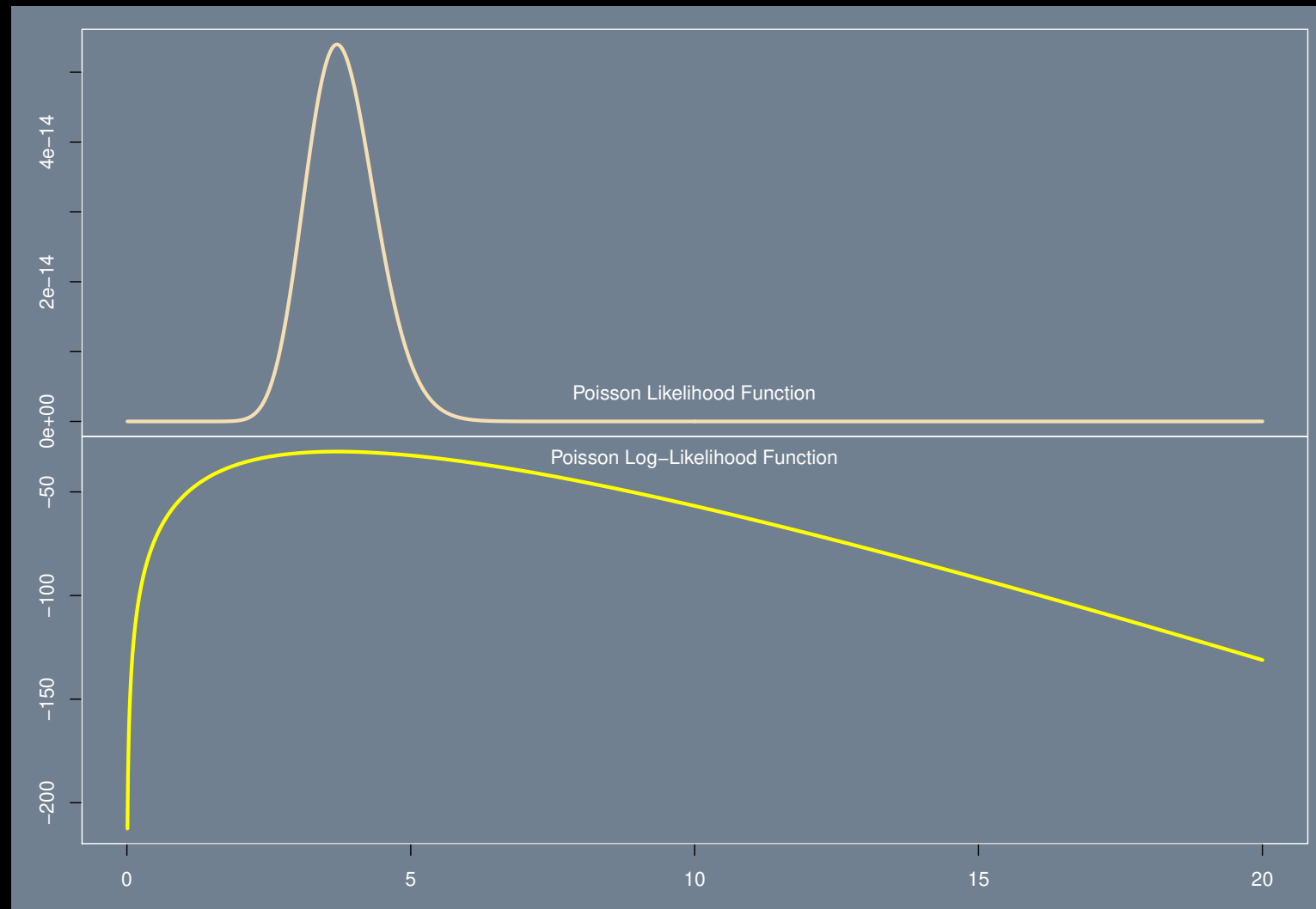
```
[9,] -4.0000 -30.000
```

```
[10,] -4.0000 -30.000
```

```
[1] -30.666 -216.114
```

Poisson Example in R

```
# USE THE R CORE FUNCTION FOR OPTIMIZING, par=STARTING VALUES,  
# control=list(fnscale=-1) INDICATES A MAXIMIZATION, bfgs=QUASI-NEWTON ALGORITHM  
mle <- optim(par=1,fn=llhfunc,X=y.vals,control=list(fnscale=-1),method="BFGS")  
  
# MAKE A PRETTY GRAPH OF THE LOG AND NON-LOG VERSIONS  
ruler <- seq(from=.01, to=20, by= .01)  
poison.ll <- llhfunc(y.vals,ruler)  
poison.l <- llhfunc(y.vals,ruler,do.log=FALSE)  
  
par(oma=c(3,3,1,1),mar=c(0,0,0,0),mfrow=c(2,1))  
plot(ruler,poison.l,col="wheat",type="l",xaxt="n",lwd=3)  
text(mean(ruler),mean(poison.l),"Poisson Likelihood Function")  
plot(ruler,poison.ll,col="yellow",type="l",lwd=3)  
text(mean(ruler),mean(poison.ll)/2,"Poisson Log-Likelihood Function")
```



Measuring the Uncertainty of the MLE

- ▶ The first derivative measures slope and the second derivative measures “curvature” of the function at a given point.
- ▶ The more peaked the function is at the MLE, the more “certain” the data are about this estimator.
- ▶ The square root of the negative inverse of the expected value of the second derivative is the SE of the MLE.
- ▶ In multivariate terms for vector $\boldsymbol{\theta}$, we take the negative inverse of the expected *Hessian*.
- ▶ Poisson example:

$$\begin{aligned}\frac{d}{d\theta}\ell(\theta|\mathbf{x}) &= -n + \frac{1}{\theta} \sum_{i=1}^n x_i \\ \frac{d^2}{d\theta^2}\ell(\theta|\mathbf{x}) &= \frac{d}{d\theta} \left(\frac{d}{d\theta}\ell(\theta|\mathbf{x}) \right) = -\theta^{-2} \sum_{i=1}^n x_i\end{aligned}$$

- ▶ The expected value (estimate) of $\boldsymbol{\theta}$ is the MLE, so:

$$SE(\hat{\theta}) = \frac{\hat{\theta}^2}{\sum_{i=1}^n x_i} = \frac{\bar{\mathbf{x}}^2}{n\bar{\mathbf{x}}} = \frac{\bar{\mathbf{x}}}{n}.$$

Multivariable MLE

► Now $\boldsymbol{\theta}$ is a vector of coefficients to be estimated (eg. regression).

► The **Score Function** is:

$$\dot{\ell}(\boldsymbol{\theta}|\mathbf{x}) = \frac{\partial}{\partial \boldsymbol{\theta}} \ell(\boldsymbol{\theta}|\mathbf{x})$$

which we use to get the MLE $\hat{\boldsymbol{\theta}}$.

► The **Hessian Matrix** is:

$$\mathbf{H} = \frac{\partial^2 \ell(\boldsymbol{\theta}|\mathbf{x})}{\partial \boldsymbol{\theta} \partial \boldsymbol{\theta}'}$$

which we use to get the SE of the MLE.

► The information matrix is:

$$\mathbf{I} = -\mathbb{E}(f) \left[\frac{\partial^2 \ell(\boldsymbol{\theta}|\mathbf{x})}{\partial \boldsymbol{\theta} \partial \boldsymbol{\theta}'} \bigg|_{\hat{\boldsymbol{\theta}}} \right] \equiv \mathbb{E}(bbbh) \left[\frac{\partial \ell(\boldsymbol{\theta}|\mathbf{x})}{\partial \boldsymbol{\theta}} \frac{\partial \ell(\boldsymbol{\theta}|\mathbf{x})}{\partial \boldsymbol{\theta}'} \bigg|_{\hat{\boldsymbol{\theta}}} \right]$$

where the equivalence of these forms is called the *information equality*.

► The variance-covariance of $\hat{\boldsymbol{\theta}}$ is produced by:

$$\boldsymbol{\Sigma} = \mathbf{I}^{-1}$$

Properties of the MLE (Birnbaum 1962)

► Consistency:

$$\text{plim} \hat{\theta} = \theta.$$

► Asymptotic Normality:

$$\hat{\theta} \underset{a}{\sim} N(\theta, I(\theta)^{-1}) \quad \text{where } I(\theta) = -\mathbb{E} \left[\frac{\partial^2 \ell(\theta)}{\partial \theta \partial \theta'} \right].$$

► Asymptotic Efficiency: no other estimator has lower variance, the variance of the MLE meets the Crámer-Rao Lower Bound.

► Invariance To Reparameterization:

$$\gamma = c(\theta) \implies \hat{\gamma} = c(\hat{\theta}).$$

Dichotomous Overview

- ▶ We will create a regression model for dichotomous outcome variables: vote/not-vote, war/no-war, pass/fail, etc.
- ▶ Note that this is different than having dichotomous explanatory variables.
- ▶ Remember that regression is really conditional average, $\mathbb{E}[\mathbf{Y}|\mathbf{X}]$, which does not have the same implications for 0/1 outcomes on the LHS.

- ▶ Consider the probability that a single case has a 0 or a 1 as the outcome:

$$\pi_i = p(Y_i) = p(Y = 1|\mathbf{X} = \mathbf{x}_i), \quad \text{where } \pi \in [0:1].$$

- ▶ So:

$$\mathbb{E}(Y_i|\mathbf{x}_i) = (\pi_i)(1) + (1 - \pi_i)(0) = \pi_i.$$

(recall that for discrete RV $\mathbb{E}(A) = \sum_{\text{over events}} P(A) \times A$)

- ▶ This means that we are *estimating* an underlying probability value for given levels of a vector of explanatory variable values.

New Conceptual Model

- ▶ Start with the linear predictor $\boldsymbol{\eta} = \boldsymbol{\alpha} + \beta \mathbf{x}$.
- ▶ Now let's specify a **link function** that relates the linear additive RHS component to the expected value of the nonlinear LHS component:

$$\pi_i = g^{-1}(\eta_i) = p(\alpha_i + \beta_i x) \Rightarrow g(\pi_i) = \eta_i = \alpha_i + \beta_i x.$$

- ▶ Objectives for $g^{-1}()$:
 - ▷ smooth on $[0:1]$
 - ▷ For a positive effect of \mathbf{x}_i on π_i :
 - $g^{-1} \rightarrow 0$ as $x_i \rightarrow, -\infty$
 - $g^{-1} \rightarrow 1$ as $x_i \rightarrow, +\infty$.
 - ▷ For a negative effect of \mathbf{x}_i on π_i :
 - $g^{-1} \rightarrow 1$ as $x_i \rightarrow, -\infty$
 - $g^{-1} \rightarrow 0$ as $x_i \rightarrow, +\infty$.

New Conceptual Model

► There are two common solutions for $g^{-1}()$.

► Logit:

$$\Lambda(\eta_i) = [1 + \exp(-\eta_i)]^{-1}$$

► Probit:

$$\Phi(\eta_i) = (2\pi)^{-\frac{1}{2}} \int_{-\infty}^{\eta_i} \exp\left[-\frac{1}{2}\eta_i^2\right] d\eta_i$$

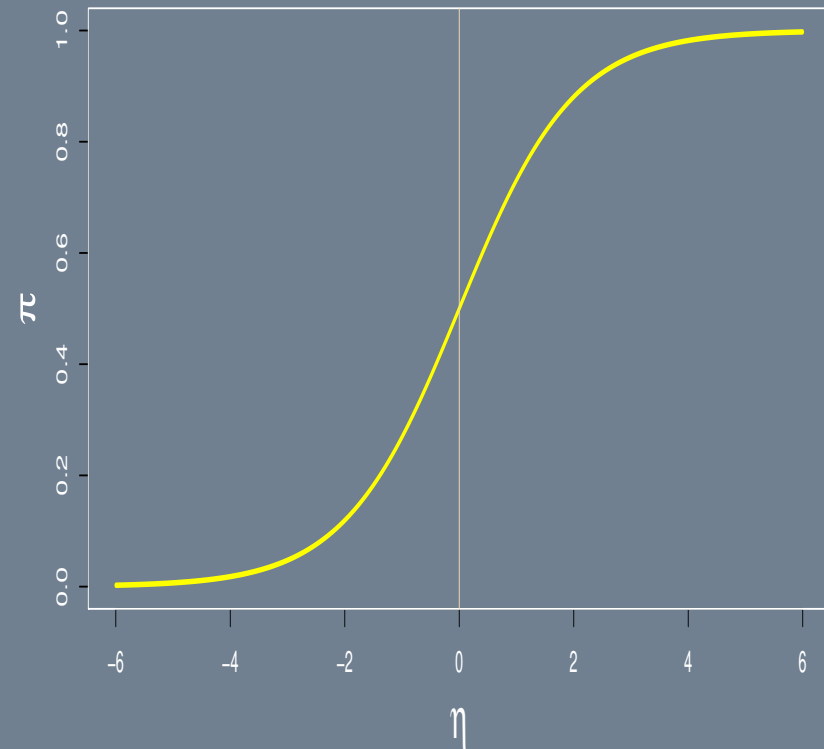
► These are sometimes given in $g()$ form: $\Phi^{-1}(\pi_i)$ and $\Lambda^{-1}(\pi_i) = \text{logit}(\pi_i) = \log\left(\frac{p_i}{1-p_i}\right)$.

► Less common is the cloglog function:

$$g(\mu) = -\log(-\log(1 - \mu)) \qquad g^{-1}(\eta) = 1 - \exp(-\exp(\eta))$$

Latent Variable Justification

- ▶ Humans make dichotomous decisions from smooth preference structures, but we only see discrete choices in the data.
- ▶ The Index Function (Utility) model states that if *benefits* - *costs* = U is greater than zero then the choice should be a one, and vice-versa.



Latent Variable Justification

- ▶ Utility model states: $U_i = \mathbf{x}_i\boldsymbol{\beta} + \boldsymbol{\epsilon}_i$ (subsume the constant into the vector), and $p(U_i > 0) = p(\mathbf{x}_i\boldsymbol{\beta} + \boldsymbol{\epsilon}_i > 0) = p(\boldsymbol{\epsilon}_i > -\mathbf{x}_i\boldsymbol{\beta})$.
- ▶ Political Example:
 - ▷ U^R , the utility of voting for the Republican candidate
 - ▷ U^D , the utility of voting for the Democratic candidate
 - ▷ direction is arbitrary, so pick $Y = 1$ the decision to vote for the Republican candidate
 - ▷ Define the two utility functions in regression terms:

$$U_i^R = \mathbf{x}_i\boldsymbol{\beta}_R + \boldsymbol{\epsilon}_{iR} \qquad U_i^D = \mathbf{x}_i\boldsymbol{\beta}_D + \boldsymbol{\epsilon}_{iD}$$

- ▷ So now:

$$\begin{aligned} p(Y_i = 1 | \mathbf{x}_i) &= p(U_i^R > U_i^D) \\ &= p(\mathbf{x}_i\boldsymbol{\beta}_R + \boldsymbol{\epsilon}_{iR} > \mathbf{x}_i\boldsymbol{\beta}_D + \boldsymbol{\epsilon}_{iD} | \mathbf{x}_i) \\ &= p(\mathbf{x}_i[\boldsymbol{\beta}_R - \boldsymbol{\beta}_D] + \boldsymbol{\epsilon}_{iR} - \boldsymbol{\epsilon}_{iD} > 0) \\ &= p(\mathbf{x}_i\boldsymbol{\beta} + \boldsymbol{\epsilon} > 0) \end{aligned}$$

which is just 1-CDF.

Binomial Regression Model

- ▶ If Y_i for $i = 1, \dots, n$ is iid binomial $B(n_i, p_i)$, then:

$$p(Y_i = y_i) = \binom{n_i}{y_i} p_i^{y_i} (1 - p_i)^{n_i - y_i}$$

- ▶ Further suppose that these are affected by the same q predictors (covariates, explanatory variables), x_{i1}, \dots, x_{iq} .
- ▶ The tool that connects these predictors to p is the linear predictor:

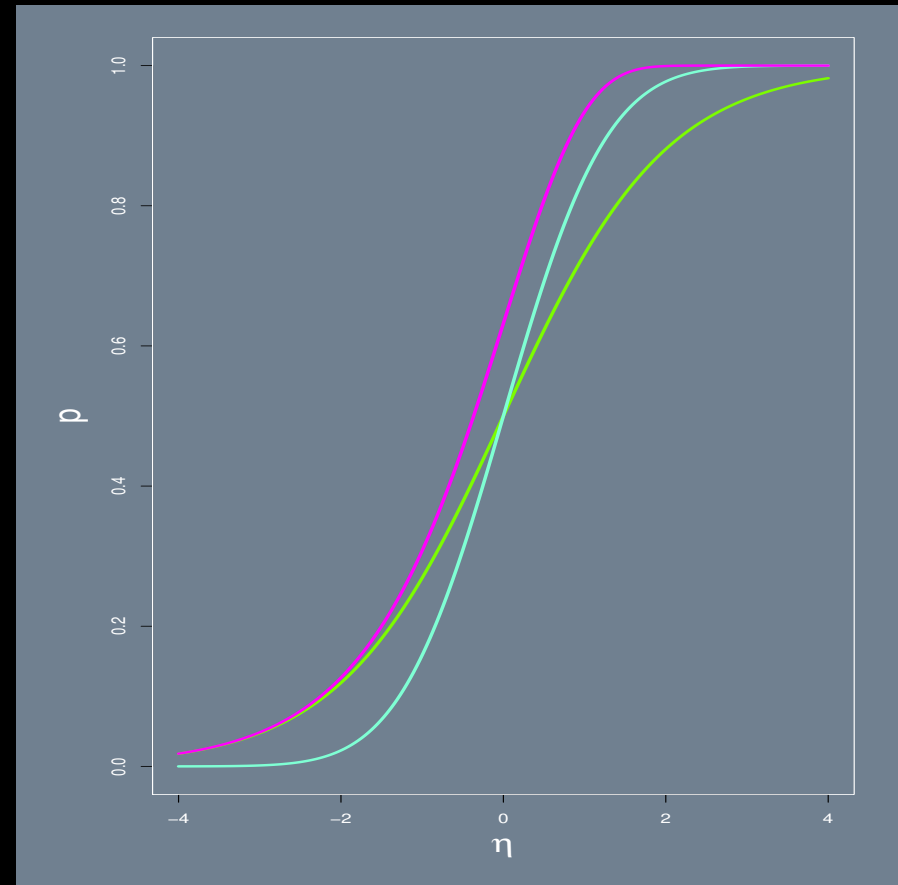
$$\eta_i = \beta_0 + \beta_1 x_{i1} + \dots + \beta_q x_{iq}.$$

- ▶ We still need a link function, $\eta_i = g(p_i)$, that is not an identity ($\eta_i = p_i$) since we need $0 \leq p_i \leq 1$.

Binomial Link Functions

- ▶ Logit (logistic): $\eta = \log\left(\frac{p}{1-p}\right)$, $p = \frac{\exp(\eta)}{1+\exp(\eta)} [1 + \exp(-\eta)]$.
- ▶ Probit: $\eta = \Phi^{-1}(p)$, $p = \Phi(\eta)$.
- ▶ Complementary log-log:
 $\eta = \log(-\log(1-p))$,
 $p = 1 - \exp(-\exp(\eta))$.

```
ruler <- seq(-4,4,length=200)
postscript("Class.MLE/faraway.ch2.fig3.ps")
par(col.axis="white",col.lab="white",col.sub="white",
    col="white", bg="slategray",cex.lab=2,mar=c(6,6,2,2))
plot(ruler,exp(ruler)/(1+exp(ruler)),type="l",lwd=3,
     col="lawngreen",ylim=c(0,1),
     xlab=expression(eta),ylab="p")
lines(ruler,pnorm(ruler),lwd=3,col="aquamarine")
lines(ruler,1-exp(-exp(ruler)),lwd=3,col="magenta")
dev.off()
```



Binomial Model Estimation

- ▶ Define a likelihood function for observed iid y_i , where $i = 1, \dots, n$ from $f(y|p)$.
- ▶ Then the *joint distribution* of these observed data is:

$$p(y_1, y_2, \dots, y_n) = p(y_1|\beta, \mathbf{x}_1)f(y_2|\beta, \mathbf{x}_2) \cdots f(y_n|\beta, \mathbf{x}_n) = \prod_{i=1}^n f(y_i|\beta, \mathbf{x}_i).$$

- ▶ If we consider that p is really the unknown and the y_i are known, then it makes sense to think of this joint function as a function that reveals something about β .
- ▶ Denote it $L(\beta|\mathbf{x}, \mathbf{y})$, which is called a *likelihood function*.

Binomial Model Estimation

- More precisely, we can incorporate the information that Y can only be 0 or 1:

$$\begin{aligned} L(\boldsymbol{\beta}|\mathbf{X}, \mathbf{Y}) &= \prod_{y_i=0} [1 - F(\mathbf{X}_i\boldsymbol{\beta})] \prod_{y_i=1} [F(\mathbf{X}_i\boldsymbol{\beta})] \\ &= \prod_{i=1}^n [1 - F(\mathbf{X}_i\boldsymbol{\beta})]^{1-y_i} [F(\mathbf{X}_i\boldsymbol{\beta})]^{y_i} \\ \ell(\boldsymbol{\beta}|\mathbf{X}, \mathbf{Y}) &= \sum_{i=1}^n [(1 - y_i) \log(1 - F(\mathbf{X}_i\boldsymbol{\beta})) + y_i \log(F(\mathbf{X}_i\boldsymbol{\beta}))] \end{aligned}$$

- The log-likelihood is concave to the x-axis for common choices of $F()$, and produces coefficient estimates that are distributed student's- t .
- Generally with the binomial setup it is easier to think in terms of the CDF, $F()$, rather than the PDF, $f()$, since the former directly describes the S-curve of theoretical interest.

Binomial Model MLE

- The **gradient** is given by:

$$G = \frac{\partial}{\partial \boldsymbol{\beta}} \ell(\boldsymbol{\beta} | \mathbf{X}, \mathbf{Y}) = \sum_{i=1}^n \left[\frac{y_i f_i}{F_i} + (1 - y_i) \frac{-f_i + 1}{1 - F_i} \right] \mathbf{x}_i$$

- The **Hessian** is given by:

$$H = \frac{\partial^2}{\partial \boldsymbol{\beta} \partial \boldsymbol{\beta}'} \ell(\boldsymbol{\beta} | \mathbf{X}, \mathbf{Y}) = \sum_{i=1}^n \frac{f_i^2}{F_i(1 - F_i)} \mathbf{x}_i \mathbf{x}_i'$$

- The **Variance-Covariance Matrix** is calculated as:

$$VC_{\boldsymbol{\beta}} = E \left[-H^{-1} \right]$$

Common Forms

► Probit, where $\phi_i = \phi_i(\mathbf{x}_i\boldsymbol{\beta})$ and $\Phi_i = \Phi_i(\mathbf{x}_i\boldsymbol{\beta})$:

$$G = \sum_{y=0} \frac{-\phi_i}{1 - \Phi_i} \boldsymbol{\beta} \mathbf{x}_i + \sum_{y_i=1} \frac{\phi_i}{\Phi_i} \boldsymbol{\beta} \mathbf{x}_i$$

$$H = \left\{ \sum_{i=0} \left[-\frac{-\phi_i^2}{(1 - \Phi_i)^2} + \frac{\mathbf{x}_i \boldsymbol{\beta} \phi_i}{1 - \Phi_i} \right] + \sum_{i=1} \left[-\frac{\mathbf{x}_i \boldsymbol{\beta} \phi_i}{\Phi_i} - \phi_i^2 \right] \right\} \mathbf{x}_i \mathbf{x}_i'$$

$$VC_{\boldsymbol{\beta}} = \sum_{i=1}^n \frac{\phi_i^2}{\Phi_i(1 - \Phi_i)} \mathbf{x}_i \mathbf{x}_i'$$

► Logit, where $\Lambda_i = 1/[1 + \exp(\mathbf{X}_i\boldsymbol{\beta})]$:

$$G = \sum_{i=1}^n (y_i - \Lambda_i) \mathbf{x}_i \quad H = \sum_{i=1}^n \{-\Lambda_i(1 - \Lambda_i)\} \mathbf{x}_i \mathbf{x}_i'$$

$$VC_{\boldsymbol{\beta}} = \left[\sum_{i=1}^n \{\Lambda_i(1 - \Lambda_i)\} \mathbf{x}_i \mathbf{x}_i' \right]^{-1}$$

Interpretation of Individual Binomial β Results

- ▶ sign of the parameter estimate
- ▶ predicted/fitted values
- ▶ marginal effects, including first differences
- ▶ derivative methods
- ▶ Note $\text{logit}(\beta) \approx \frac{\pi}{\sqrt{3}}\text{probit}(\beta)$
- ▶ Wald (t-tests) for significance:

$$W = (R\hat{\beta} - q) \left[R(VC_{\hat{\beta}})R' \right]^{-1} (R\hat{\beta} - q)$$

for $H_0: R\hat{\beta} = q$ (commonly $R = 1, q = 0$, so that $W \sim F_{df=J, n-K}$. (where J is the number of restrictions stipulated in R). For individual coefficients, this reduces to:

$$W_k = (\hat{\beta}'_k \hat{\beta}_k / VC_{\hat{\beta}}[k, k])^{\frac{1}{2}} \sim t_{df=n-k}$$

(where $n \times k$ is the dimension of the \mathbf{X} matrix).

- ▶ Note that the F-test is more robust than the t-test (Hauck-Donner effect, JASA 1977).

Percent Predicted Correctly

- Compares actual against predicted in a 2-by-2 table:

		<i>Prediction</i>	
		0	1
<i>Data</i>	0	correct	incorrect
	1	incorrect	correct

- But wait! These models do not produce predicted 0/1 values, for instance:

```
round(logitmod2$fitted.values,3)
```

```

      1      2      3      4      5      6      7      8      9     10     11     12     13
0.939 0.859 0.829 0.603 0.430 0.375 0.375 0.375 0.322 0.274 0.230 0.230 0.230
     14     15     16     17     18     19     20     21     22     23
0.230 0.158 0.130 0.086 0.086 0.069 0.069 0.045 0.036 0.023
```

from the Bernoulli treatment.

Percent Predicted Correctly

- The naïve criteria:

$$p_i = 1 \text{ if, } F(\mathbf{x}_i\boldsymbol{\beta}) > 0.5 \qquad p_i = 0 \text{ if, } F(\mathbf{x}_i\boldsymbol{\beta}) < 0.5$$

- Create the table:

```
ppc <- cbind(orings2$damage, round(logitmod2$fitted.values,3))
( naive <- matrix(c(
  nrow(ppc[(ppc[,1] == 0) & (ppc[,2] < 0.5),])/nrow(ppc),
  nrow(ppc[(ppc[,1] == 0) & (ppc[,2] > 0.5),])/nrow(ppc),
  nrow(ppc[(ppc[,1] == 1) & (ppc[,2] < 0.5),])/nrow(ppc),
  nrow(ppc[(ppc[,1] == 1) & (ppc[,2] > 0.5),])/nrow(ppc)),
  byrow=TRUE,ncol=2) )
```

```
      [,1]      [,2]
[1,] 0.69565 0.00000
[2,] 0.13043 0.17391
```

- Better criteria: mean of \hat{y}_i , substantive/theoretical point.

Binomial Model Comparison

- ▶ Compare two models, one with ℓ parameters and one with s parameters such that $\ell > s$ and every parameter in the s set is also in the ℓ set: nesting.
- ▶ Denote the first as $L(p|\mathbf{y}, \mathbf{X}_L) = L_L$ and the second as $L(p|\mathbf{y}, \mathbf{X}_S) = L_S$.
- ▶ A tool for comparing these models is the **likelihood ratio statistic**:

$$LRT = 2 \log \frac{L_L}{L_S} = 2(\log(L_L) - \log(L_S)) = -2 \log \frac{L_S}{L_L} = -2(\log(L_S) - \log(L_L)).$$

- ▶ This is distributed asymptotically χ^2 with degrees of freedom the difference between the number of parameters in the two models.
- ▶ Tail values support the nesting values, meaning that the restricted values are not supported.

Binomial Model Comparison

- ▶ The most extreme case of L_L fits a “covariate” to every datapoint as an indicator function, and is thus a regression model where every datapoint is a separate inference.
- ▶ This is called the saturated model and provides no data-reduction and no modeling value, but serves as a reference point.
- ▶ For the binomial model, the saturated model can be described by $\hat{p}_i = y_i/n_i$, which is the number of success over the number of trials for the i th case (frequently $n_i = 1$).
- ▶ Another reference point is a model that uses β_0 only and is called a *mean model*.
- ▶ Thus any model we specify “lives” between these two extremes of model fit.
- ▶ Residuals in the nonlinear regression sense are called *deviances* to distinguish them from the assumptions in linear models.

Binomial Model Comparison

- So it should be clear that:

$$\sum D_{\text{saturated model}} < \sum D_{\text{our specified model}} < \sum D_{\text{mean model}}$$

- For the binomial model, the LRT reduces to a ratio of the saturated model to the specified model, given by:

$$D = 2 \sum_{i=1}^n \{y_i \log(y_i/\hat{y}_i) + (n_i - y_i) \log((n_i - y_i)/(n_i - \hat{y}_i))\},$$

where \hat{y}_i are the fitted values from the smaller (specified) model.

- The mean model provides a large value of D called the *null deviance*.
- D for assessing a model with p covariates is asymptotically distributed χ_{n-p}^2 , where $n - p$ is the degrees of freedom.
- Returning the Challenger example ($n = 23$), I left off the following information before:

```
summary(logitmod)
:
Null deviance: 38.898  on 22  degrees of freedom
Residual deviance: 16.912  on 21  degrees of freedom
```

Binomial Model Comparison

► Formal tests:

- ▷ Specified model versus saturated model:

```
pchisq(deviance(logitmod),df.residual(logitmod),lower=FALSE)  
0.71641
```

which is not in the χ^2_{21} tail, so it is statistically “close” to the saturated model and therefore a good fit.

- ▷ Mean model versus saturated model:

```
pchisq(38.9,22,lower=FALSE)  
0.014489
```

which is in the χ^2_{22} tail, so it is statistically “far” from the saturated model and therefore not a good fit.

- ▷ Specified model (with temperature) versus mean model ($D_S - D_L$):

```
pchisq(38.9-16.9,1,lower=FALSE)  
2.7265e-06
```

which is in the χ^2_{22} tail, so L_S is statistically “far” from L_L .

Binomial Model Comparison

► Cautions:

- ▷ The approximation of D to a χ^2 distributed statistic is poor for small n_i and “lumpy” distribution of n_i as well.
- ▷ Most texts recommend $n_i \geq 5, \forall i$, but this is just a rule-of-thumb.
- ▷ We could also have done a Wald test on temperature:

	Estimate	Std. Error	z value	Pr(> z)
temp	-0.2162	0.0532	-4.07	4.8e-05

but differences of deviances are usually more accurate than tests on a single deviance.

- ▷ When Wald provides significant results but a deviance comparison doesn't (the Hauck-Donner effect).

Binomial Model Comparison

► Confidence interval for the j th coefficient: $\hat{\beta}_j \pm z^{\alpha/2} se(\hat{\beta}_j)$.

► Low-tech method:

```
c(-0.2162-1.96*0.0532,-0.2162+1.96*0.0532)
-0.32047 -0.11193
```

► Hi-tech method:

```
summary(logitmod)$coefficients[,1]
      + qnorm(0.975) * t(c(-1,1) %o% summary(logitmod)$coefficients[,2])
(Intercept)  5.20243 18.12355
temp          -0.32046 -0.11201
```

► Profile likelihood version (accounts for covariance):

```
library(MASS)
confint(logitmod)
Waiting for profiling to be done...
      2.5 %    97.5 %
(Intercept)  5.57520 18.73760
temp          -0.33266 -0.12018
```

Real Example: Model of Vote Choice 1994 American National Election Study

	Parameter Estimate	Standard Error	z-statistic	p-value
Choice Parameters				
Intercept	-1.116	0.387	-2.882	0.004
Democratic Support for Clinton	-0.015	0.008	-1.943	0.052
Republican Support for Clinton	0.030	0.011	2.701	0.007
Democratic Crime Concern	0.044	0.009	4.960	0.000
Republican Crime Concern	0.007	0.009	0.699	0.485
Democratic Gvt. Help Disadv.	0.029	0.011	2.698	0.007
Republican Gvt. Help Disadv.	-0.006	0.013	-0.438	0.661
Democratic Gvt. Spending	0.114	0.025	4.633	0.000
Republican Gvt. Spending	-0.100	0.025	-4.030	0.000
Democratic Federal Healthcare	0.031	0.008	3.670	0.000
Republican Federal Healthcare	-0.017	0.010	-1.691	0.091
Democratic Ideology Entropy	0.104	0.131	0.794	0.427
Republican Ideology Entropy	0.303	0.068	4.437	0.000
Party Identification Scale	0.368	0.028	13.158	0.000

Goodness of Fit Test: $LRT = 359.3869, p < 0.0001$ for $\chi^2_{df=19}$

Percent Correctly Classified: 78.66% (using the “naive criteria”)

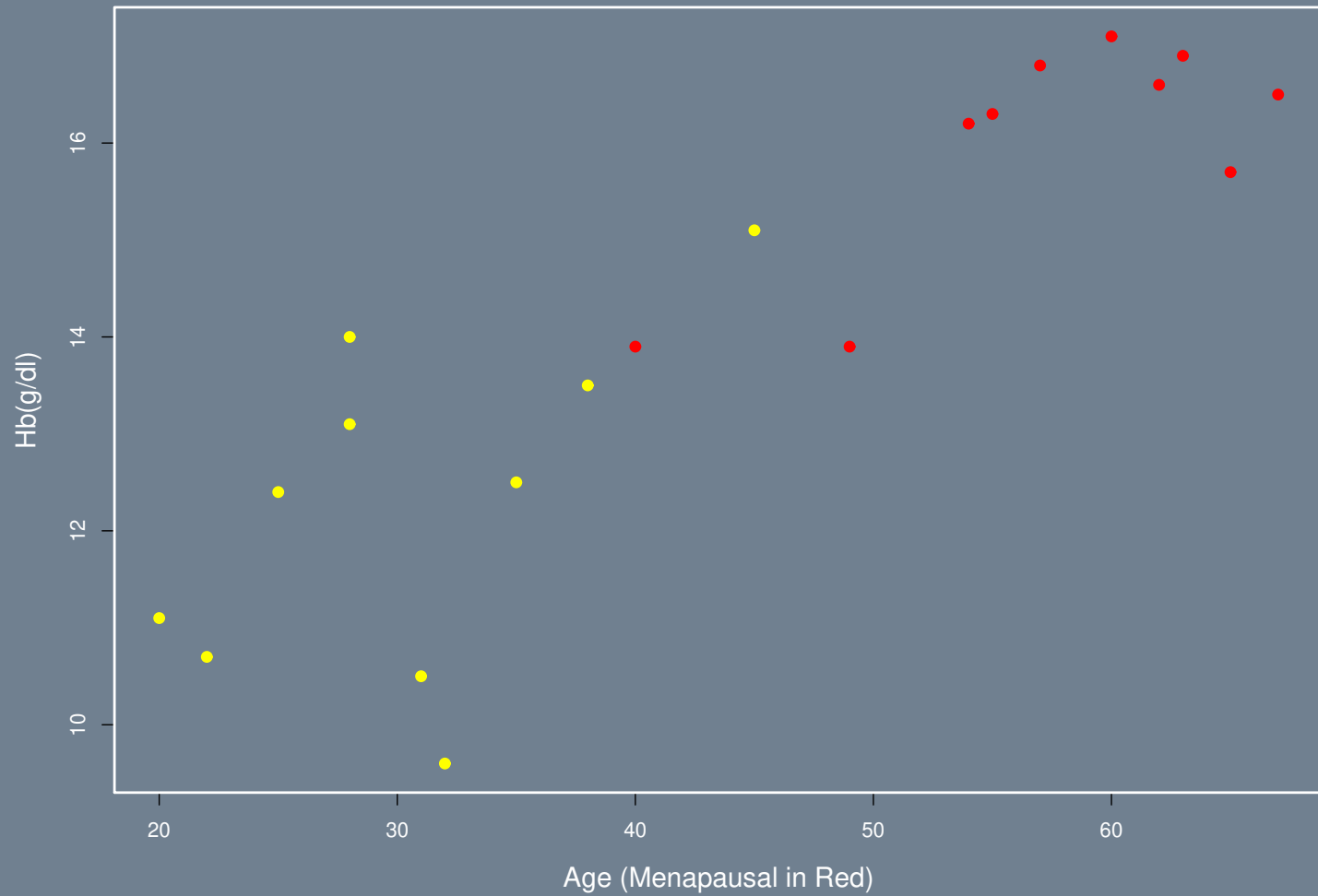
Example: Anaemia

- ▶ Consider again the study of anaemia in women in a given clinic where 20 cases are chosen at random from the full study to get the data here.
- ▶ From a blood sample we get:
 - ▷ haemoglobin level (Hb) in grams per deciliter (12–15 g/dl is normal in adult females)
 - ▷ packed cell volume (PCV) in percent of blood volume that is occupied by red blood cells (also called hematocrit, Ht or HCT, or erythrocyte volume fraction, EVF). 38% to 46% is normal in adult females.
- ▶ We also have:
 - ▷ age in years
 - ▷ menopausal (0=no, 1=yes)
- ▶ There is an obvious endogeneity problem in modeling Hb(g/dl) versus PCV(%).

Anaemia Data

Subject	Hb(g/dl)	PCV(%)	Age	Menopausal
1	11.1	35	20	0
2	10.7	45	22	0
3	12.4	47	25	0
4	14.0	50	28	0
5	13.1	31	28	0
6	10.5	30	31	0
7	9.6	25	32	0
8	12.5	33	35	0
9	13.5	35	38	0
10	13.9	40	40	1
11	15.1	45	45	0
12	13.9	47	49	1
13	16.2	49	54	1
14	16.3	42	55	1
15	16.8	40	57	1
16	17.1	50	60	1
17	16.6	46	62	1
18	16.9	55	63	1
19	15.7	42	65	1
20	16.5	46	67	1

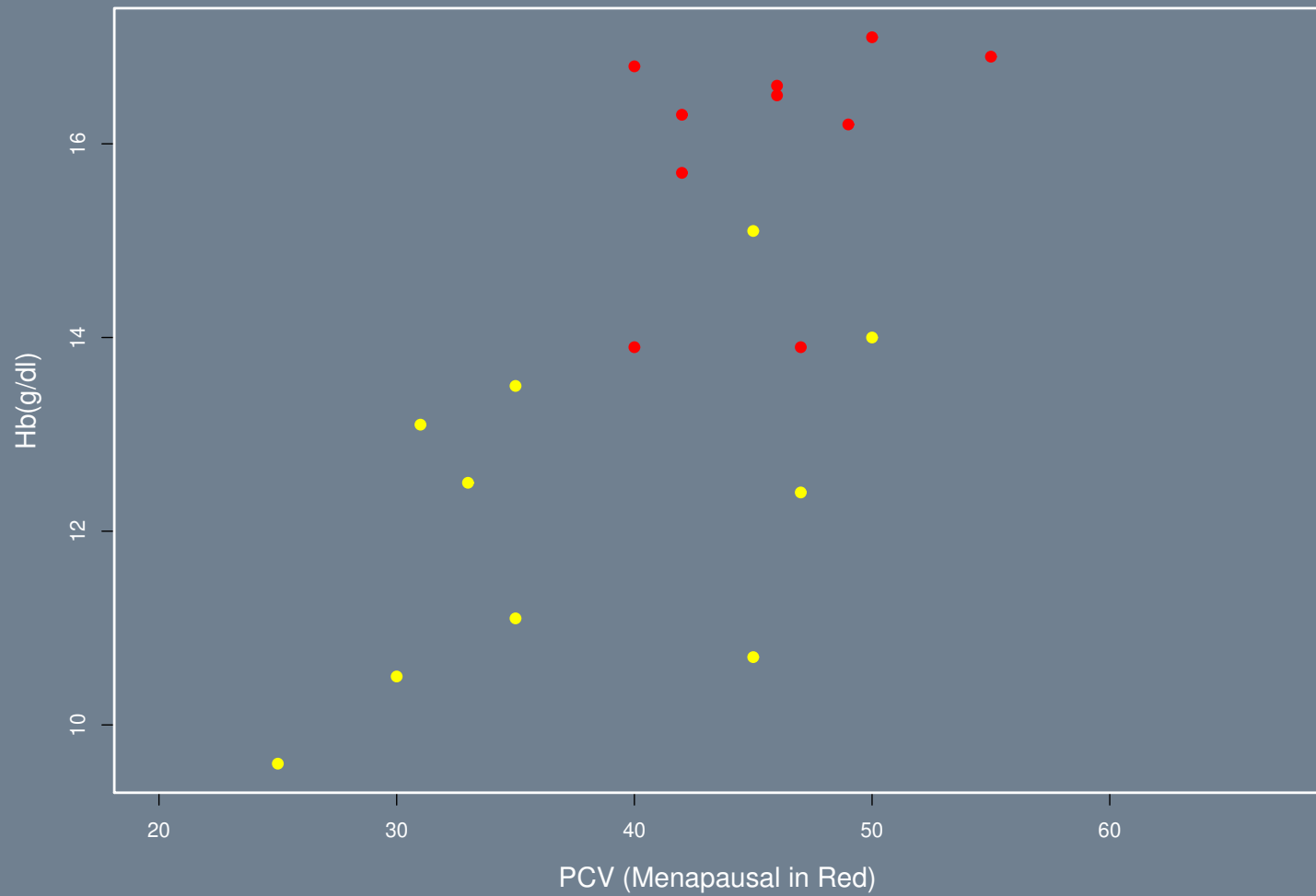
Scatterplot of the Anaemia Data



Scatterplot of the Anaemia Data

```
postscript("Class.PreMed.Stats/Images/anaemia1.fig.ps")
par(mfrow=c(1,1),mar=c(5,5,2,2),lwd=2,col.axis="white",col.lab="white",
    col.sub="white", col="white",bg="slategray", cex.lab=1.3)
plot(anaemia$Age[anaemia$Menopause==0],anaemia$Hb[anaemia$Menopause==0],
     pch=19,col="yellow",
     xlim=range(anaemia$Age),ylim=range(anaemia$Hb),
     xlab="Age (Menapausal in Red)",ylab="Hb(g/dl)")
points(anaemia$Age[anaemia$Menopause==1],anaemia$Hb[anaemia$Menopause==1],
       pch=19,col="red")
dev.off()
```

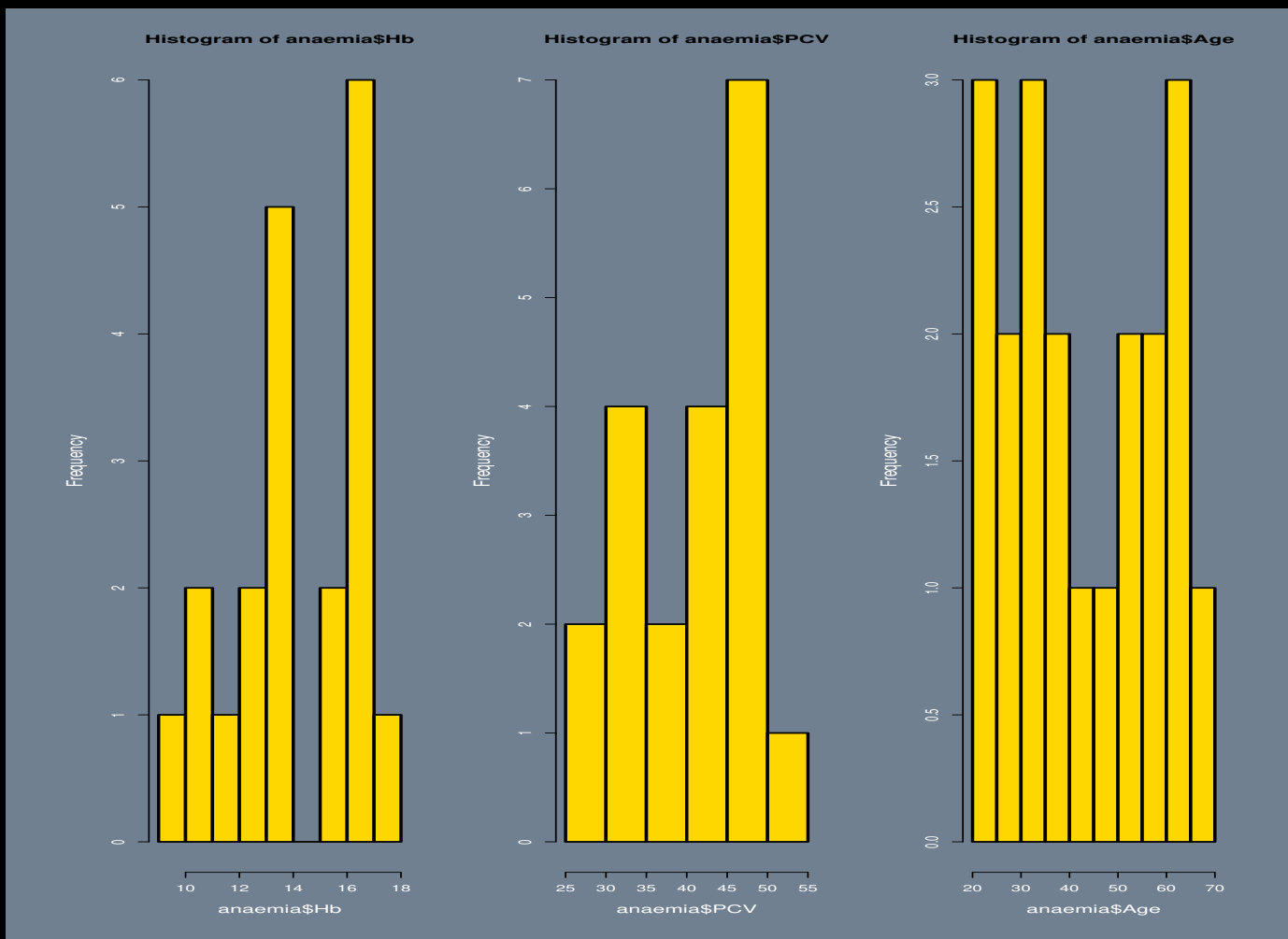
Scatterplot of the Anaemia Data



Scatterplot of the Anaemia Data

```
postscript("Class.PreMed.Stats/Images/anaemia2.fig.ps")
par(mfrow=c(1,1),mar=c(5,5,2,2),lwd=2,col.axis="white",col.lab="white",
    col.sub="white",col="white",bg="slategray", cex.lab=1.3)
plot(anaemia$PCV[anaemia$Menapause==0],anaemia$Hb[anaemia$Menapause==0],
     pch=19,col="yellow",
     xlim=range(anaemia$Age),ylim=range(anaemia$Hb),
     xlab="PCV (Menapausal in Red)",ylab="Hb(g/dl)")
points(anaemia$PCV[anaemia$Menapause==1],anaemia$Hb[anaemia$Menapause==1],
       pch=19,col="red")
dev.off()
```

Distribution of the Anaemia Data?



Logistic Regression: Anaemia Example

```
summary( glm(Menapause~Age, data=anaemia, family=binomial(link=logit)) )
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-1.45227	-0.13139	-0.00176	0.09818	1.63990

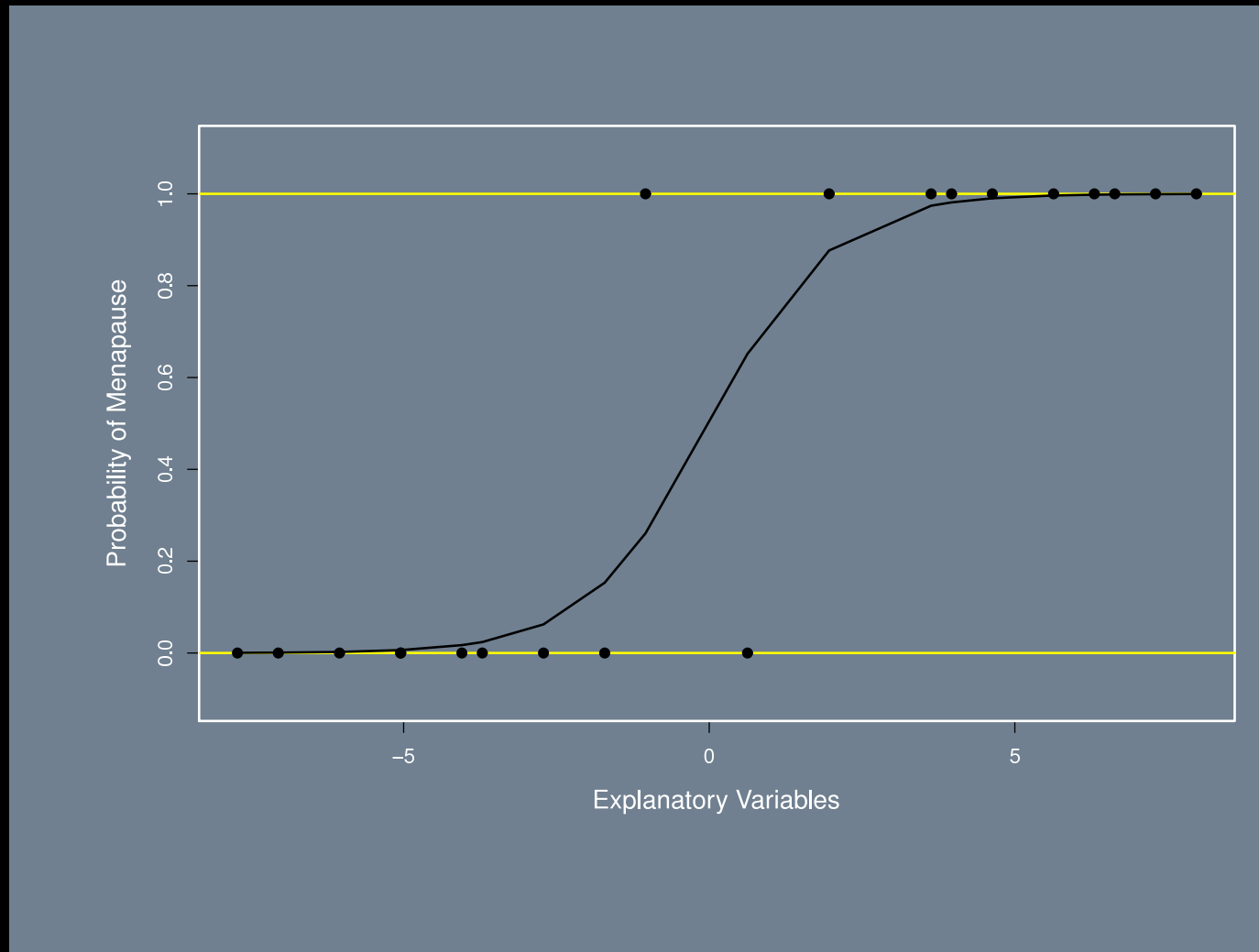
Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-14.395	7.462	-1.93	0.054
Age	0.334	0.174	1.92	0.055

Null deviance: 27.7259 on 19 degrees of freedom

Residual deviance: 5.7632 on 18 degrees of freedom

Logistic Illustration



Logistic Illustration

```
inv.logit <- function(mu)  log(mu/(1-mu))
logit <- function(Xb)  1/(1+exp(-Xb))
ana.logit <- glm(Menopause ~ Age, data=anaemia, family=binomial(link=logit))
postscript("Class.PreMed.Stats/Images/logit.anaemia1.fig.ps")
par(mfrow=c(1,1),mar=c(5,5,2,2),lwd=2,col.axis="white",col.lab="white",
     col.sub="white",col="white",bg="slategray",
     cex.lab=1.3,oma=c(4,2,2,2))
xbeta <- as.matrix(cbind(rep(1,length=nrow(anaemia)),anaemia$Age))
      %*% coef(ana.logit)
plot(range(xbeta),c(-0.1,1.1),type="n",xlab="Explanatory Variables",
     ylab="Probability of Menopause")
abline(h=c(0,1),col="yellow")
x <- seq(from=min(xbeta),to=max(xbeta),length=100)
points(xbeta,anaemia$Menopause,col="black",pch=19)
lines(xbeta,logit(xbeta),col="black")
dev.off()
```

Logit Model for Survey Responses in Scotland

- ▶ These data come from the British General Election Study, Scottish Election Survey, 1997 (ICPSR Study Number 2617).
- ▶ These data contain 880 valid cases, each from an interview with a Scottish national after the election.
- ▶ Our outcome variable of interest is their party choice in the UK general election for Parliament where we collapse all non-Conservative party choices (abstention, Labour, Liberal Democrat, Scottish National, Plaid Cymru, Green, Other, Referendum) to one category, which produces 104 Conservative votes.
- ▶ For probit, $\sigma^2 = 1$ to establish the scale and provide an intuitive (standard) probit metric.

Logit Model for Survey Responses in Scotland, Explanatory Variables

- ▶ **POLITICS**, which asks how much interest the respondent has in political events (increasing scale: none at all, not very much, some, quite a lot, a great deal).
- ▶ **READPAP**, which asks about daily morning reading of the newspapers (yes=1 or no=0).
- ▶ **PTYTHNK**, how strong that party affiliation is for the respondent (categorical by party name).
- ▶ **IDSTRNG** (increasing scale: not very strong, fairly strong, very strong).
- ▶ **TAXLESS** asks if “it would be better if everyone paid less tax and had to pay more towards their own healthcare, schools and the like” (measured on a five point increasing Likert scale).
- ▶ **DEATHPEN** asks whether the UK should bring back the death penalty ((measured on a five point increasing Likert scale).
- ▶ **LORDS** queries whether the House of Lords should be reformed (asked as *remain as is* coded as zero and *change is needed* coded as one).
- ▶ **SCENGBEN** asks how economic benefits are distributed between England and Scotland with the choices: England benefits more = -1 , neither/both lose = 0 , Scotland benefits more = 1 .

Logit Model for Survey Responses in Scotland, Explanatory Variables

- ▶ **INDPAR** asks which of the following represents the respondent's view on the role of the Scottish government in light of the new parliament: (1) Scotland should become independent, separate from the UK and the European Union, (2) Scotland should become independent, separate from the UK but part of the European Union, (3) Scotland should remain part of the UK, with its own elected parliament which has some taxation powers, (4) Scotland should remain part of the UK, with its own elected parliament which has no taxation powers, and (5) Scotland should remain part of the UK without an elected parliament.
- ▶ **SCOTREF1** asks "should there be a Scottish parliament within the UK? (yes=1, no=0).
- ▶ **RSEX**, the respondent's sex.
- ▶ **RAGE**, the respondent's age.
- ▶ **RSOCCLA2**, the respondents social class (7 category ascending scale).
- ▶ **TENURE1**, whether the respondent rents (0) or owns (1) their household.
- ▶ **PRESB** is a categorical variable for church affiliation, measurement of religion is collapsed down to one for the dominant historical religion of Scotland (Church of Scotland/Presbyterian) and zero otherwise and designated

Logit Model for Survey Responses in Scotland

- ▶ Run a probit model for the conservative/not-conservative outcome with these covariates:
- ▶ Results give across two slides...

```
scot.mat <- read.table("http://jeffgill.org/data/scotland.dat",sep=",",header=TRUE)
Y        <- as.numeric(scot.mat[,1])
X        <- as.matrix(scot.mat[,2:ncol(scot.mat)])
glm.out  <- glm(Y ~ X, family=binomial(link=probit))
```

Logit Model for Survey Responses in Scotland, Results (not in order)

```
summary(glm.out)
```

Call:

```
glm(formula = Y ~ X[, -1], family = binomial(link = probit))
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-2.223	-0.287	-0.120	-0.022	3.598

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 639.38 on 879 degrees of freedom
Residual deviance: 338.98 on 864 degrees of freedom
AIC: 371

Number of Fisher Scoring iterations: 8

Logit Model for Survey Responses in Scotland, Results (not in order)

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-0.8032	0.5655	-1.42	0.1555
X[, -1]POLITICS	0.1999	0.0777	2.57	0.0101
X[, -1]READPAP	0.2626	0.1840	1.43	0.1536
X[, -1]PTYTHNK	-0.5765	0.0928	-6.21	5.3e-10
X[, -1]IDSTRNG	0.2114	0.0775	2.73	0.0064
X[, -1]TAXLESS	0.1059	0.0736	1.44	0.1501
X[, -1]DEATHPEN	0.0817	0.0578	1.41	0.1573
X[, -1]LORDS	-0.4267	0.1597	-2.67	0.0075
X[, -1]SCENGBEN	0.3279	0.1107	2.96	0.0031
X[, -1]SCOPREF1	-0.9728	0.1889	-5.15	2.6e-07
X[, -1]RSEX	0.3785	0.1712	2.21	0.0270
X[, -1]RAGE	0.0118	0.0043	2.74	0.0062
X[, -1]RSOCCLA2	-0.1218	0.0582	-2.09	0.0363
X[, -1]TENURE1	0.4634	0.1808	2.56	0.0104
X[, -1]PRESB	-0.1417	0.1675	-0.85	0.3975
X[, -1]IND.PAR	0.2500	0.1925	1.30	0.1940

Percent Predicted Correctly

```
scot.pred <- scot.out$fitted.values
scot.pred[scot.pred < 0.5] <- 0
scot.pred[scot.pred > 0.5] <- 1
table(scot.pred,scot.mat$VOTE)
```

```
scot.pred    0    1
           0 750  50
           1  26  54
```

```
sum(diag(table(scot.pred,scot.mat$VOTE)))/nrow(scot.mat)
[1] 0.91364
```

Percent Predicted Correctly

```
mean(scot.pred)
[1] 0.09091
scot.pred <- scot.out$fitted.values
scot.pred[scot.pred < mean(scot.pred)] <- 0
scot.pred[scot.pred > mean(scot.pred)] <- 1
table(scot.pred,scot.mat$VOTE)

scot.pred    0    1
           0 663  11
           1 113  93

sum(diag(table(scot.pred,scot.mat$VOTE)))/nrow(scot.mat)
[1] 0.85909
```

Tolerance Distribution (related to IRT)

- ▶ A student taking a test has aptitude $T \sim N(\mu, \sigma^2)$, which we would like to measure.
- ▶ A particular question has difficulty d_i , and the student will get it right if $d_i < T$.
- ▶ Consider d_i to be fixed, so that the probability that the student gets the question *wrong* is:

$$p_i = p(T \leq d_i) = \Phi \left(\frac{d_i - \mu}{\sigma} \right),$$

and from rearranging:

$$\begin{aligned} \Phi(p_i) &= \frac{d_i - \mu}{\sigma} \\ &= -\mu/\sigma + d_i/\sigma \\ &= \beta_0 + \beta_1 d_i \end{aligned}$$

meaning that this is really a probit regression model with a *tolerance distribution* for T .

- ▶ Not much more here except that this shows the connection between a normal assumption and probit regression.

Tabular Analysis of Binary Outcomes

- ▶ Binary outcomes are often called *events*, meaning they either happened or didn't.
- ▶ Usually these are labeled 0 and 1, where the one denotes “happened.”
- ▶ Sometimes the 1 is called a “success.”
- ▶ These are only labels and switching the assignment never changes the construction or reliability of the statistical model.
- ▶ Tables of events have a very specific construction:

2×2 Contingency Table

<i>Outcome</i>	<i>Experimental-Manipulation</i>		Row Total
	Treatment	Control	
Positive	a	b	$a + b$
Negative	c	d	$c + d$
Column Total	$a + c$	$b + d$	

- ▶ Hypothesized relationships are usually down the primary diagonal of the table.

Odds and Odds Ratios

- **Odds** of an event is the ratio of the probability of an event *happening* to the probability of the event *not happening*:

$$\text{Odds} = \frac{p}{1-p},$$

where p is the probability of the event.

- **Odds Ratio** compares the odds of an event under treatment to odds under control:

$$OR = \frac{\left(\frac{p_T}{1-p_T}\right)}{\left(\frac{p_C}{1-p_C}\right)} = \frac{\frac{\frac{a}{a+c}}{1-\frac{a}{a+c}}}{\frac{\frac{b}{b+d}}{1-\frac{b}{b+d}}} = \frac{\frac{\frac{a}{a+c}}{\frac{a+c-a}{a+c}}}{\frac{\frac{b}{b+d}}{\frac{b+d-b}{b+d}}} = \frac{\left(\frac{a}{c}\right)}{\left(\frac{b}{d}\right)} = \frac{ad}{bc}.$$

- For rare events, the odds and probability are close since $a \ll c$, so $a/c \approx a/(a+c)$, and the OR is close to the RR ($RR \approx \frac{p_T}{p_C}$).
- Nicely, the OR for failure is just the inverse of the OR for success (symmetry).

Interpreting Odds

- Some people prefer to think in terms of *odds* rather than probability:

$$o = \frac{p}{1-p} = \frac{p(y=1)}{p(y=0)} \qquad p = \frac{o}{1+o}$$

where o is obviously on the support $(0 : \infty)$.

- This is essentially how logit works since:

$$\log(\text{odds}) = \log\left(\frac{p}{1-p}\right) = \beta_0 + \beta_1 x_1 + \beta_2 x_2.$$

- So if x_2 is held constant, then a one-unit change in x_1 gives a β_1 change in the log-odds of success (or a $\exp(\beta_1)$ change in the odds).
- Relatedly, if p_1 is the probability of success under condition 1 and p_2 is the probability of success under condition 2, then the **relative risk** is simply:

$$RR = \frac{p_1}{p_2}$$

Example: Cohort Study of Adolescents

- ▶ A random sample of size 2437, asking about cannabis and psychotic symptoms up to 4 years later(!).
- ▶ Summary table (Henquet, et al. 2005):

Cannabis Use and Psychosis			
	<i>Cannabis</i>	<i>No Cannabis</i>	Total
Event	82	342	424
No Event	238	1775	2013
Total	320	2117	2437

- ▶ Thus the odds ratio for psychosis is:

$$OR = \frac{ad}{bc} = \frac{82 \times 1775}{342 \times 238} = 1.79.$$

- ▶ Since psychosis is a relatively rare event, this close to the relative risk:

$$RR = \frac{p_T}{p_C} = \frac{\left(\frac{82}{320}\right)}{\left(\frac{342}{2117}\right)} = 1.59.$$

Interpreting Odds, Respiratory Disease

- Respiratory Disease in < 1 year-olds:

```
library(MASS); data(babyfood)
xtabs(disease/(disease+nondisease)~sex+food,babyfood)
```

	Bottle	Breast	Suppl
Boy	0.168122	0.095142	0.129252
Girl	0.125000	0.066810	0.125984

```
mdl <- glm(cbind(disease,nondisease) ~ sex + food, family=binomial,babyfood)
summary(mdl)
```

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-1.613	0.112	-14.35	< 2e-16
sexGirl	-0.313	0.141	-2.22	0.027
foodBreast	-0.669	0.153	-4.37	1.2e-05
foodSuppl	-0.173	0.206	-0.84	0.401

Null deviance: 26.37529 on 5 degrees of freedom

Residual deviance: 0.72192 on 2 degrees of freedom

Interpreting Odds, Respiratory Disease

- ▶ The interaction model is the saturated model for these data since $k - 1$ degrees of freedom gets consumed by 1 sex and 2 food categories.
- ▶ A deviance (not Wald) test for each of the main effects relative to the full is done with:

```
drop1 mdl, test="Chi")
```

Single term deletions

Model:

```
cbind(disease, nondisease) ~ sex + food
```

	Df	Deviance	AIC	LRT	Pr(Chi)
<none>		0.7	40.2		
sex	1	5.7	43.2	5.0	0.026
food	2	20.9	56.4	20.2	4.2e-05

where the LRTs show strong evidence for inclusion.

Interpreting Odds, Respiratory Disease

► Coefficient interpretations:

- ▷ **foodBreast -0.669**, so $\exp(-0.669) = 0.51222$, meaning that breast feeding reduces the odds of respiratory disease to 51% of bottle only feeding (the reference).
- ▷ Computing a confidence interval on the log-odds scale (better coverage properties for categorical variables):

```
exp(c(-0.669-1.96*0.153,-0.669+1.96*0.153))
0.37951 0.69134
```

or:

```
library(MASS); exp(confint mdl))
Waiting for profiling to be done...
              2.5 %   97.5 %
(Intercept) 0.15920 0.24743
sexGirl      0.55362 0.96292
foodBreast   0.37819 0.68952
foodSuppl    0.55554 1.24643
```

Overdispersion in Dichotomous Choice Models

- ▶ If we meet the described assumptions, then the two times the residual (summed) deviance is approximately χ^2 with $n - p$ degrees of freedom.
- ▶ However, sometimes we are in the tail of this distribution not because we have chosen the wrong explanatory variables, but because of:
 - ▷ outliers,
 - ▷ sparse data,
 - ▷ overdispersion: $\text{Var}(Y) \gg mp(1 - p)$, where m is the size of the binomial trial group (often denoted n_i when there are differences).
- ▶ Underdispersion is rare.
- ▶ Typical causes of overdispersion:
 - ▷ variation in p across binomial trials (violates iid assumption),
 - ▷ unmeasured clustering in the data,
 - ▷ dependence between trials (which can come from clustering).
- ▶ One diagnostic: plot $\hat{\mu}$ versus $(y - \hat{\mu})^2$.

Overdispersion in Dichotomous Choice Models

- ▶ In regular models $\sigma^2 = \phi = 1$, and **R** even reminds us of this assumption.
- ▶ A test for $\phi > 1$ can be constructed by modifying the Pearson statistic according to:

$$\hat{\sigma}^2 = X^2/(n - k) = \frac{1}{n - k} \sum_{i=1}^n \frac{(y_i - n_i \hat{p}_i)^2}{n_i \hat{p}_i (1 - \hat{p}_i)}.$$

- ▶ Then the variance of the coefficient variance is adjusted with:

$$\widehat{\text{Var}}\hat{\boldsymbol{\beta}} = \hat{\sigma}^2(\mathbf{X}'\mathbf{W}\mathbf{X})^{-1},$$

where $\mathbf{W} = \text{diag}(mp(1 - p))$ (the coefficient estimate is still unbiased).

- ▶ This added uncertainty replaces the chi-square model comparison with an approximate F-test:

$$F \approx \frac{D_{small} - D_{large}}{\widehat{\text{Var}}\hat{\boldsymbol{\beta}}(df_{small} - df_{large})}.$$

Overdispersion Example: boxes of trout eggs buried in 5 places

```
data(troutegg)
ftable(xtabs(cbind(survive,total) ~ location+period, troutegg))
```

		survive	total
location	period		
1	4	89	94
	7	94	98
	8	77	86
	11	141	155
2	4	106	108
	7	91	106
	8	87	96
	11	104	122
3	4	119	123
	7	100	130
	8	88	119
	11	91	125
4	4	104	104
	7	80	97
	8	67	99
	11	111	132
5	4	49	93
	7	11	113
	8	18	88
	11	0	138

Overdispersion Example: boxes of trout eggs buried in 5 places

```
bmod <- glm(cbind(survive,total-survive) ~ location+period, family=binomial,troutegg)
bmod
```

Coefficients:

(Intercept)	location2	location3	location4	location5	period7	period8
4.636	-0.417	-1.242	-0.951	-4.614	-2.170	-2.326
period11						
-2.450						

Degrees of Freedom: 19 Total (i.e. Null); 12 Residual

Null Deviance: 1020

Residual Deviance: 64.5 AIC: 157

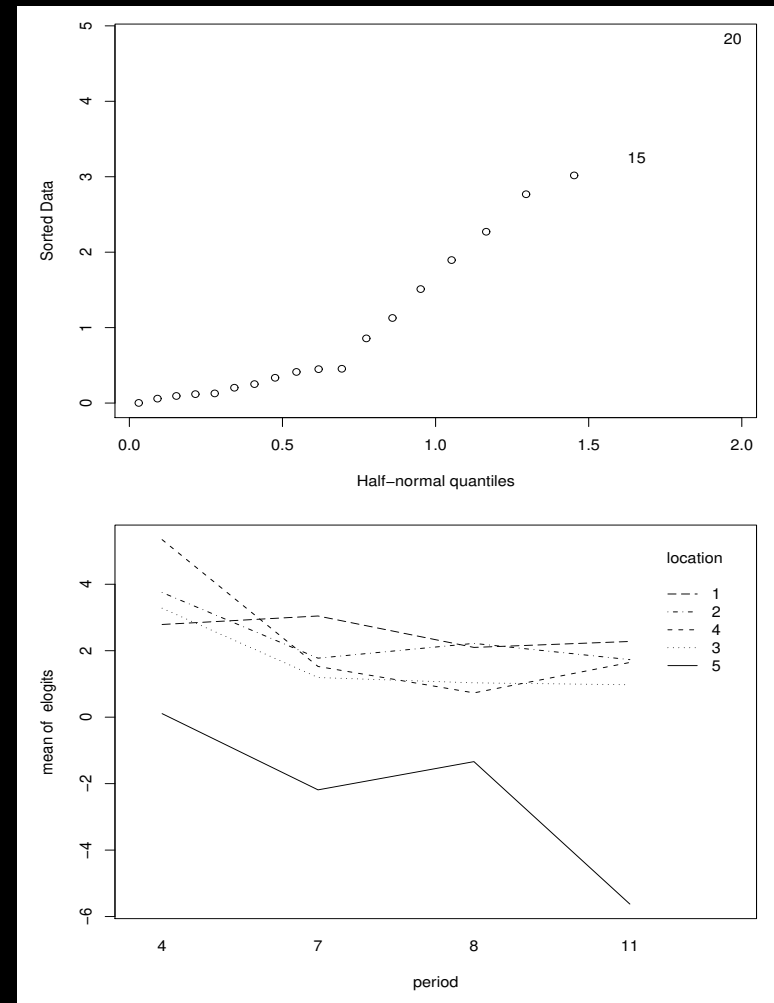
► Since 64.5 is way into the tail of a χ^2_{12} distribution, we know to be worried.

Overdispersion Example: boxes of trout eggs buried in 5 places

- Sparseness? No, `min(troutegg$total)` returns 86.
- Outliers? No, `halfnorm(residuals(bmod))` shows no problems.
- Specification error? No, an interaction plot of the *empirical logits* ($\log(y + 0.5) - \log(m - y + 0.5)$) shows no major relationships.

```
e logits <- log((troutegg$survive+0.5)/
(troutegg$total-troutegg$survive+0.5))
```

```
with(troutegg, interaction.plot(period,
location, e logits))
```



Overdispersion Example: boxes of trout eggs buried in 5 places

- Estimating $\hat{\sigma}^2$ shows it to be much larger than 1:

```
(sigma2 <- sum(residuals(bmod,type="pearson")^2)/12)
5.3303
```

- Now do an F-test of the predictors using the new $\hat{\sigma}^2$:

```
drop1(bmod,test="Chi")
Single term deletions
scale: 5.3303
```

	Df	Deviance	AIC	F value	Pr(F)
<none>		64	157		
location	4	914	308	39.5	8.1e-07
period	3	229	182	10.2	0.0013

Overdispersion Example: boxes of trout eggs buried in 5 places

- And summarize the new results using the new value of $\hat{\sigma}^2$:

```
summary(bmod,dispersion=sigma2)
```

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	4.636	0.649	7.14	9.5e-13
location2	-0.417	0.568	-0.73	0.463
location3	-1.242	0.507	-2.45	0.014
location4	-0.951	0.528	-1.80	0.072
location5	-4.614	0.578	-7.99	1.4e-15
period7	-2.170	0.550	-3.94	8.1e-05
period8	-2.326	0.561	-4.15	3.4e-05
period11	-2.450	0.540	-4.53	5.8e-06

(Dispersion parameter for binomial family taken to be 5.3303)

The Poisson PMF

- probability mass function:

$$f(Y|\mu) = \frac{(\mu)^Y e^{-\mu}}{Y!}, \quad y = 0, 1, 2, \dots, \mu > 0$$

where μ is the intensity parameter.

- This is the probability that exactly Y arrivals occur.
- The chapter uses Faraway's Galapagos Island data:

```
data(gala)
head(gala)
```

	Species	Endemics	Area	Elevation	Nearest	Scruz	Adjacent
Baltra	58	23	25.09	346	0.6	0.6	1.84
Bartolome	31	21	1.24	109	0.6	26.3	572.33
Caldwell	3	3	0.21	114	2.8	58.7	0.78
Champion	25	9	0.10	46	1.9	47.4	0.18
Coamano	2	1	0.05	77	1.9	1.9	903.82
Daphne.Major	18	11	0.34	119	8.0	8.0	1.84

Poisson Assumptions

- ▶ **Infinitesimal Interval.** The probability of an arrival in the interval: $(t : \delta t)$ equals $\mu \delta t + o(\delta t)$ where μ is the intensity parameter discussed above and $o(\delta t)$ is a time interval with the property: $\lim_{\delta t \rightarrow 0} \frac{o(\delta t)}{\delta t} = 0$. In other words, as the interval δt reduces in size towards zero, $o(\delta t)$ is negligible compared to δt . This assumption is required to establish that μ adequately describes the intensity or expectation of arrivals. Typically there is no problem meeting this assumption provided that the time measure is adequately granular with respect to arrival rates.
- ▶ **Non-Simultaneity of Events.** The probability of more than one arrival in the interval: $(t : \delta t)$ equals $o(\delta t)$. Since $o(\delta t)$ is negligible with respect to $\mu \delta t$ for sufficiently small $\mu \delta t$, the probability of simultaneous arrivals approaches zero in the limit.
- ▶ **I.I.D. Arrivals.** The number of arrivals in any two consecutive or non-consecutive intervals are independent and identically distributed. More specifically, $P(Y = y) \in (T_j : T_{j+1})$ does not depend on $P(Y = y) \in (T_k : T_{k+1})$ for any $j \neq k$.

Poisson Features

- ▶ The intensity parameter (μ) is both the mean and variance for a single Poisson distributed random variable.
- ▶ The intensity parameter is tied to a time interval, and rescaling time rescales the intensity parameter.
- ▶ Sums of independent Poisson random variables are themselves Poisson.
- ▶ We can also specifically model time by including it in the intensity parameter: $\mu^* = \mu t$.

Relationships to Other Forms

- ▶ Poisson assumption is that there is no upper limit; if there is one use a binomial PMF.
- ▶ If $\mu = np$ as $n \rightarrow \infty$, then the Poisson is a good approximation for the binomial.
- ▶ If n is small, then $\text{logit}(p) \approx \log(p)$, so the logit model is close to the Poisson model.
- ▶ If counts are bins, then use the multinomial PMF (Chapter 5).

Derivation of MLE

► PMF:

$$p(Y = y|\mu) = \frac{e^{-\mu}\mu^y}{y!}$$

► Likelihood function:

$$L(\mu|\mathbf{y}) = \prod_{i=1}^n \frac{e^{-\mu}\mu^{y_i}}{y_i!}$$

► Log-likelihood function:

$$\ell(\mu|\mathbf{y}) = -n\mu + \log(\mu) \sum_{i=1}^n y_i - \sum_{i=1}^n \log(y_i!)$$

► MLE:

$$\frac{d}{d\mu}\ell(\mu|\mathbf{y}) = -n + \frac{1}{\mu} \sum_{i=1}^n y_i \equiv 0 \Rightarrow n\mu = \sum_{i=1}^n y_i \Rightarrow \hat{\mu} = \bar{y}$$

Derivation of the Variance

- Second derivative of the LL:

$$\frac{d^2}{d\mu^2}\ell(\mu|\mathbf{y}) = \frac{d}{d\mu} \left(-n + \frac{1}{\mu} \sum_{i=1}^n y_i \right) = -\mu^{-2} \sum_{i=1}^n y_i,$$

called the Hessian.

- Fisher Information:

$$FI = -E_{\mu} \left[\frac{d^2}{d\mu^2}\ell(\mu|\mathbf{y}) \right] = -E_{\mu} \left[-\mu^{-2} \sum_{i=1}^n y_i \right] = n\bar{y}E_{\mu} [\mu^{-2}] = \frac{n}{\bar{y}}$$

since $E\mu = \bar{y}$.

- Variance:

$$\text{Var}[\mu] = (FI)^{-1} = \bar{y}/n.$$

Link Function for Poisson Regression

► Definition:

$$\log(\mu_i) = \eta_i \Rightarrow \mu_i = \exp(\eta_i) = \exp(\mathbf{X}_i \boldsymbol{\beta})$$

► Start with the substitution:

$$L(\boldsymbol{\beta}|\mathbf{y}) = \prod_{i=1}^n \frac{e^{-\mu} \mu^{y_i}}{y_i!} \Big|_{\mu_i = \exp(\mathbf{X}_i \boldsymbol{\beta})} = \prod_{i=1}^n e^{-\exp(\mathbf{X}_i \boldsymbol{\beta})} \exp(\mathbf{X}_i \boldsymbol{\beta})^{y_i} / y_i!$$

► Take the log:

$$\ell(\boldsymbol{\beta}|\mathbf{y}) = \sum_{i=1}^n [-\exp(\mathbf{X}_i \boldsymbol{\beta}) + y_i(\mathbf{X}_i \boldsymbol{\beta}) - \log(y_i!)]$$

► Now take the first derivative:

$$\frac{d}{d\boldsymbol{\beta}} \ell(\boldsymbol{\beta}|\mathbf{y}) = \sum_{i=1}^n [\exp(\mathbf{X}_i \boldsymbol{\beta}) \mathbf{X}_j + \mathbf{y}_i \mathbf{X}_j], \quad \forall j$$

► Or in full matrix terms: $\mathbf{X}'\mathbf{y} = \mathbf{X}'\hat{\boldsymbol{\mu}}$, where $\hat{\boldsymbol{\mu}} = \mathbf{X}\hat{\boldsymbol{\beta}}$ (the normal equation for the Poisson model).

► Problem: there does not exist a closed form solution for $\hat{\boldsymbol{\beta}}$, so we use numerical methods.

Application: Poisson Model of Military Coups.

- ▶ Sub-Saharan Africa has experienced a disproportionately high proportion of regime changes due to the military takeover of government for a variety of reasons, including ethnic fragmentation, arbitrary borders, economic problems, outside intervention, and poorly developed governmental institutions.
- ▶ These data, selected from a larger set given by Bratton and Van De Walle (1994), look at potential causal factors for counts of military coups (ranging from 0 to 6 events) in 33 sub-Saharan countries over the period from each country's colonial independence to 1989.
- ▶ Seven explanatory variables are chosen here to model the count of military coups: **Military Oligarchy** (the number of years of this type of rule); **Political Liberalization** (0 for no observable civil rights for political expression, 1 for limited, and 2 for extensive); **Parties** (number of legally registered political parties); **Percent Legislative Voting**; **Percent Registered Voting**; **Size** (in one thousand square kilometer units); and **Population** (given in millions).

Application: Poisson Model of Military Coups.

- ▶ A generalized linear model for these data with the Poisson link function is specified as:

$$g^{-1}(\boldsymbol{\theta}) = g^{-1}(\mathbf{X}\boldsymbol{\beta}) = \exp[\mathbf{X}\boldsymbol{\beta}] = \mathbb{E}[\mathbf{Y}] = \mathbb{E}[\mathbf{Military\ Coups}].$$

- ▶ In this specification, the systematic component is $\mathbf{X}\boldsymbol{\beta}$, the stochastic component is $\mathbf{Y} = \mathbf{Military\ Coups}$, and the link function is $\boldsymbol{\theta} = \log(\mathbf{M})$.
- ▶ We can re-express this model by moving the link function to the left-hand side exposing the linear predictor: $g(\mathbf{M}) = \log(\mathbb{E}[\mathbf{Y}]) = \mathbf{X}\boldsymbol{\beta}$ (although this is now a less intuitive form for understanding the outcome variable).
- ▶ The R language GLM call for this model is:

```
africa.out <- glm(MILTCOUP ~ MILITARY+POLLIB+PARTY93+PCTVOTE+PCTTURN
                  +SIZE*POP+NUMREGIM*NUMLEC, family=poisson).
```

- ▶ The new part is `family=poisson`, where poisson is not capitalized.

Application: Poisson Model of Military Coups.

	Parameter Estimate	Standard Error	95% Confidence Interval
(Intercept)	2.9209	1.3368	[0.3008: 5.5410]
Military Oligarchy	0.1709	0.0509	[0.0711: 0.2706]
Political Liberalization	-0.4654	0.3319	[-1.1160: 0.1851]
Parties	0.0248	0.0109	[0.0035: 0.0460]
Percent Legislative Voting	0.0613	0.0218	[0.0187: 0.1040]
Percent Registered Voting	-0.0361	0.0137	[-0.0629:-0.0093]
Size	-0.0018	0.0007	[-0.0033:-0.0004]
Population	-0.1188	0.0397	[-0.1965:-0.0411]
Regimes	-0.8662	0.4571	[-1.7621: 0.0298]
Elections	-0.4859	0.2118	[-0.9010:-0.0709]
(Size)(Population)	0.0001	0.0001	[0.0001: 0.0002]
(Regimes)(Elections)	0.1810	0.0689	[0.0459: 0.3161]

Application: Poisson Model of Military Coups.

- ▶ Note that the two interaction terms are specified by using the multiplication character. The iteratively weighted least squares algorithm converged in only four iterations using Fisher scoring, and the results are provided in the table.
- ▶ The model appears to fit the data quite well:
 - ▷ an improvement from the null deviance of 62 on 32 degrees of freedom to a residual deviance of 7.5 on 21 degrees of freedom
 - ▷ evidence that the model does not fit would be supplied by a model deviance value in the tail of a χ^2_{n-k} distribution
 - ▷ and nearly all the coefficients have 95% confidence intervals bounded away from zero and therefore appear reliable in the model.

Back to Residuals and Model Fit

- ▶ General Deviance Notation: $D = \sum_{i=1}^n d(\boldsymbol{\eta}, y_i)$, where the individual deviance function is defined as: $d(\boldsymbol{\eta}, y_i) = -2 [\ell(\hat{\boldsymbol{\eta}}, \psi|y_i) - \ell(\tilde{\boldsymbol{\eta}}, \psi|y_i)]$, where $\hat{\boldsymbol{\eta}}$ is the model estimate and $\tilde{\boldsymbol{\eta}}$ is the saturated estimate.
- ▶ Linear Model Residual Vector: $\mathbf{R}_{standard} = \mathbf{Y} - \mathbf{X}\boldsymbol{\beta}$.
- ▶ Response Residual Vector: $\mathbf{R}_{Response} = \mathbf{Y} - g^{-1}(\mathbf{X}\boldsymbol{\beta}) = \mathbf{Y} - \hat{\boldsymbol{\mu}}$.
- ▶ Pearson Residual Vector: $\mathbf{R}_{Pearson} = \frac{\mathbf{Y} - \hat{\boldsymbol{\mu}}}{\sqrt{VAR[\boldsymbol{\mu}]}}$ (the sum of the Pearson residuals for a Poisson generalized linear model is the Pearson χ^2 goodness-of-fit measure).
- ▶ Working Residual Vector: $\mathbf{R}_{Working} = (\mathbf{y} - \boldsymbol{\mu}) \frac{\partial}{\partial \boldsymbol{\eta}} \boldsymbol{\mu}$ (from the last step of Iteratively Reweighted Least Squares algorithm).

Deviance for the Poisson Model

- The “G-statistic” (summed deviance) for this model is:

$$D_{\text{Poisson}} = 2 \sum_{i=1}^n (y_i \log(y_i/\hat{\mu}_i) - (y_i - \hat{\mu}_i)) \underset{\text{a}}{\sim} \chi_{n-p}^2,$$

where p is the number of explanatory variables including the constant, and $\hat{\mu}_i$ is the predicted outcome for the i th case.

- Individual Deviance Function:

$$R_{\text{Deviance}} = \frac{(y_i - \hat{\mu}_i)}{|y_i - \hat{\mu}_i|} \sqrt{|d(\boldsymbol{\eta}, y_i)|} \quad \text{where:} \quad d(\boldsymbol{\eta}, y_i) = -2 [\ell(\hat{\boldsymbol{\eta}}, \psi|y_i) - \ell(\tilde{\boldsymbol{\eta}}, \psi|y_i)].$$

- Recall also the Pearson’s statistic:

$$X^2 = \sum_{i=1}^n \frac{(y_i - \hat{\mu}_i)^2}{\hat{\mu}_i} \underset{\text{a}}{\sim} \chi_{n-p}^2.$$

- Generally the summed deviance is more robust.

Deviance Summary (again)

Table 1: DEVIANCE FUNCTIONS

Distribution	Canonical Parameter	Deviance Function
Poisson($\hat{\mu}$)	$\eta = \log(\hat{\mu})$	$2 \sum \left[y_i \log \left(\frac{y_i}{\hat{\mu}_i} \right) - y_i + \hat{\mu}_i \right]$
Binomial(m, p)	$\eta = \log \left(\frac{\hat{\mu}}{1 - \hat{\mu}} \right)$	$2 \sum \left[y_i \log \left(\frac{y_i}{\hat{\mu}_i} \right) + (m_i - y_i) \log \left(\frac{m_i - y_i}{m_i - \hat{\mu}_i} \right) \right]$
Normal($\hat{\mu}, \sigma$)	$\eta = \hat{\mu}$	$\sum [y_i - \hat{\mu}_i]^2$
Gamma($\hat{\mu}, \delta$)	$\eta = -\frac{1}{\hat{\mu}}$	$2 \sum \left[-\log \left(\frac{y_i}{\hat{\mu}_i} \right) \frac{y_i - \hat{\mu}_i}{\hat{\mu}_i} \right]$
Negative Binom($\hat{\mu}, p$)	$\eta = \log(1 - \hat{\mu})$	$2 \sum \left[y_i \log \left(\frac{y_i}{\hat{\mu}_i} \right) + (1 + y_i) \log \left(\frac{1 + \hat{\mu}_i}{1 + y_i} \right) \right]$

Poisson GLM of Capital Punishment Data

The model is developed from the Poisson link function, $\boldsymbol{\eta} = \log(\boldsymbol{\mu})$, with the objective of finding the best $\boldsymbol{\beta}$ vector in:

$$\begin{aligned}
 \underbrace{g^{-1}(\boldsymbol{\eta})}_{17 \times 1} &= g^{-1}(\mathbf{X}\boldsymbol{\beta}) \\
 &= \exp[\mathbf{X}\boldsymbol{\beta}] \\
 &= \exp[\mathbf{1}\beta_0 + \mathbf{INC}\beta_1 + \mathbf{POV}\beta_2 + \mathbf{BLK}\beta_3 + \mathbf{CRI}\beta_4 + \mathbf{SOU}\beta_5 + \mathbf{DEG}\beta_6] \\
 &= \mathbb{E}[\mathbf{Y}] = \mathbb{E}[\mathbf{EXE}].
 \end{aligned}$$

```

dp.97 <- read.table("http://jeffgill.org/files/jeffgill/files/cpunish.dat_.txt",header=
PROPDEGREE <- matrix(apply(dp.97[,12:14],1,sum)/apply(dp.97[8:14],1,sum),
                      nrow(dp.97),1,dimnames=list(dimnames(dp.97)[[1]],"PROPDEGREE"))
dp.97 <- cbind(dp.97,PROPDEGREE)
dp.out <- glm(EXECUTIONS ~ INCOME + PERPOVERTY + PERBLACK + log(VC100k96) + SOUTH
              + PROPDEGREE, family=poisson, data=dp.97)

```


Poisson GLM of Capital Punishment Data, 1997

State	Executions	Median Income	Percent Poverty	Percent Black	Violent Crime/100K	South	Proportion w/Degrees
Texas	37	34453	16.7	12.2	644	1	0.16
Virginia	9	41534	12.5	20.0	351	1	0.27
Missouri	6	35802	10.6	11.2	591	0	0.21
Arkansas	4	26954	18.4	16.1	524	1	0.16
Alabama	3	31468	14.8	25.9	565	1	0.19
Arizona	2	32552	18.8	3.5	632	0	0.25
Illinois	2	40873	11.6	15.3	886	0	0.25
South Carolina	2	34861	13.1	30.1	997	1	0.21
Colorado	1	42562	9.4	4.3	405	0	0.31
Florida	1	31900	14.3	15.4	1051	1	0.24
Indiana	1	37421	8.2	8.2	537	0	0.19
Kentucky	1	33305	16.4	7.2	321	0	0.16
Louisiana	1	32108	18.4	32.1	929	1	0.18
Maryland	1	45844	9.3	27.4	931	0	0.29
Nebraska	1	34743	10.0	4.0	435	0	0.24
Oklahoma	1	29709	15.2	7.7	597	0	0.21
Oregon	1	36777	11.7	1.8	463	0	0.25
	EXE	INC	POV	BLK	CRI	SOU	DEG

Source: United States Census Bureau, United States Department of Justice.

Poisson GLM of Capital Punishment Data

Table 2: MODELING CAPITAL PUNISHMENT IN THE UNITED STATES: 1997

	Coefficient	Standard Error	95% Confidence Interval
(Intercept)	-6.30665	4.17678	[-14.49299: 1.87969]
Median Income	0.00027	0.00005	[0.00017: 0.00037]
Percent Poverty	0.06897	0.07979	[-0.08741: 0.22534]
Percent Black	-0.09500	0.02284	[-0.13978: -0.05023]
log(Violent Crime)	0.22124	0.44243	[-0.64591: 1.08838]
South	2.30988	0.42875	[1.46955: 3.15022]
Degree Proportion	-19.70241	4.46366	[-28.45102:-10.95380]
Null deviance: 136.573, <i>df</i> = 16			Maximized $\ell()$: -31.7375
Summed deviance: 18.212, <i>df</i> = 11			AIC: 77.475

Poisson GLM of Capital Punishment Data

$$\mathbf{VC} = (-\mathbf{A})^{-1} =$$

Int	INC	POV	BLK	<i>log(CRI)</i>	SOU	DEG
17.445501654	-0.000131052	-0.198325558	0.017689695	-1.484011921	0.368916884	-4.651658695
-0.000131052	0.000000003	0.000001862	0.000000113	0.000004171	-0.000006245	-0.000094858
-0.198325558	0.000001862	0.006365688	0.000158039	0.003911954	-0.017825119	0.121451892
0.017689695	0.000000113	0.000158039	0.000521871	-0.003283494	-0.005090192	-0.033679253
-1.484011921	0.000004171	0.003911954	-0.003283494	0.195742167	-0.001384018	0.397439934
0.368916884	-0.000006245	-0.017825119	-0.005090192	-0.001384018	0.183825030	0.298730196
-4.651658695	-0.000094858	0.121451892	-0.033679253	0.397439934	0.298730196	19.924250374

First Differences for Non-Linear Models

- ▶ We can no longer use “a one unit change in \mathbf{X} gives a β change in Y .”
- ▶ Main idea:
 - ▷ pick one covariate of interest, \mathbf{X}_q
 - ▷ choose 2 levels of this variable, $\mathbf{X}_{1,q}$, $\mathbf{X}_{2,q}$
 - ▷ set all other covariates at their mean, $\bar{\mathbf{X}}_{-q}$
 - ▷ create two predictions by running these values through the link function:

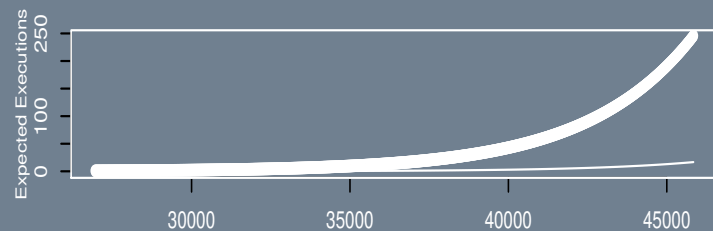
$$\hat{Y}_1 = g^{-1}(\bar{\mathbf{X}}_{-q}\hat{\boldsymbol{\beta}}_{-q} + \mathbf{X}_{1,q}\hat{\boldsymbol{\beta}}_q)$$

$$\hat{Y}_2 = g^{-1}(\bar{\mathbf{X}}_{-q}\hat{\boldsymbol{\beta}}_{-q} + \mathbf{X}_{2,q}\hat{\boldsymbol{\beta}}_q)$$

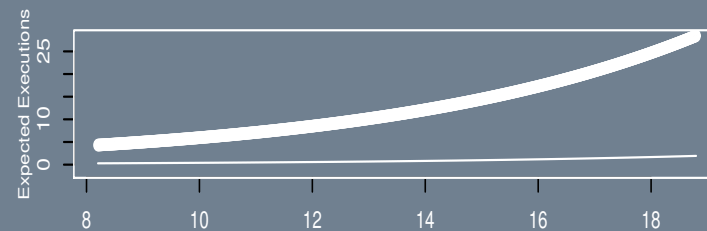
- ▷ Look at $\hat{Y}_1 - \hat{Y}_2$.

- ▶ For example:

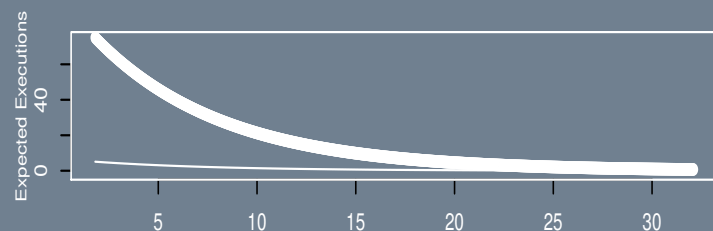
```
dp.1 <- dp.2 <- c(1,apply(dp.97[,c(3,4,5,6,7,15)],2,mean))
dp.1[6] <- 0; dp.2[6] <- 1
y.1 <- exp(dp.1 %*% dp.out$coef); y.2 <- exp(dp.2 %*% dp.out$coef)
y.2 - y.1
```



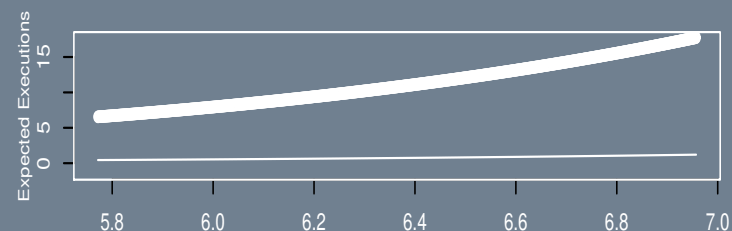
Levels of INCOME



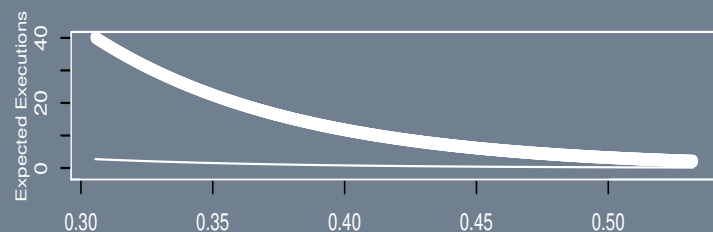
Levels of PERPOVERTY



Levels of PERBLACK



Levels of log(VC100k96)



Levels of PROPDEGREE

— South State
— Non-South State

Poisson GLM of Capital Punishment, First Difference Code

```
X <- cbind(rep(1,nrow(dp.97)), as.matrix(dp.97[,3:5]), as.matrix(log(dp.97[,6])),
          as.matrix(dp.97[,7]), as.matrix(dp.97[,15]))
X.0 <- cbind(X[,1:5],rep(0,length=nrow(X)),X[,7])
dimnames(X.0)[[2]] <- names(dp.out$coefficients)
X.1 <- cbind(X[,1:5],rep(1,length=nrow(X)),X[,7])
dimnames(X.1)[[2]] <- names(dp.out$coefficients)

postscript("/Users/jgill/Class.MLE/glm.fig2.ps")
par(mfrow=c(3,2),mar=c(4,3,2,2),oma=c(3,1,1,1),col.axis="white",col.lab="white",
    col.sub="white",col="white",bg="slategray")
```

Poisson GLM of Capital Punishment, First Difference Code

```

for (i in 2:(ncol(X.0)-1)) {
  if (i==6) i <- i+1
  ruler <- seq(min(X.0[,i]),max(X.0[,i]),length=1000)
  xbeta0 <- exp(dp.out$coefficients[-i]%*%apply(X.0[, -i], 2, mean)
              + dp.out$coefficients[i]*ruler)
  xbeta1 <- exp(dp.out$coefficients[-i]%*%apply(X.1[, -i], 2, mean)
              + dp.out$coefficients[i]*ruler)
  plot(ruler,xbeta0,type="l",xlab="",ylab="",
       ylim=c(min(xbeta0,xbeta1)-2,max(xbeta0,xbeta1)))
  lines(ruler,xbeta1,type="b")
  mtext(outer=F,side=1,paste("Levels of",dimnames(X.0)[[2]][i]),cex=0.8,line=3)
  mtext(outer=F,side=2,"Expected Executions",cex=0.6,line=2)
}
plot(ruler[100:200],rep(ruler[400],101),bty="n",xaxt="n",yaxt="n",xlab="",ylab="",
     type="l",xlim=range(ruler),ylim=range(ruler))
lines(ruler[100:200],rep(ruler[600],101),type="b")
text(ruler[445],ruler[400],"Non-South State",cex=1.4)
text(ruler[390],ruler[700],"South State",cex=1.4)
dev.off()

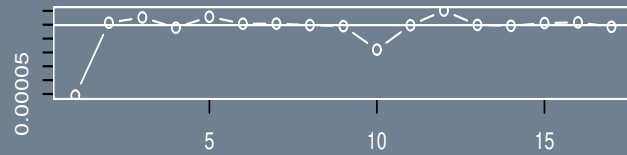
```

Poisson GLM of Capital Punishment, Continued

Table 3: RESIDUALS FROM POISSON MODEL OF CAPITAL PUNISHMENT

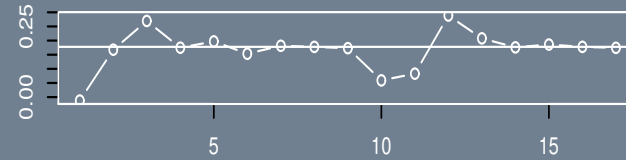
	Response	Pearson	Working	Deviance	Anscombe
Texas	1.70755431	0.28741478	0.04837752	0.28515874	0.28292493
Virginia	0.87407687	0.30671010	0.10762321	0.30136452	0.29629097
Missouri	4.59530299	3.86395636	3.24898061	2.86925916	2.27854829
Arkansas	0.26481208	0.13694108	0.07081505	0.13544624	0.13391171
Alabama	0.95958171	0.67097152	0.46916278	0.62736060	0.58874967
Arizona	0.95395198	0.93375106	0.91397549	0.82741022	0.74425671
Illinois	0.13924315	0.10197129	0.07467388	0.10084230	0.09963912
South Carolina	-0.38227185	-0.24752186	-0.16027167	-0.25478237	-0.26235519
Colorado	-0.95901329	-0.68428704	-0.48826435	-0.75706323	-0.84845827
Florida	-1.82216650	-1.08543456	-0.64657649	-1.25272634	-1.49557143
Indiana	-2.17726883	-1.21566195	-0.67880001	-1.42915840	-1.74185735
Kentucky	-2.31839936	-1.26926054	-0.69489994	-1.49593905	-1.83715998
Louisiana	-1.60160305	-0.99359914	-0.61640776	-1.13620002	-1.33738726
Maryland	0.10161119	0.10709684	0.11287657	0.10527242	0.10341466
Nebraska	0.07022962	0.07261924	0.07506941	0.07194451	0.07107841
Oklahoma	0.49917358	0.70406163	0.99304011	0.62019695	0.55401828
Oregon	-0.90510552	-0.65451282	-0.47330769	-0.72189767	-0.80517526

INCOME



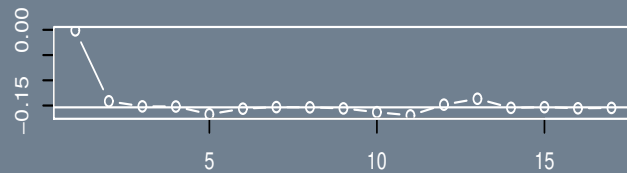
Index Number

PERPOVERTY



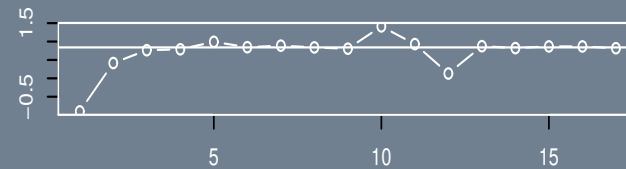
Index Number

PERBLACK



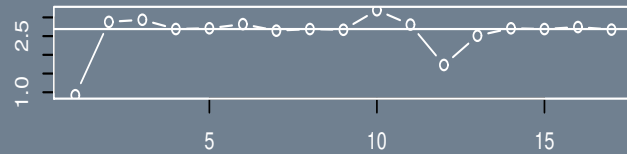
Index Number

log(VC100k96)



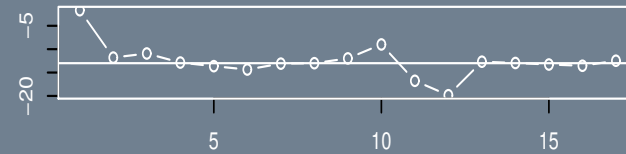
Index Number

SOUTH



Index Number

PROPDEGREE



Index Number

New and Old Ways to Look at Model Fit

- Approximation to Pearson's Statistic.

$$X^2 = \sum_{i=1}^n \mathbf{R}_{Pearson}^2 = \sum_{i=1}^n \left[\frac{\mathbf{Y} - \boldsymbol{\mu}}{\sqrt{VAR[\boldsymbol{\mu}]}} \right]^2.$$

- If the sample size is sufficiently large, then $\frac{X^2}{a(\psi)} \sim \chi_{n-p}^2$ where n is the sample size, p is the number of explanatory variables including the constant, and $a(\psi)$ is the scale function that we'll see in Chapter 6.
- For the summed deviance with sufficient sample size it is also true that $D(\boldsymbol{\eta}, \mathbf{y})/a(\psi) \sim \chi_{n-p}^2$.
- Recall that it is also common to contrast this with the *null deviance*: the deviance function calculated for a model with no covariates (mean function only).

New and Old Ways to Look at Model Fit

- Akaike Information Criterion.

minimizes the negative likelihood penalized by the number of parameters:

$$\text{AIC} = -2\ell(\hat{\boldsymbol{\beta}}|\mathbf{y}) + 2p$$

where $\ell(\hat{\boldsymbol{\beta}}|\mathbf{y})$ is the maximized model log likelihood value and p is the number of explanatory variables in the model (including the constant). (AIC has a bias towards models that overfit with extra parameters since the penalty component is obviously linear with increases in the number of explanatory variables, and the log likelihood often increases more rapidly.)

- Schwartz Criterion/Bayesian Information Criterion (BIC).

$$\text{BIC} = -2\ell(\hat{\boldsymbol{\beta}}|\mathbf{y}) + p\log(n)$$

where n is the sample size.

- There is also a Deviance Information Criterion (DIC) used in Bayesian MCMC estimation.

Congressional Cosponsoring of Bills

- Fowler (2006) looks at patterns of sponsorship and cosponsorship in Congress from 1973 to 2004.

```
cosponsor <- read.table("http://jeffgill.org/files/jeffgill/files/fowler.dat_.txt",
summary(cosponsor)
```

Congress	Period	Total.Sponsors	Total.Bills	Mean.Bills.Per.Leg
100th: 2	1974: 2	Min. : 99.0	Min. : 4188	Min. : 15.00
101st: 2	1976: 2	1st Qu.:101.0	1st Qu.: 7278	1st Qu.: 19.00
102nd: 2	1978: 2	Median :267.0	Median : 7849	Median : 44.50
103rd: 2	1980: 2	Mean :268.9	Mean : 8814	Mean : 47.62
104th: 2	1982: 2	3rd Qu.:437.0	3rd Qu.: 8832	3rd Qu.: 75.00
105th: 2	1984: 2	Max. :442.0	Max. :20994	Max. :111.00

Mean.Cos.Per.Leg	Mean.Cos.Per.Bill	Cos.Per.Leg	Mean.Dist	Senate
Min. :121.0	Min. : 2.000	Min. : 49.0	Min. :1.170	Min. :0.0
1st Qu.:174.5	1st Qu.: 3.000	1st Qu.: 70.0	1st Qu.:1.300	1st Qu.:0.0
Median :260.0	Median : 4.000	Median : 80.5	Median :1.545	Median :0.5
Mean :247.5	Mean : 7.969	Mean :101.5	Mean :1.515	Mean :0.5
3rd Qu.:303.8	3rd Qu.:14.250	3rd Qu.:143.2	3rd Qu.:1.673	3rd Qu.:1.0
Max. :376.0	Max. :19.000	Max. :184.0	Max. :1.950	Max. :1.0

Application to Congressional Cosponsoring of Bills

- Look at summary statistics:

```
mean(cosponsor$Mean.Bills.Per.Leg)
```

```
[1] 47.625
```

```
var(cosponsor$Mean.Bills.Per.Leg)
```

```
[1] 828.24
```

```
mean(cosponsor$Mean.Cos.Per.Leg)
```

```
[1] 247.5
```

```
var(cosponsor$Mean.Cos.Per.Leg)
```

```
[1] 6134.7
```

- This is clear evidence of *overdispersion* in the original unconditional count data.
- We are actually more interested in overdispersion in the modeled counts, which are conditional on the form of the model specification including the link function and the collection of covariates.

Over/Under Dispersion

- ▶ For Poisson models the mean and the variance of a single random variable are assumed to be the same.
- ▶ For the likelihood function as a statistic, the variance is scaled by n .
- ▶ Overdispersion, $\text{Var}(Y) > \mathbb{E}(Y)$, is relatively common, whereas underdispersion, $\text{Var}(Y) < \mathbb{E}(Y)$ is rare.
- ▶ Biggest effect is to make the standard errors wrong.
- ▶ One diagnostic: plot $\hat{\mu}$ versus $(y - \hat{\mu})^2$.
- ▶ Solution: make μ a random variable rather than a fixed constant to be estimated, with a gamma distribution: $G[\mu\alpha, \alpha]$. So

$$\mathbb{E}[Y] = \mu \qquad \text{Var}[Y] = \frac{\mu}{\phi}$$

- ▶ This is called the “Poisson-Gamma” model and it means that Y is distributed *negative binomial*.

Negative Binomial

- ▶ Negative binomial distribution has the same sample space (i.e. on the counting measure) as the Poisson, but contains an additional parameter which can be thought of as gamma distributed and therefore used to model a variance function.
- ▶ Used by many to fit a count model with overdispersion.
- ▶ The binomial distribution measures the number of successes in a given number of fixed trials, whereas the negative binomial distribution measures *the number of failures, y before the r^{th} success*.
- ▶ An alternative but equivalent form,

$$f(y|r, p) = \binom{y-1}{r-1} p^r (1-p)^{y-r},$$

measures the number of trials necessary to get r successes.

- ▶ An important application of the negative binomial distribution is in survey research design. If the researcher knows the value of p from previous surveys, then the negative binomial can provide the number of subjects to contact in order to get the desired number of responses for analysis.

Negative Binomial

- The PMF is:

$$f(Y|k, p) = \binom{y-1}{k-1} p^k (1-p)^{y-k}, \quad y = 0, 1, 2, \dots, \quad 0 \leq p \leq 1.$$

- For this parameterization, we get:

$$\mathbb{E}[Y] = \mu, \quad \text{Var}[Y] = \frac{\mu(1 + \phi)}{\phi}.$$

- If ϕ (the dispersion parameter) is unknown, use the estimate:

$$\hat{\phi} = \frac{X^2}{n-p} = \frac{\sum_{i=1}^n \frac{(y_i - \hat{\mu}_i)^2}{\hat{\mu}_i}}{n-p}.$$

- This gives an F-test for comparing models (big values implies a difference in models).

Negative Binomial

- ▶ There are two interpretations:
 - ▷ as a generalized Poisson,
 - ▷ with probability p , modeling the number of trials, Y , before the k th success (alternatively failure) where k is fixed in advance.
- ▶ For estimation, use `library(MASS)`, which has `glm.nb`.
- ▶ Note that there is also:

```
dnbinom(x, size, prob, mu, log = FALSE)
pnbinom(q, size, prob, mu, lower.tail = TRUE, log.p = FALSE)
qnbinom(p, size, prob, mu, lower.tail = TRUE, log.p = FALSE)
rnbinom(n, size, prob, mu)
```

Negative Binomial GLM, Congressional Activity: 1995

- ▶ Compare the number of bills assigned to committee in the first 100 days of the 103rd and 104th Houses as a function of the number of members on the committee, the number of subcommittees, the number of staff assigned to the committee, and a dummy variable indicating whether or not it is a high prestige committee.
- ▶ The model is developed with the link function:

$$\eta = g(\mu) = \log \left(\frac{\mu}{\mu + \frac{1}{k}} \right) \quad \longrightarrow \quad \mu = g^{-1}(\eta) = \frac{\exp(\eta)}{k(1 - \exp(\eta))},$$

where $\eta = \mathbf{X}\boldsymbol{\beta}$, and $k \geq 1$ is the overdispersion term.

Negative Binomial GLM, Bills Assigned to Committed, First 100 Days

Committee	Size	Subcommittees	Staff	Prestige	Bills-103 rd	Bills-104 th
Appropriations	58	13	109	1	9	6
Budget	42	0	39	1	101	23
Rules	13	2	25	1	54	44
Ways and Means	39	5	23	1	542	355
Banking	51	5	61	0	101	125
Economic/Educ. Opportunities	43	5	69	0	158	131
Commerce	49	4	79	0	196	271
International Relations	44	3	68	0	40	63
Government Reform	51	7	99	0	72	149
Judiciary	35	5	56	0	168	253
Agriculture	49	5	46	0	60	81
National Security	55	7	48	0	75	89
Resources	44	5	58	0	98	142
Transport./Infrastructure	61	6	74	0	69	155
Science	50	4	58	0	25	27
Small Business	43	4	29	0	9	8
Veterans Affairs	33	3	36	0	41	28
House Oversight	12	0	24	0	233	68
Standards of Conduct	10	0	9	0	0	1
Intelligence	16	2	24	0	2	4

Model Code

```
committee.dat <- read.table("http://jeffgill.org/files/jeffgill/files/committee.dat_.txt",
                             header=TRUE)

committee.poisson <- glm(BILLS104 ~ SIZE + SUBS * (log(STAFF)) + PRESTIGE +
                        BILLS103, family=poisson, data=committee.dat)
1 - pchisq(summary(committee.poisson)$deviance,
            summary(committee.poisson)$df.residual)
[1] 0    # IN THE TAIL INDICATES OVERDISPERSION

committee.out <- glm.nb(BILLS104 ~ SIZE + SUBS * (log(STAFF)) + PRESTIGE +
                        BILLS103, data=committee.dat)

resp <- resid(committee.out,type="response")
pears <- resid(committee.out,type="pearson")
working <- resid(committee.out,type="working")
devs <- resid(committee.out,type="deviance")
cbind(resp,pears,working,devs)
```

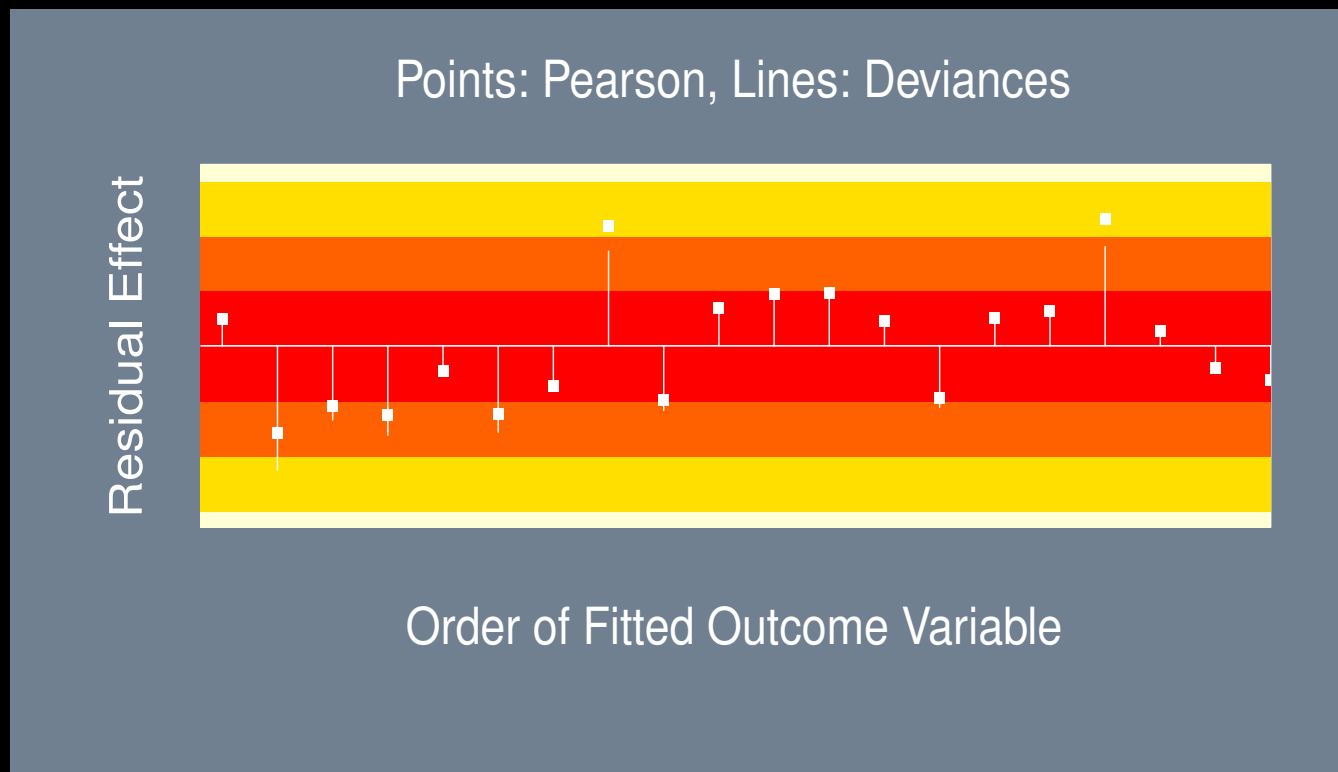
Negative Binomial GLM, Congressional Activity: 1995

	resp	pears	working	devs
Appropriations	-7.38308	-0.99451	-0.55167	-1.22671
Budget	-6.17325	-0.40931	-0.21161	-0.43997
Rules	22.54158	1.98665	1.05048	1.56745
Ways_and_Means	-135.06135	-0.56848	-0.27560	-0.63081
Banking	21.00117	0.40998	0.20194	0.38568
Economic_Educ_Oppor	-93.92104	-0.85695	-0.41757	-1.01572
Commerce	-58.03818	-0.36306	-0.17639	-0.38675
International_Relations	-49.33480	-0.89295	-0.43918	-1.06810
Government_Reform	32.60986	0.57003	0.28018	0.52480
Judiciary	27.80878	0.25343	0.12349	0.24378
Agriculture	24.21181	0.85168	0.42635	0.75680
National_Security	27.14348	0.87911	0.43881	0.77861
Resources	26.13708	0.45893	0.22559	0.42884
TransInfrastructure	79.10378	2.10068	1.04226	1.64133
Science	-34.35454	-1.12146	-0.55993	-1.43001
Small_Business	-12.50419	-1.14887	-0.60984	-1.48074
Veterans_Affairs	-14.18802	-0.66378	-0.33630	-0.75200
House_Oversight	16.14917	0.62009	0.31145	0.56716
Stdsof_Conduct	0.37836	0.44850	0.60864	0.40700
Intelligence	-13.58498	-1.43490	-0.77253	-2.05981

Modeling Bill Assignment – 104th House, Results

	Coefficient	Standard Error	95% Confidence Interval
(Intercept)	-6.80543	2.54651	[-12.30683:-1.30402]
Size	-0.02825	0.02093	[-0.07345: 0.01696]
Subcommittees	1.30159	0.54370	[0.12701: 2.47619]
log(Staff)	3.00971	0.79450	[1.29329: 4.72613]
Prestige	-0.32367	0.44102	[-1.27644: 0.62911]
Bills in 103 rd	0.00656	0.00139	[0.00355: 0.00957]
Subcommittees:log(STAFF)	-0.32364	0.12489	[-0.59345:-0.05384]
Null deviance: 107.314, $df = 19$			Maximized $\ell()$: 10559
Summed deviance: 20.948, $df = 13$			AIC: 121130

Modeling Bill Assignment – 104th House, Residuals Diagnostics



Rate Models

- ▶ Accounts for occurrences, maximum possible events, time.
- ▶ Note that the binomial does not account for repeat events on the same unit.
- ▶ A key problem is that units may differ in size: crime events are higher in bigger cities.
- ▶ Focus on rate:

$$\text{Rate} = \frac{\text{\#events}}{\text{unit}} = \frac{\text{occurrences}}{\text{possibilities}}$$

- ▶ Example from Faraway:
 - ▷ gamma radiation leads to cell abnormalities,
 - ▷ **ca** is the count of chromosomal abnormalities,
 - ▷ **cells** is the number (in hundreds) of exposed cells,
 - ▷ **doseamt** = dose amount,
 - ▷ **doserate** = rate of application.

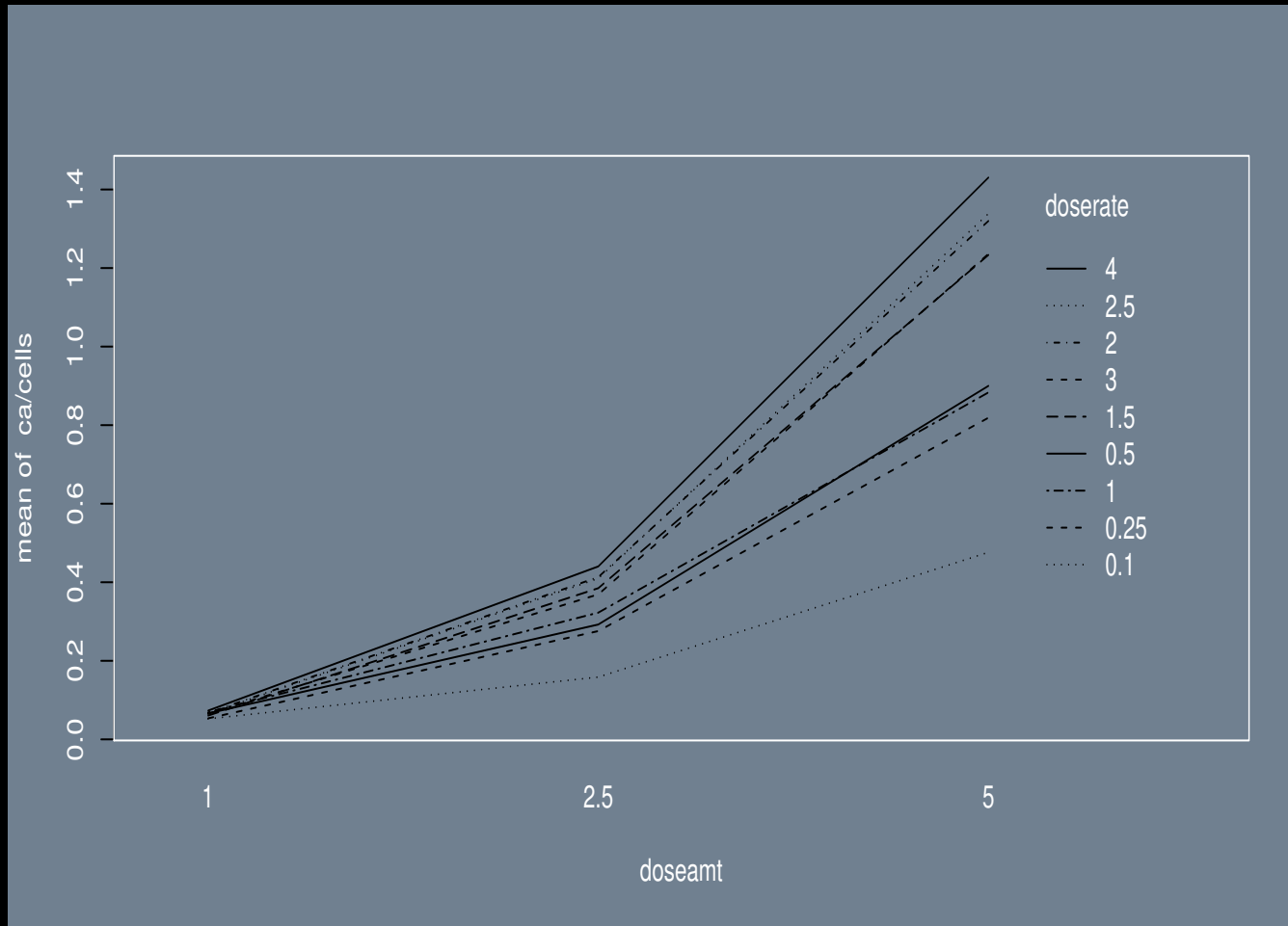
Rate Models

```
library(faraway)
data(dicentric)
round(xtabs(ca/cells ~ doseamt + doserate, dicentric),2)
```

	doserate									
doseamt	0.1	0.25	0.5	1	1.5	2	2.5	3	4	
1	0.05	0.05	0.07	0.07	0.06	0.07	0.07	0.07	0.07	
2.5	0.16	0.28	0.29	0.32	0.38	0.41	0.41	0.37	0.44	
5	0.48	0.82	0.90	0.88	1.23	1.32	1.34	1.24	1.43	

```
postscript("Class.MLE/dicentric.ps")
par(mfrow=c(1,1),col.axis="white",col.lab="white",col.sub="white",col="white",
     bg="slategray")
with(dicentric,interaction.plot(doseamt,doserate,ca/cells))
dev.off()
```

Rate Models



Rate Models

- MODEL 1: Linearly modeling the ratio directly seems to fit well, but there is overdispersion.

```
lmod <- lm(ca/cells ~ log(doserate)*factor(doseamt), dicentric); summary(lmod)
```

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	0.06349	0.01953	3.25	0.0038
log(doserate)	0.00457	0.01669	0.27	0.7868
factor(doseamt)2.5	0.27631	0.02762	10.01	1.9e-09
factor(doseamt)5	1.00412	0.02762	36.36	< 2e-16
log(doserate):factor(doseamt)2.5	0.06393	0.02361	2.71	0.0132
log(doserate):factor(doseamt)5	0.23913	0.02361	10.13	1.5e-09

Residual standard error: 0.0586 on 21 degrees of freedom

Multiple R-squared: 0.987, Adjusted R-squared: 0.984

F-statistic: 330 on 5 and 21 DF, p-value: <2e-16

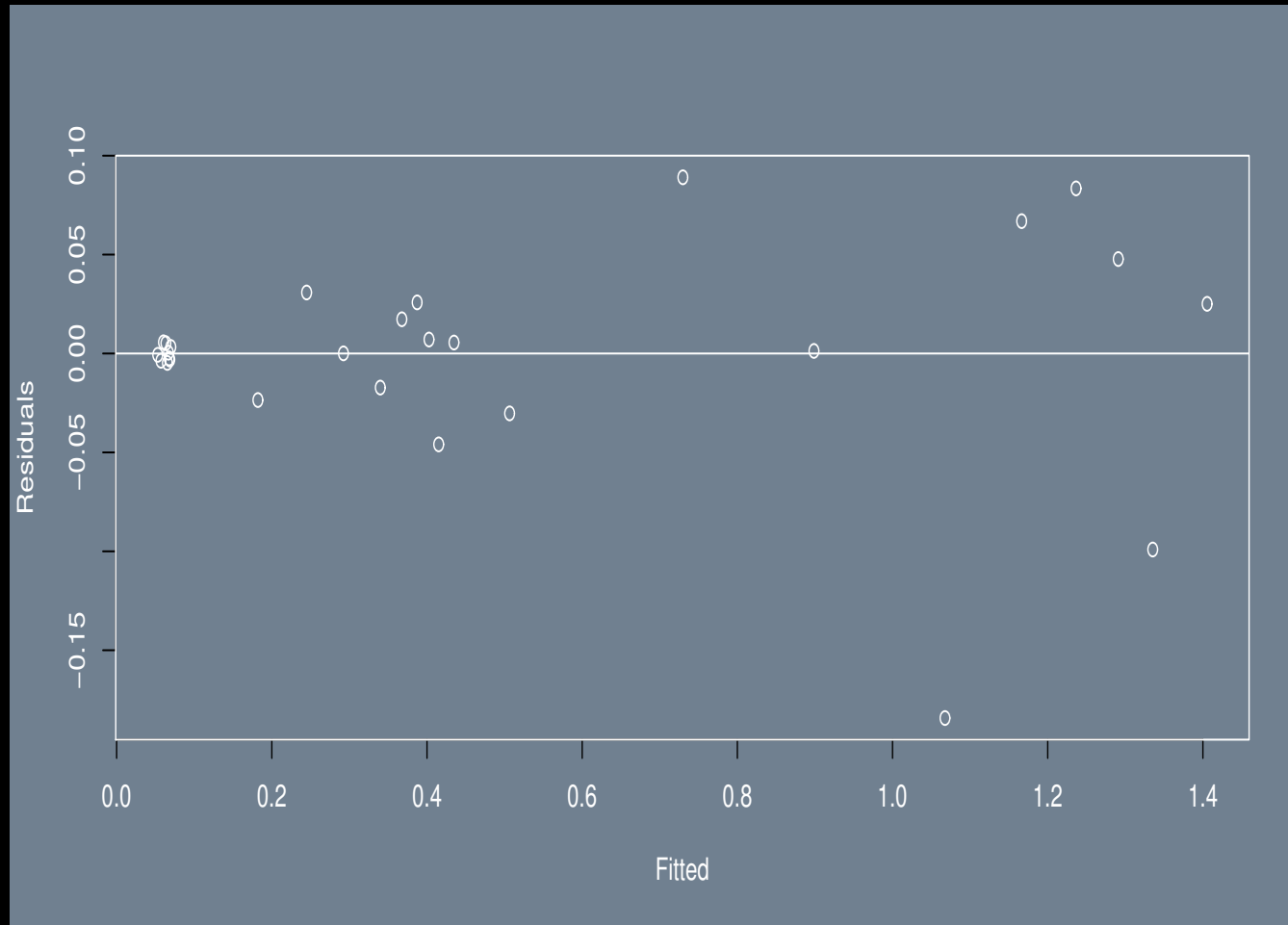
[1]

Rate Models

```
pchisq(sum(lmod$residual), lmod$df.residual)
[1]
```

```
postscript("Class.MLE/rate.diag.ps")
par(mfrow=c(1,1),col.axis="white",col.lab="white",col.sub="white",
     col="white",bg="slategray")
plot(residuals(lmod) ~ fitted(lmod),xlab="Fitted",ylab="Residuals")
abline(h=0)
dev.off()
```

Rate Models



Rate Models

- MODEL 2: Poisson modeling directly the counts, starting with logging the number of cells since it has a multiplicative effect on the outcome, and make `doseamt` a factor:

```
dicentric$dosef <- factor(dicentric$doseamt)
pmod <- glm(ca ~ log(cells)+log(doserate)*dosef,family=poisson,dicentric)
summary(pmod)
```

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-2.7653	0.3812	-7.25	4e-13
log(cells)	1.0025	0.0514	19.52	< 2e-16
log(doserate)	0.0720	0.0355	2.03	0.04240
dosef2.5	1.6298	0.1027	15.87	< 2e-16
dosef5	2.7667	0.1229	22.52	< 2e-16
log(doserate):dosef2.5	0.1611	0.0484	3.33	0.00087
log(doserate):dosef5	0.1932	0.0430	4.49	7e-06

(Dispersion parameter for poisson family taken to be 1)

```
Null deviance: 916.127 on 26 degrees of freedom
Residual deviance: 21.748 on 20 degrees of freedom
AIC: 211.2
```

Using an Offset

- We just modeled these as counts independent of the amount of exposure.
- But the deaths are actually out of a number of cases exposed.
- This is called a rate model in the count literature: events per unit of exposed.
- Thus we want to put exposure on the RHS of the model, being careful about logs:

$$\log \left(\frac{\mathbb{E}[Y|\boldsymbol{\beta}, \mathbf{X}]}{\text{exposure}} \right) = \mathbf{X}\boldsymbol{\beta}$$

$$\log(\mathbb{E}[Y|\boldsymbol{\beta}, \mathbf{X}]) - \log(\text{exposure}) = \mathbf{X}\boldsymbol{\beta}$$

$$\log(\mathbb{E}[Y|\boldsymbol{\beta}, \mathbf{X}]) = \mathbf{X}\boldsymbol{\beta} + \log(\text{exposure})$$

$$\mathbb{E}[Y|\boldsymbol{\beta}, \mathbf{X}] = \exp [\mathbf{X}\boldsymbol{\beta} + \log(\text{exposure})]$$

which justifies putting a log-constant on the RHS to reflect the number exposed in each case.

- In R this is done with the `offset()` specification, for example:

```
glm(Y ~ X1 + X2 + offset(X3), family=poisson, data=swe07)
```

Rate Models

- MODEL 3: make this intuitive like a standard Poisson model:

$$\log\left(\frac{\text{ca}}{\text{cells}}\right) = \mathbf{X}\boldsymbol{\beta} \quad \implies \quad \log(\text{ca}) = \log(\text{cells}) + \mathbf{X}\boldsymbol{\beta}.$$

- Note also the estimate `log(cells) 1.0025` in the previous model, which suggests that this parameter is really just 1, so fix it at one using an offset:

```
rmod <- glm(ca ~ offset(log(cells))+log(doserate)*dosef, family=poisson,dicentric);
```

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-2.7467	0.0343	-80.16	< 2e-16
log(doserate)	0.0718	0.0352	2.04	0.04130
dosef2.5	1.6254	0.0495	32.86	< 2e-16
dosef5	2.7611	0.0435	63.49	< 2e-16
log(doserate):dosef2.5	0.1612	0.0483	3.34	0.00084
log(doserate):dosef5	0.1935	0.0424	4.56	5.1e-06

(Dispersion parameter for poisson family taken to be 1)

```
Null deviance: 4753.00 on 26 degrees of freedom
Residual deviance: 21.75 on 21 degrees of freedom
AIC: 209.2
```


Zero-Inflated Poisson Model

- ▶ Zero-inflated Poisson (ZIP) regression is first introduced Lambert (1992) although the ZIP distribution, without covariates, has been discussed early in literatures (Cohen 1963, Yip 1988).
- ▶ The main advantage of this model is to deal with so called “structural” zeros in modeling count data.
- ▶ The ZIP regression model assumes that zeros are observed with probability π , and the rest of observations come from a $\text{Poisson}(\lambda)$ with probability $1 - \pi$.

Zero-Inflated Poisson Model

► Let Y_1, \dots, Y_N be a sample of size N independently drawn from

$$Y_i \sim \begin{cases} 0 & \text{with probability } \pi_i \\ \text{Poisson}(\lambda_i) & \text{with probability } 1 - \pi_i \end{cases}$$

► So the probability mass function is given by

$$P(Y_i = h) = \begin{cases} \pi_i + (1 - \pi_i)e^{-\lambda_i} & \text{for } h = 0 \\ (1 - \pi_i)e^{-\lambda_i}\lambda_i^h/h! & \text{for } h = 1, 2, \dots \end{cases}$$

Zero-Inflated Poisson Model

- ▶ The regression model with this zero-inflated Poisson distribution now consists of two generalized linear models.
- ▶ The first part is a logistic regression, specified by $\text{logit}(\pi_i) = \mathbf{u}_i^T \boldsymbol{\gamma}$, where the response variable states zero or nonzero status and $\boldsymbol{\gamma}$ is a regression coefficient vector for covariates \mathbf{u}_i^T .
- ▶ The second part is a poisson regression, specified by $\log(\lambda_i) = \mathbf{x}_i^T \boldsymbol{\beta}$, where the response variable is a non-negative count from a $\text{Poisson}(\lambda_i)$ and $\boldsymbol{\beta}$ is a regression coefficient vector for covariates \mathbf{x}_i^T .
- ▶ This separation allows the predictors in each model to perform different roles; for example, what causes exact zeros (no-movement) is different from what causes vigorous activities.

Hurdle Model

- ▶ A similar approach to handle zero-inflated count data is also introduced in Mullahy (1986) referred as a hurdle model.
- ▶ This model utilizes a zero-truncated Poisson distribution:

$$P(Y_i = h | Y_i > 0) = \lambda_i^h / \{(e^{\lambda_i} - 1)h!\}$$

- ▶ The probability mass function in the ZIP model is modified to

$$P(Y_i = h) = \begin{cases} \pi_i & \text{for } h = 0 \\ (1 - \pi_i)\lambda_i^h / \{(e^{\lambda_i} - 1)h!\} & \text{for } h = 1, 2, \dots \end{cases}$$

- ▶ The hurdle model has the advantage of handling both zero-inflated and zero-deflated count data.

Congress and the Supreme Court

► Zorn (1996) observes...

Whether due to institutional deference, agreement with case outcomes, or simple inattention, the typical Supreme Court decision is final: Congress rarely intervenes to modify or overturn the high Court's ruling. As a result, the vast majority of Supreme Court cases are never addressed by the Congress.

► So this is a perfect application for ZIP and hurdle models.

Descriptive Statistics for Dependent and Independent Variables

Variables	Mean	Std. Dev.	Min.	Max.
Number of Actions Taken	0.11	0.64	0	11
ln(Exposure)	2.04	0.55	0	2.30
Year of Decision	1972.4	9.85	1953	1988
Liberal Decision	0.52	0.50	0	1
Lower Court Disagreement	0.23	0.42	0	1
Alteration of Precedent	0.02	0.15	0	1
Declaration of Unconstitutionality	0.08	0.27	0	1
Unanimous Vote	0.34	0.47	0	1

Note: N = 4052. Data are all Supreme Court decisions handed down during the 1953-1987 terms and which fall under the jurisdiction of House and Senate Judiciary committees. See Zorn and Caldeira (1995) and Eskridge (1991) for a fuller description of how the cases were selected and coded for analysis.

Congress and the Supreme Court

- ▶ The vast majority of decisions received no Congressional scrutiny.
- ▶ Of those that did, the total number of such actions ranged from one to eleven, with a mean of 2.6.
- ▶ The data contain significantly more zeros than would be predicted by a Poisson with a mean of 0.11.
- ▶ In nearly 96 percent of all cases analyzed here no Congressional response occurred during the 1979-1988 period.

Frequencies: Numbers of House and Senate Actions Taken in Response to Supreme Court Decisions, 1979-1988

Number of Actions	Frequency	Percentage
0	3882	95.80
1	63	1.55
2	38	0.94
3	32	0.79
4	8	0.20
5	12	0.30
6	12	0.30
7	3	0.07
10	1	0.02
11	1	0.02
Total	4052	100.0

Model Results (Numbers in parentheses are t-ratios)

Variables	Poisson	Negative Binomial
(Constant)	-160.125 (-9.91)	-134.411 (-4.93)
log(Exposure)	0.544 (4.77)	0.178 (0.67)
Year of Decision	0.079 (9.82)	0.067 (4.89)
Liberal Decision	0.296 (3.02)	0.099 (0.45)
Lower Court Disagreement	-0.212 (-1.79)	-0.321 (-1.22)
Alteration of Precedent	-0.254 (-0.67)	-0.102 (-0.13)
Declaration of Unconstitutionality	-1.838 (-4.78)	-1.538 (-2.89)
Unanimous Decision	-0.407 (-3.74)	-0.297 (-1.28)
(σ)	-	32.233 (30.96)
Log-Likelihood	-1636.308	-989.542

Variables	Zero-Inflated Poisson		Hurdle Poisson	
	Prob(Y=0)	E(Y)	Prob(Y>0)	E(Y)
(Constant)	153.580 (6.35)	-8.793 (-0.63)	-153.217 (-5.86)	-9.967 (-0.60)
log(Exposure)	-0.487 (-2.64)	0.089 (0.65)	0.510 (2.76)	0.079 (0.62)
Year of Decision	-0.076 (-6.24)	0.005 (0.68)	0.076 (5.77)	0.005 (0.64)
Liberal Decision	-0.091 (-0.54)	0.190 (2.08)	0.139 (0.87)	0.192 (1.70)
Lower Court Disagreement	0.043 (0.22)	-0.138 (-1.30)	-0.079 (-0.43)	-0.147 (-1.01)
Alteration of Precedent	-0.401 (-0.65)	-0.582 (-1.08)	0.171 (0.34)	-0.601 (-1.11)
Declaration of Unconstitutionality	1.590 (2.42)	-0.421 (-0.69)	-1.696 (-2.88)	-0.367 (-0.78)
Unanimous Decision	0.499 (2.58)	0.098 (0.96)	-0.460 (-2.59)	0.088 (0.70)
Log-Likelihood	-979.483		-671.428	

Gamma Regression

- ▶ The Gamma GLM is used when the support of the outcome variable is $[0:\infty]$.
- ▶ Assume Y is distributed gamma indexed by two parameters: the shape parameter, and the inverse-scale parameter.
- ▶ The gamma distribution is most commonly written in “rate” format:

$$f(y|\alpha, \beta) = \frac{1}{\Gamma(\alpha)} \beta^\alpha y^{\alpha-1} e^{-\beta y}, \quad y, \alpha, \beta > 0.$$

- ▶ R uses as a default the “scale” format:

$$f(y|\alpha, \beta) = \frac{1}{\Gamma(\alpha)} \beta^{-\alpha} y^{\alpha-1} e^{-y/\beta}, \quad y, \alpha, \beta > 0.$$

Gamma Regression

- ▶ The canonical link for the gamma family variable μ , is $\theta = -\frac{1}{\mu}$.
- ▶ So $b(\theta) = \log(\mu) = \log\left(-\frac{1}{\theta}\right)$ with the restriction: $\theta < 0$. Therefore: $b(\theta) = -\log(-\theta)$.
- ▶ The χ^2 distribution is $\text{gamma}(\frac{\rho}{2}, \frac{1}{2})$ for ρ degrees of freedom, and the exponential distribution is $\text{gamma}(1, \beta)$.

Gamma GLM of Electoral Politics in Scotland

- On September 11, 1997 Scottish voters overwhelming (74.3%) approved the establishment of the first Scottish national parliament in nearly three hundred years.
- On the same ballot, the voters gave strong support (63.5%) to granting this parliament taxation powers.
- Data: 32 *Unitary Authorities* (also called council districts), U.K. government sources, includes 40 potential explanatory variables
- Used here: CouncilTax (COU), PerClaimantFemale (PCR), StdMortalityRatio (MOR), Active (ACT), GDP (GDP), Percentage5to15 (PER).

The model for these data using the gamma link function is produced by:

$$\begin{aligned}
 \underbrace{g^{-1}(\boldsymbol{\theta})}_{32 \times 1} &= g^{-1}(\mathbf{X}\boldsymbol{\beta}) \\
 &= -\frac{1}{\mathbf{X}\boldsymbol{\beta}} \\
 &= -[\mathbf{1}\beta_0 + \mathbf{COU}\beta_1 + \mathbf{PCR}\beta_2 + \mathbf{MOR}\beta_3 + \mathbf{ACT}\beta_4 + \mathbf{GDP}\beta_5]^{-1} \\
 &= E[\mathbf{Y}] = E[\mathbf{YES}].
 \end{aligned}$$

The systematic component here is $\mathbf{X}\boldsymbol{\beta}$, the stochastic component is $\mathbf{Y} = \mathbf{YES}$, and the link function is $\boldsymbol{\theta} = -\frac{1}{\mu}$.

Gamma GLM

```
scotland.df <- read.table(  
  "http://jeffgill.org/files/jeffgill/files/scotvote.dat_.txt",  
  header=TRUE)  
  
scottish.vote.glm <- glm((PerYesTax/100) ~ CouncilTax * PerClaimantFemale  
  + StdMortalityRatio + Active + GDP + Percentage5to15,  
  family=Gamma, data=scotland.df)  
  
graph.summary(scottish.vote.glm)
```

Gamma GLM

Family: Gamma

Link function: inverse

	Coef	Std.Err.	0.95 Lower	0.95 Upper	CI's:ZE+R0
(Intercept)	-1.777	1.148	-4.026	0.473	--o--
CouncilTax	0.005	0.002	0.002	0.008	o
PerClaimantFemale	0.203	0.053	0.099	0.308	o
StdMortalityRatio	-0.007	0.003	-0.012	-0.002	o
Active	0.011	0.004	0.003	0.019	o
GDP	0.000	0.000	0.000	0.000	o
Percentage5to15	-0.052	0.024	-0.099	-0.005	o
CouncilTax:PerClaimantFemale	0.000	0.000	0.000	0.000	o

N: 32 log-likelihood: 59.892 AIC: -111.784 Dispersion Parameter: 0.0035842
 Null deviance: 0.536 on 31 degrees of freedom
 Residual deviance: 0.087 on 24 degrees of freedom