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Faraway Chapter 5, Count Data

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The Poisson PMF

- probability mass function:

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

  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 $\mu\delta t + \circ(\delta t)$ where μ is the intensity parameter discussed above and $\circ(\delta t)$ is a time interval with the property: $\lim_{\delta t \to 0} \frac{\circ(\delta t)}{\delta t} = 0$. In other words, as the interval δt reduces in size towards zero, $\circ(\delta t)$ 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 $\circ(\delta t)$. Since $\circ(\delta t)$ 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 $n \to \infty$, 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:

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

Graphical View of the MLE

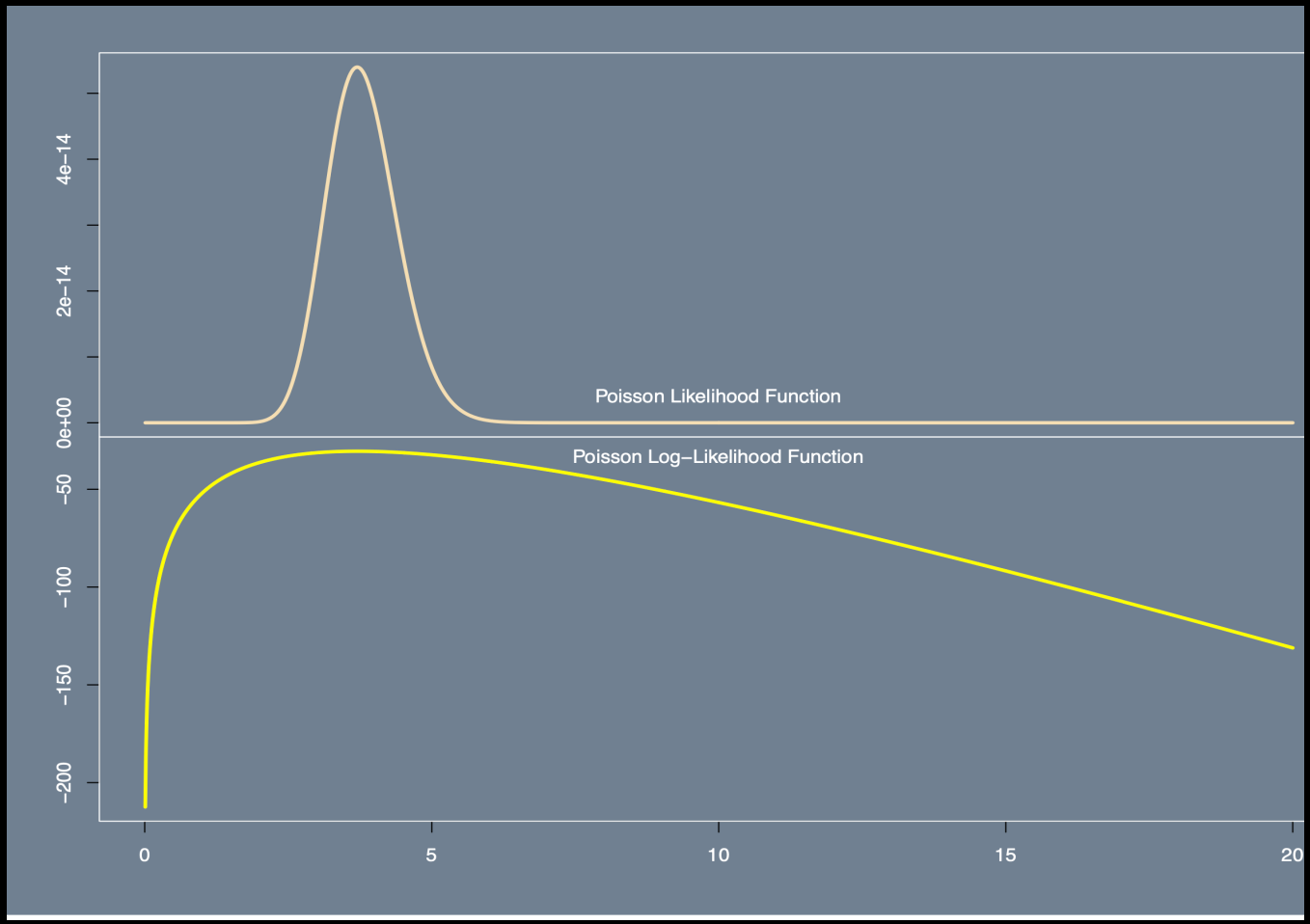
```
y.vals<-c(1,3,1,5,2,6,8,11,0,0)

# POISSON LIKELIHOOD AND LOG-LIKELIHOOD FUNCTION
llhfunc<-function(X,p,do.log=TRUE) {
        d <- rep(X,length(p))
        print(d)
        u.vec <- rep(p,each=length(X))
        print(u.vec)
        d.mat <- matrix(dpois(d,u.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)
}
```

Test Function

```
llhfunc(y.vals,c(4,30))
 [1]  1  3  1  5  2  6  8 11  0  0  1  3  1  5  2  6  8 11  0  0

 [1]  4  4  4  4  4  4  4  4  4  4 30 30 30 30 30 30 30 30 30 30

          [,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
```

Graphical View of the MLE

```
# THIS IS A VERSION OF THE mle CALL FROM, fnscale=-1 MAKES IT A MAXIMIZATION
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)

postscript("Class.MLE/poisson.like.ps")
par(oma=c(3,3,1,1),mar=c(0,0,0,0),mfrow=c(2,1),col.axis="white",
    col.lab="white",col.sub="white",col="white", bg="slategray")
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")
dev.off()
```


Poisson Likelihood Function
Poisson Log−Likelihood Function
4e−14
2e−14
0e+00
−50
−100
−150
−200
0
5
10
15
20

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:

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

  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:

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

- Now take the first deriviative:

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

- Or in full matrix terms: $\mathbf{X}'\mathbf{y} = \mathbf{X}'\hat{\mu}$, where $\hat{\mu} = \mathbf{X}\hat{\boldsymbol{\beta}}$ (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:

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

- In this specification, the systematic component is $\mathbf{X}\boldsymbol{\beta}$, the stochastic component is $\mathbf{Y} = \textbf{Military Coups}$, and the link function is $\boldsymbol{\theta} = \log(\boldsymbol{\mu})$.

- We can re-express this model by moving the link function to the left-hand side exposing the linear predictor: $g(\boldsymbol{\mu}) = \log(\mathbb{E}[\mathbf{Y}]) = \mathbf{X}\boldsymbol{\beta}$ (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 * NUMELEC, 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 in Vector Notation

- General Summed Deviance Notation: $D = \sum_{i=1}^{n} d(\boldsymbol{\eta}, y_i)$, where the individual deviance function is defined as: $d(\boldsymbol{\eta}, y_i) = -2\left[\ell(\hat{\boldsymbol{\eta}}|y_i) - \ell(\tilde{\boldsymbol{\eta}}|y_i)\right]$, where the first likelihood comes from the fitted model and the second likelihood comes from the saturated model. Thus D is a generalizion of the well-known linear *regression sum of squares*.
- Linear Model Residual Vector: $\mathbf{R}_{standard} = \mathbf{Y} - \mathbf{X}\beta$.
- Response Residual Vector: $\mathbf{R}_{Response} = \mathbf{Y} - g^{-1}(\boldsymbol{X\beta}) = \mathbf{Y} - \hat{\boldsymbol{\mu}}$.
- 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: $\mathbf{R}_{Working} = (\mathbf{y} - \boldsymbol{\mu})\frac{\partial}{\partial \eta}\boldsymbol{\mu}$ (from the last step of Iteratively Reweighted Least Squares algorithm).

Deviance for the Poisson Model

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

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

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

- Individual Deviance Function in the General Case:

$$D_i = \frac{(y_i - \hat{\mu}_i)}{|y_i - \hat{\mu}_i|}\sqrt{|d(\boldsymbol{\eta}, y_i)|} \qquad \text{where:} \qquad d(\boldsymbol{\eta}, y_i) = -2\left[\ell(\hat{\boldsymbol{\eta}}|y_i) - \ell(\tilde{\boldsymbol{\eta}}|y_i)\right].$$

- The Individual Deviance Function for Poisson Regression uses:

$$\ell(\eta_i|y_i) = [-\exp(\mathbf{X}_i\boldsymbol{\beta}) + y_i(\mathbf{X}_i\boldsymbol{\beta}) - \log(y_i!)] \qquad \text{where } \boldsymbol{\beta} \text{ is either } \hat{\boldsymbol{\beta}} \text{ or } \tilde{\boldsymbol{\beta}}.$$

- Recall also the Pearson's statistic:

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

- 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:

$$\underbrace{g^{-1}(\boldsymbol{\eta})}_{17\times 1} = g^{-1}(\boldsymbol{X}\boldsymbol{\beta})$$

$$= \exp\left[\boldsymbol{X}\boldsymbol{\beta}\right]$$

$$= \exp\left[\mathbf{1}\beta_0 + \mathbf{INC}\beta_1 + \mathbf{POV}\beta_2 + \mathbf{BLK}\beta_3 + \mathbf{CRI}\beta_4 + \mathbf{SOU}\beta_5 + \mathbf{DEG}\beta_6\right]$$

$$= \mathbb{E}[\mathbf{Y}] = \mathbb{E}[\mathbf{EXE}].$$

```
dp.97 <- read.table("https://jeffgill.org/wp-content/uploads/2024/08/cpunish.dat_.txt",
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, $df = 16$ Maximized $\ell()$: -31.7375

Summed deviance: 18.212, $df = 11$ AIC: 77.475

Poisson GLM of Capital Punishment Data

$\mathbf{VC} = E[(-\mathbf{H})^{-1}] =$

Int	**INC**	**POV**	**BLK**	log(**CRI**)	**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

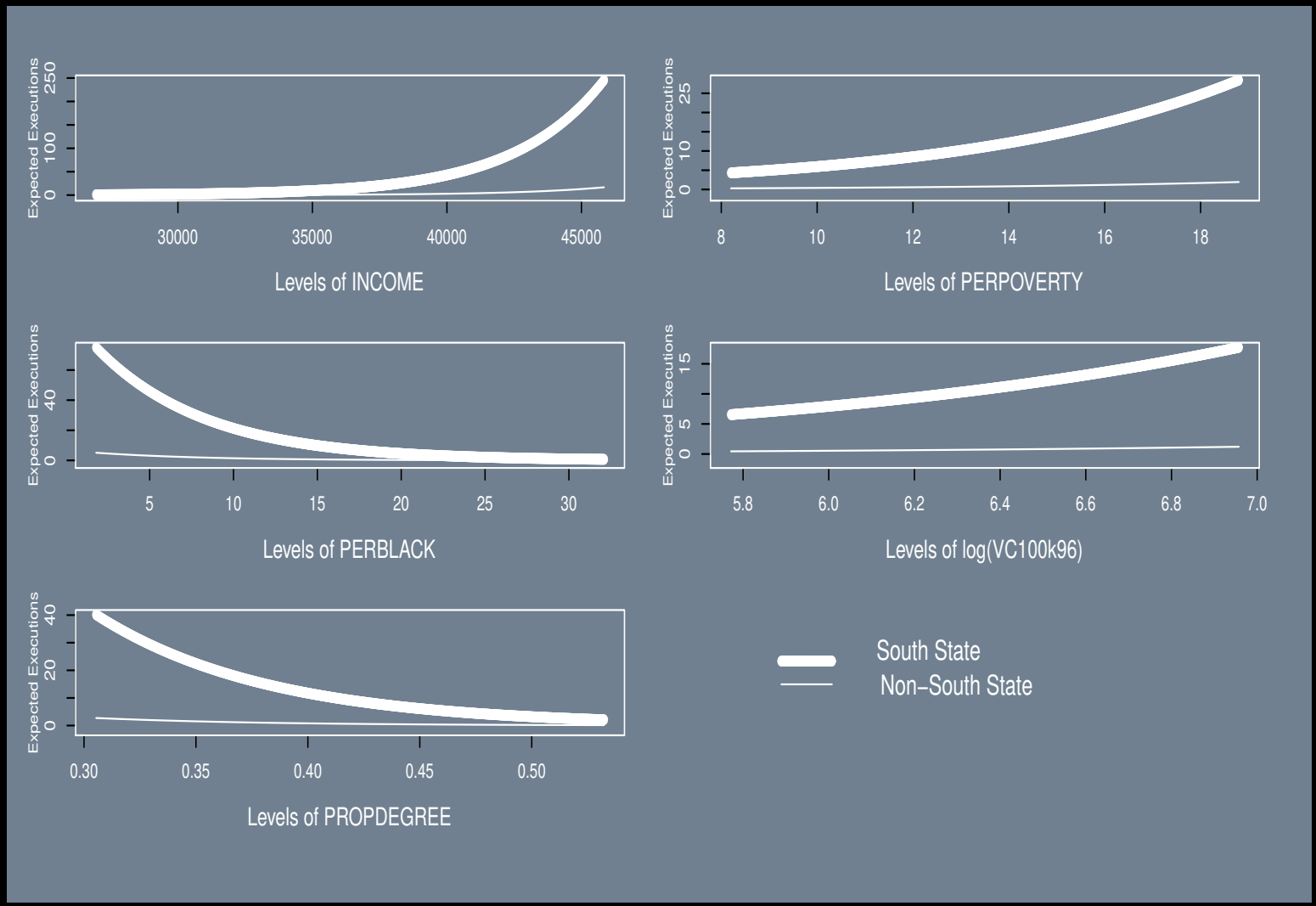
- We can no longer use "a one unit change in X gives a β change in Y."
- Main idea:
  - pick one covariate of interest, $\mathbf{X}_q$
  - choose 2 levels of this variable, $\mathbf{X}_{1,q}$, $\mathbf{X}_{2,q}$
  - set all other covarates at their mean, $\bar{\mathbf{X}}_{-q}$
  - create two predictions 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
```


Expected Executions
0
100
250
30000
35000
40000
45000
Levels of INCOME
Expected Executions
0
10
25
8
10
12
14
16
18
Levels of PERPOVERTY
Expected Executions
0
40
5
10
15
20
25
30
Levels of PERBLACK
Expected Executions
0
5
15
5.8
6.0
6.2
6.4
6.6
6.8
7.0
Levels of log(VC100k96)
Expected Executions
0
20
40
0.30
0.35
0.40
0.45
0.50
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")
```

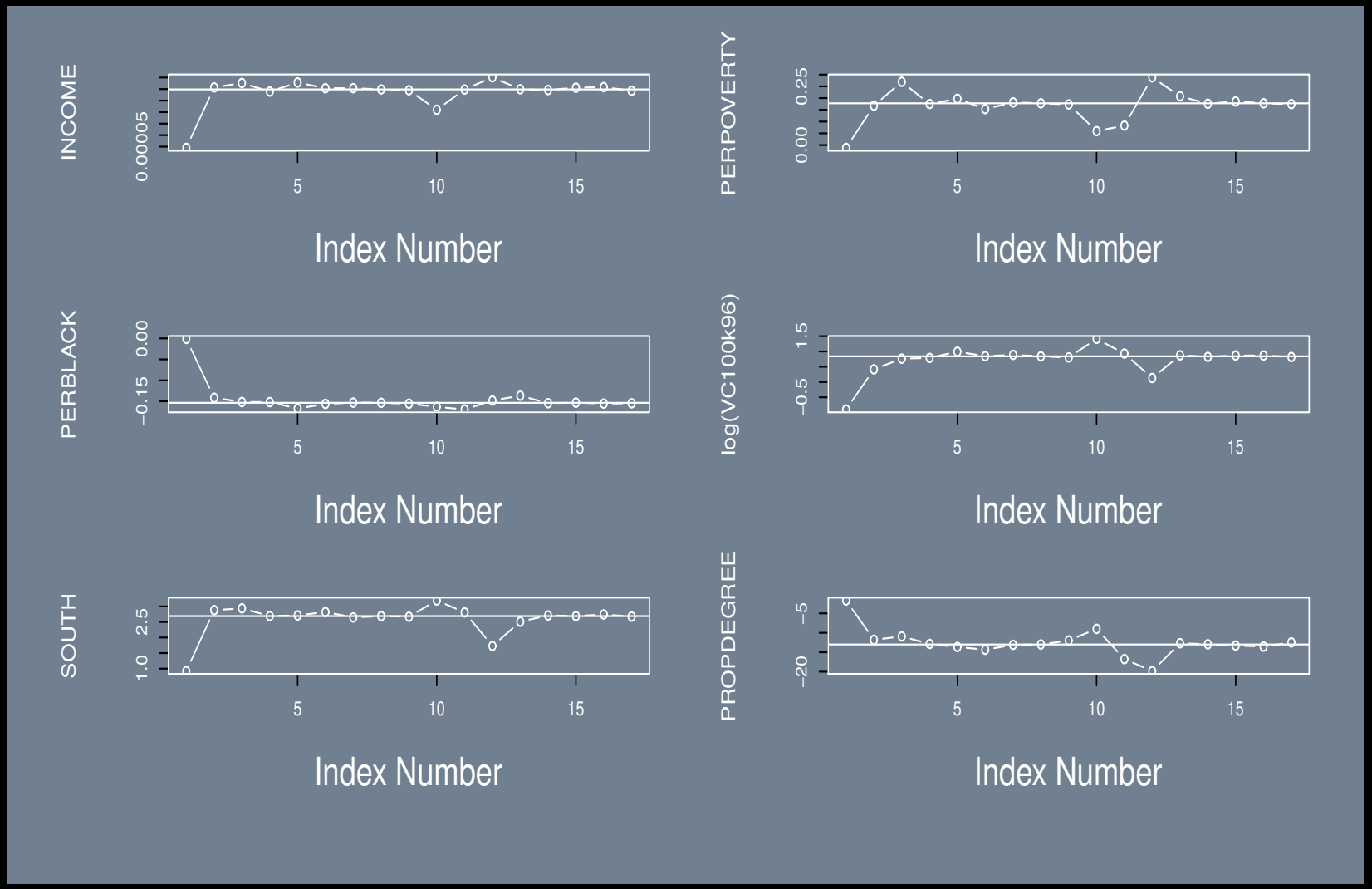
Poisson GLM of Capital Punishment, First Difference Code

```
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
0.00005
5
10
15
Index Number
PERPOVERTY
0.00
0.25
5
10
15
Index Number
PERBLACK
−0.15
0.00
5
10
15
Index Number
log(VC100k96)
−0.5
1.5
5
10
15
Index Number
SOUTH
1.0
2.5
5
10
15
Index Number
PROPDEGREE
−20
−5
5
10
15
Index Number

New and Old Ways to Look at Model Fit

- Approximation to Pearson's Statistic.

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

- If the sample size is sufficiently large, then $\frac{X^2}{a(\psi)} \sim \chi^2_{n-p}$ 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 $D(\boldsymbol{\eta}, \mathbf{y})/a(\psi) \sim \chi^2_{n-p}$.
- 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.

Application to Congressional Cosponsoring of Bills

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

```
cosponsor <- read.table("fowler.dat", header=TRUE);  head(cosponsor,4)
```

- 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 interesed 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

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

- 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* k^{th} *success.*
- An alternative but equivalent form,

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

  measures the number of trials necessary to get k 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:

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

- For this parameterization, we get:

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

- 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 kth 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 103^{rd} and 104^{th} 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–103rd	Bills–104th
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("https://jeffgill.org/wp-content/uploads/2024/08/committe.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
Stds_of_Conduct	0.37836	0.44850	0.60864	0.40700
Intelligence	-13.58498	-1.43490	-0.77253	-2.05981

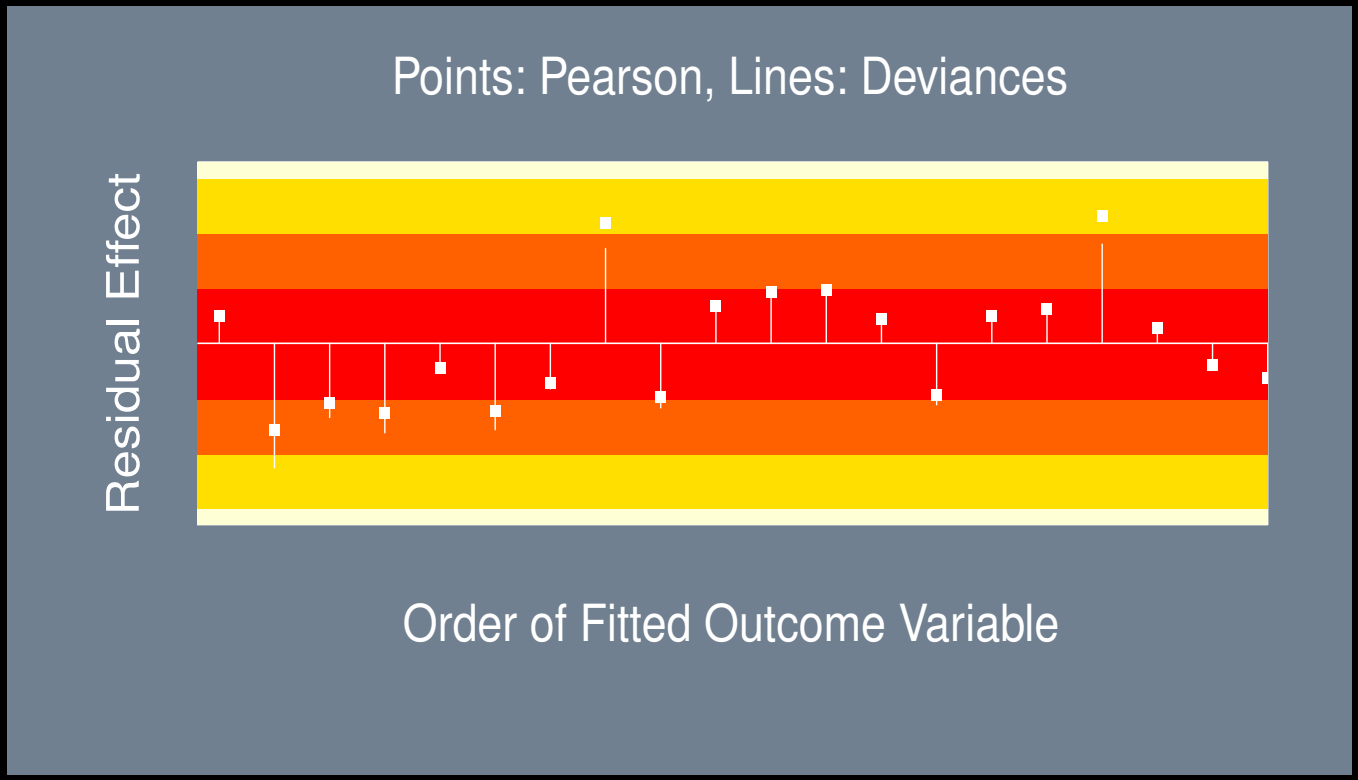
Modeling Bill Assignment – 104th House, Results

	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 occurrances, 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 more common in bigger cities.
- Focus on rate:

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

- Example from Faraway:
  - gamma radiation leads to cell abnormalities,
  - `ca` is the count of chromosonal abnormalities,
  - `cells` is the number (in hundreds) of exposed cells,
  - `doseamt` = dose amount = `(1,2.5,5)`,
  - `doserate` = rate of application = `(0.1,0.25,0.5,1,1.5,2,2.5,3,4)`.

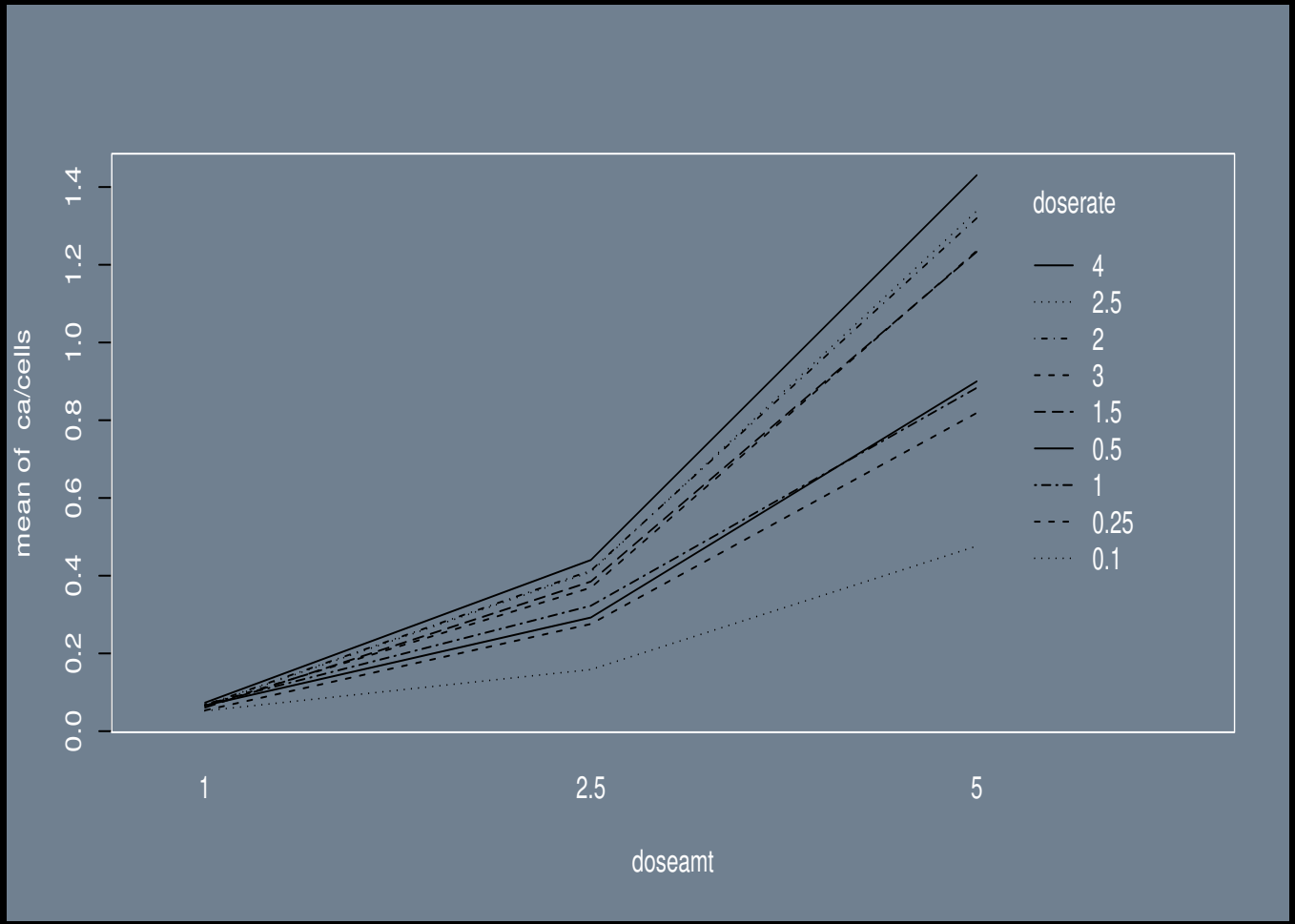
Rate Models

```
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


mean of ca/cells
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1.4
1
2.5
5
doseamt
doserate
4
2.5
2
3
1.5
0.5
1
0.25
0.1

Rate Model 1

- MODEL 1: Linearly modeling the ratio directly seems to fit well.

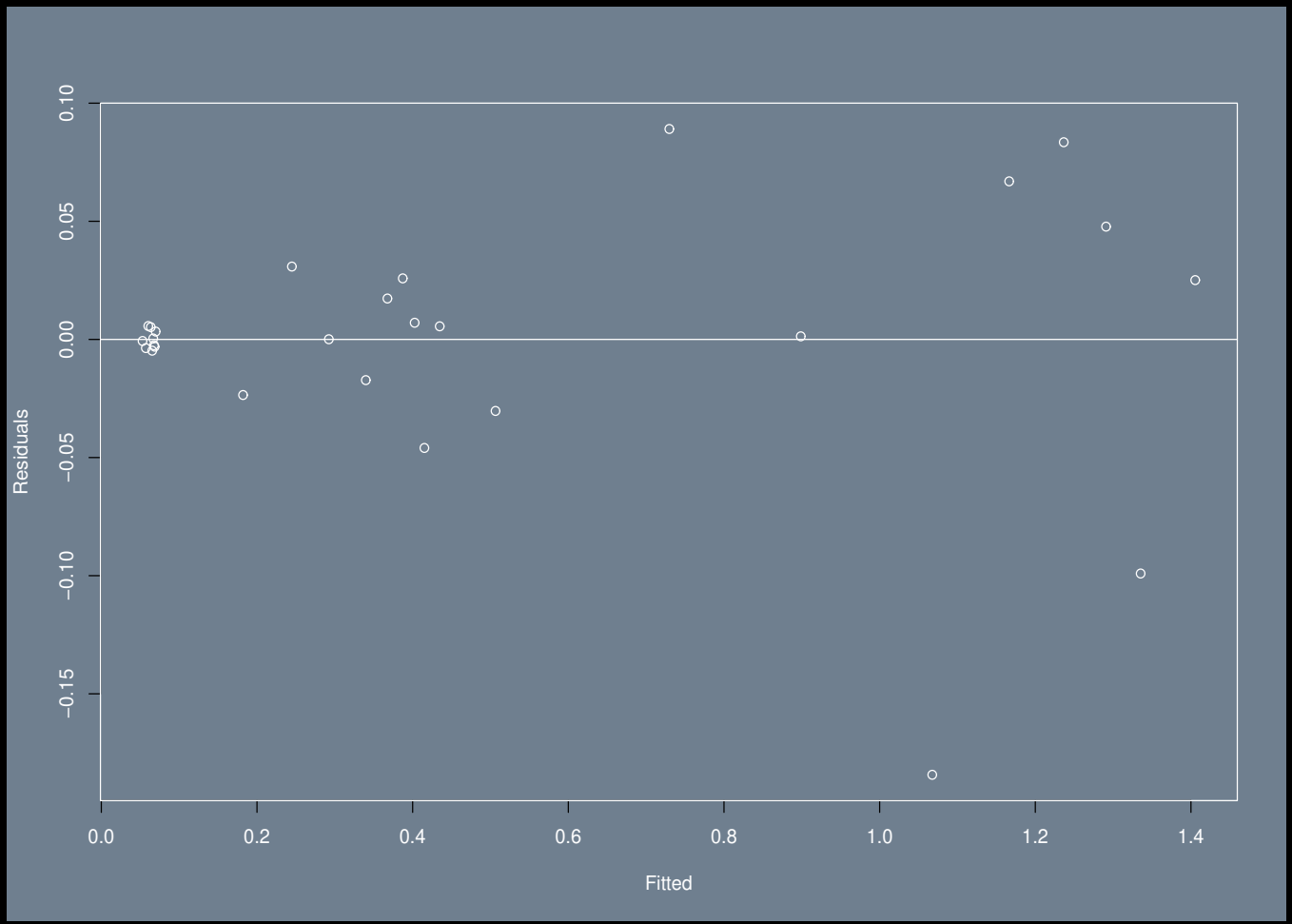
```
lmod <- lm(ca/cells ~ log(doserate)*factor(doseamt), dicentric)
summary(lmod)

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
```

Rate Model 1

- However, there is overdispersion:

```
 sum(lmod$residual)
[1] 2.417771e-17
pchisq(sum(lmod$residual), lmod$df.residual,lower.tail=FALSE)
[1] 1

postscript("CLASSES/Class.MLE/Images/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 Model 1



Rate Model 2

- 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 outside the function call:

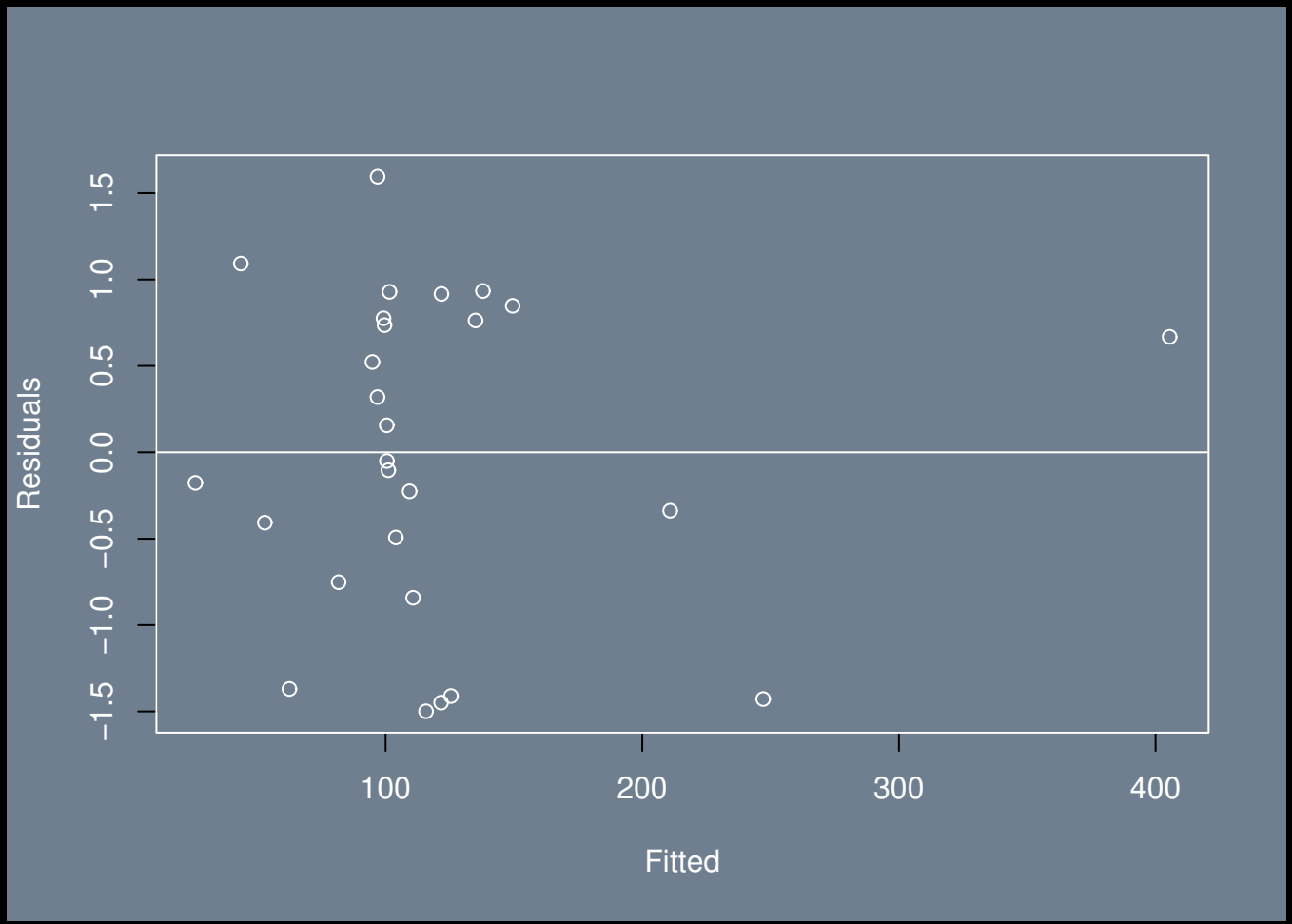
```
dicentric$dosef <- factor(dicentric$doseamt)
pmod <- glm(ca ~ log(cells)+log(doserate)*dosef,family=poisson,dicentric)
summary(pmod)
                      Estimate Std. Error z value Pr(>|z|)
(Intercept)            -2.7653     0.3812   -7.25    4e-13
log(cells)              1.0025     0.0514   19.52  < 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
```

Rate Model 2

- However, there is a strange pattern to the residuals:

```
pchisq(sum(pmod$residual), pmod$df.residual,lower.tail=FALSE)
[1] 1

postscript("CLASSES/Class.MLE/Images/rate.diag2.ps",width=7,height=5)
par(mfrow=c(1,1),col.axis="white",col.lab="white",col.sub="white",
    col="white",bg="slategray")
plot(residuals(pmod) ~ fitted(pmod),xlab="Fitted",ylab="Residuals")
abline(h=0)
dev.off()
system("open CLASSES/Class.MLE/Images/rate.diag2.ps")
```

Rate Model 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:

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

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

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

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

  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 Model 3

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

$$\log\left(\frac{\texttt{ca}}{\texttt{cells}}\right) = \mathbf{X}\boldsymbol{\beta} \qquad \Longrightarrow \qquad \log(\texttt{ca}) = \log(\texttt{cells}) + \mathbf{X}\boldsymbol{\beta}.$$

- 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:

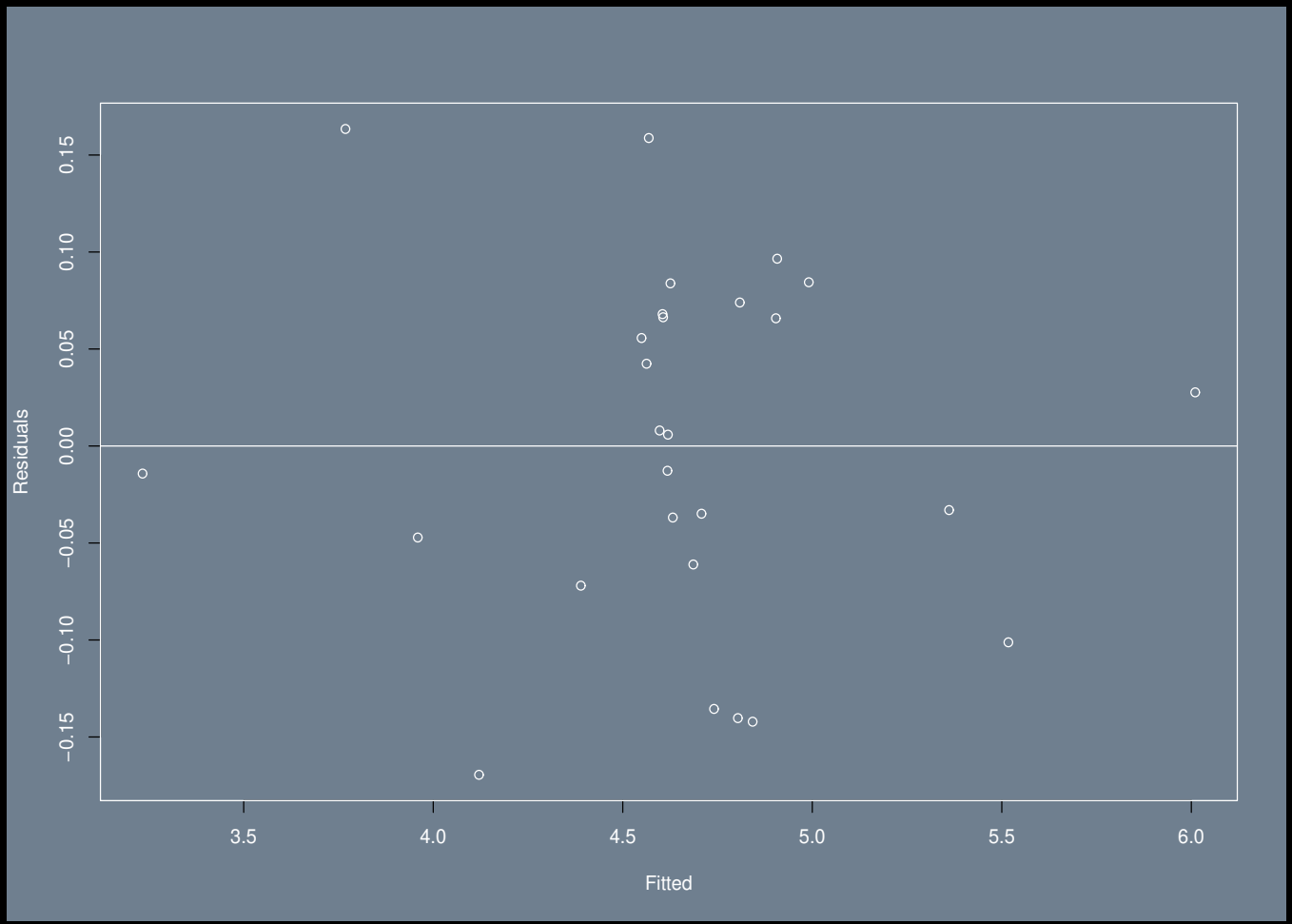
```
rmod <- lm(log(ca) ~ offset(log(cells))+log(doserate)*dosef, dicentric)
summary(rmod)
                      Estimate Std. Error z value Pr(>|z|)
(Intercept)           -2.76243    0.03352 -82.402  < 2e-16
log(doserate)          0.07561    0.02866   2.638 0.015364
dosef2.5               1.64378    0.04741  34.672  < 2e-16
dosef5                 2.77866    0.04741  58.610  < 2e-16
log(doserate):dosef2.5 0.16483    0.04053   4.067 0.000553
log(doserate):dosef5   0.19480    0.04053   4.807 9.47e-05

Residual standard error: 0.1006 on 21 degrees of freedom
Multiple R-squared:  0.9709,        Adjusted R-squared:  0.964
F-statistic: 140.3 on 5 and 21 DF,  p-value: 2.128e-15
```

Rate Model 3

- Better?

```
postscript("CLASSES/Class.MLE/Images/rate.diag3.ps")
par(mfrow=c(1,1),col.axis="white",col.lab="white",col.sub="white",
    col="white",bg="slategray")
plot(residuals(rmod) ~ fitted(rmod),xlab="Fitted",ylab="Residuals")
abline(h=0)
dev.off()
system("open CLASSES/Class.MLE/Images/rate.diag3.ps")
```

Rate Model 3



Zero-Inflated Poisson Model

- When there are *many* zeros in the data then the coefficient estimates from a Poisson regression model are biased.
- 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 Poisson(λ) with probability $1 - \pi$.
- So this can be thought of as a type of mixture model.

Zero-Inflated Poisson Model, Setup

- Let $Y_1, \ldots, Y_N$ be a sample of size N independently drawn from

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

- There are actually three categories of events:
  - Zero counts in the always zero group: $P(Y_i = 0|\mathbf{X}_i, \boldsymbol{\beta}) = \pi_i$
  - Zero counts in the not-always zero group: $P(Y_i = 0|\mathbf{X}_i, \boldsymbol{\beta}) = (1 - \pi_i)\frac{e^{-\lambda_i}\lambda_i^0}{0!} = (1 - \pi_i)e^{-\lambda_i}$
  - Non-zero counts in the not-always zero group: $P(Y_i = y_i|\mathbf{X}_i, \boldsymbol{\beta}) = (1 - \pi_i)\frac{e^{-\lambda_i}\lambda_i^{y_i}}{y_i!}$

- So the probability mass function is given by:

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

- With mean and variance:

$$\mathcal{E}[y_i|\mathbf{X}_i, \boldsymbol{\beta}] = (0 \times pi_i) + (\mu \times (1 - \pi_i))$$
$$\text{Var}[y_i|\mathbf{X}_i, \boldsymbol{\beta}] = \lambda_i(1 - \pi_i)(1 + \lambda_i\pi_i)$$

Zero-Inflated Poisson Model, Context

- 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 $\text{logit}(\pi_i) = \mathbf{u}_i^{\text{T}}\boldsymbol{\gamma}$, where the response variable states zero or nonzero status and $\boldsymbol{\gamma}$ is a regression coefficient vector for covariates $\mathbf{u}_i^{\text{T}}$.
- The second part is a poisson regression, specified by $\log(\lambda_i) = \mathbf{x}_i^{\text{T}}\boldsymbol{\beta}$, 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 $\mathbf{x}_i^{\text{T}}$.
- 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.
- See: Jung Ae Lee and Jeff Gill. "Missing Value Imputation for Physical Activity Data Measured by Accelerometer." Statistical Methods in Medical Research. Volume 27, Issue 2, 490-506, (March) 2016.

Zero-Inflated Poisson Model, Example Code

```
library(pscl)
accel <- read.csv(
  "/Users/jgill/ARTICLES/Article.Accelerometer/Election.Study/LYN2B08080256.csv")
accel <- as.numeric(accel[[1]])
accel <- accel[-c(1:10)]
accel.df <- data.frame(accel)
zip.md <- zeroinfl(accel ~ ., data=accel.df, dist="poisson"); summary(zip.md)

Pearson residuals:
    Min      1Q  Median      3Q     Max
-0.6369 -0.6369 -0.6369 -0.5786 13.8524

Count model coefficients (poisson with log link):
            Estimate Std. Error z value Pr(>|z|)
(Intercept) 6.577279   0.001056    6229   <2e-16

Zero-inflation model coefficients (binomial with logit link):
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  0.90046    0.03357   26.82   <2e-16
```

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:

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

- Notice that this uses $Y_i > 0$ in this conditional instead of $Y = 0$ in the conditional of the ZIP model.
- The probability mass function in the ZIP model is modified to

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

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

Hurdle Model, Example Code

```
zip.hurdle <- hurdle(accel ~ ., data=accel.df, dist="poisson")
summary(zip.hurdle)

Pearson residuals:
    Min      1Q  Median      3Q     Max
-0.6369 -0.6369 -0.6369 -0.5786 13.8524

Count model coefficients (truncated poisson with log link):
            Estimate Std. Error z value Pr(>|z|)
(Intercept) 6.577274   0.001056    6229   <2e-16
Zero hurdle model coefficients (binomial with logit link):
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -0.90046    0.03357  -26.82   <2e-16

Number of iterations in BFGS optimization: 8
Log-likelihood: -7.621e+05 on 2 Df
```

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

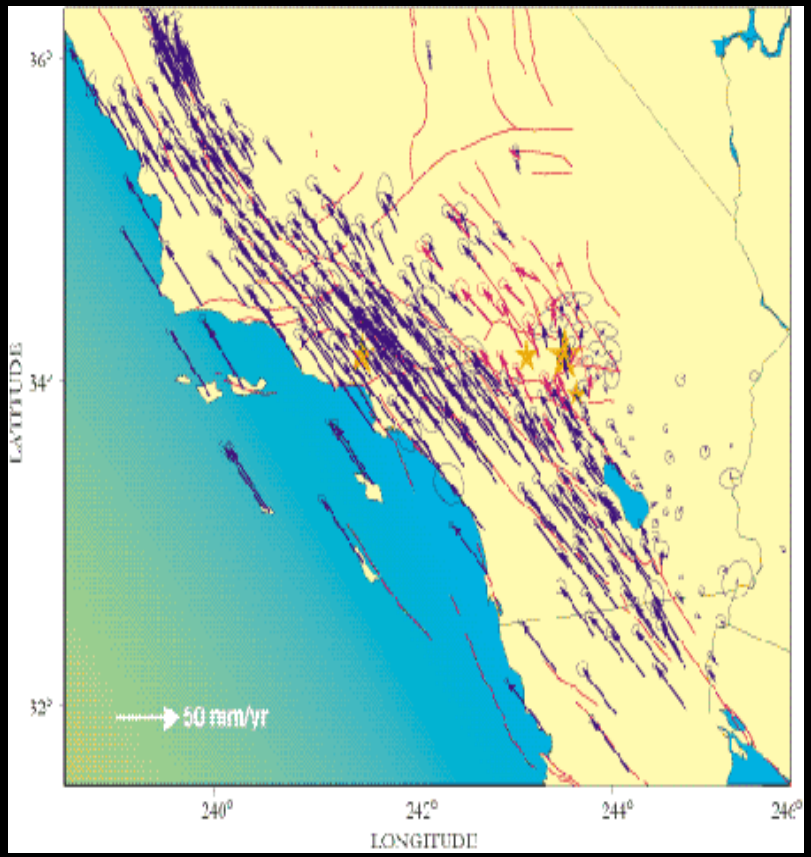
Number of Actions	Frequency	Percentage
0	3882	95.80
1	63	1.55
2	38	0.94
3	32	0.79
4	8	0.20
5	12	0.30
6	12	0.30
7	3	0.07
10	1	0.02
11	1	0.02
Total	4052	100.0

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

	Zero-Inflated Poisson		Hurdle Poisson	
Variables	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	

Multivariate Application: the Predicting Earthquake Aftershocks



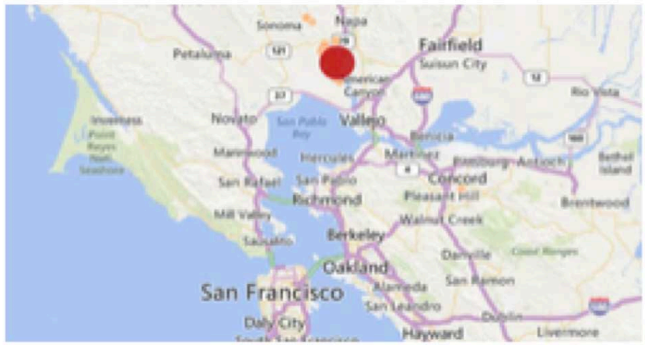
- Topical.
- Immediately after a powerful earthquake in a high population density area decisions must be made about operating powerplants, schools, and transportation facilities.
- A series of aftershocks can be equally deadly and destructive as a mainshock.
- Predicting aftershocks based on empirical evidence is far reliable than predicting mainshocks.

Multivariate Application: the Predicting Earthquake Aftershocks (cont.)

- Why is this relevant?
- Some geopolitical events are very hard to predict, but their after-effects may be much more reliably anticipated.
- Examples: terrorist attacks, unannounced nuclear tests, civil wars, coups.
- Bayesian learning may (over time) increase our knowledge.
- The need for real-time analysis parallels necesary government reactions after such events.

How Aftershocks Are Described

Infographic



Bay Area's 6.0 quake and aftershocks

READ THE STORY >

A little more than two hours after the quake, a shallow magnitude 3.6 tremor was reported by the USGS. The aftershock occurred at 5:47 a.m. at a depth of five miles. The National California Seismic System put the chance of a strong aftershock in the next week at 54%. Scientists at UC Berkely released a video showing an early-warning system that sent an alert 10 seconds before the earthquake.

Multivariate Application: the Predicting Earthquake Aftershocks (cont.)

- Model aftershocks as a *non-homogeneous* Poisson process with the intensity parameter:

$$N(t) \propto \frac{1}{(t+c)^p}.$$

  This is actually called "Omori's Law" where t is time, and the rest are constants: c is a time offset, p is a rate of decay.

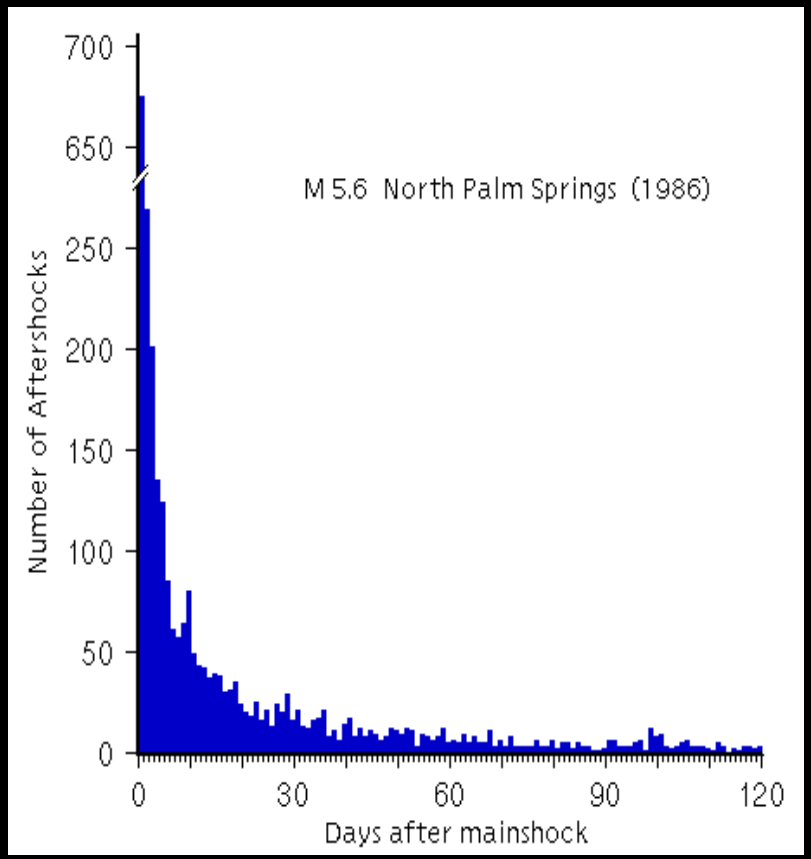
- So the probability of n aftershocks at time period t is: $\boxed{P(n|t) = \frac{N(t)^n e^{-N(t)}}{n!}.}$

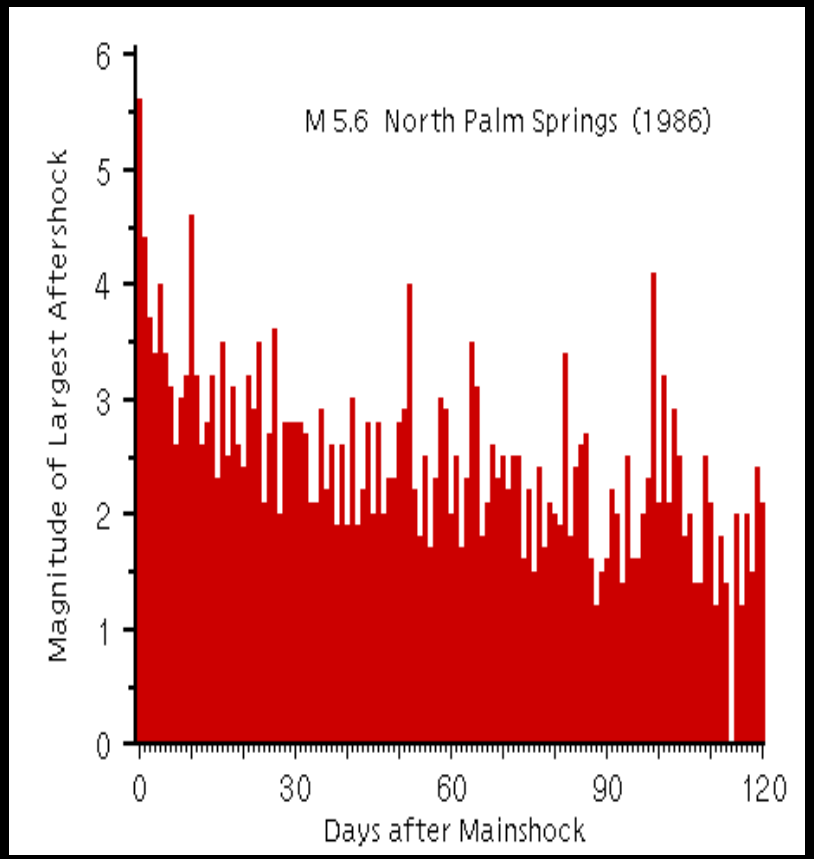
- Use the Gutenberg-Richter relation (an empirical law), aftershock version:

$$\log_{10} N(M) = a + b(M_{\text{mainshock}} - M_{\text{aftershock}})$$

  where $N(M)$ is the number per year of aftershocks of magnitude greater than $M_{\text{aftershock}}$ following a mainshock of magnitude $M_{\text{mainshock}}$, a and b are constants.

Multivariate Application: the Predicting Earthquake Aftershocks (cont.)





Multivariate Application: the Predicting Earthquake Aftershocks (cont.)

- Putting these two principles together gives the rate of aftershocks of magnitude $M_{\text{aftershock}}$ or larger at time t following a mainshock:

$$\lambda(t, M) = 10^{a+b(M_{\text{mainshock}}-M_{\text{aftershock}})}(t+c)^{-p}$$

- More usefully, the probability of an aftershock between M_1 and M_2, both less than $M_{\text{mainshock}}$, and between time t_1 and t_2 after the mainshock:

$$p(t, M) = 1 - \exp\left[-\int_{M_1}^{M_2}\int_{t_1}^{t_2}\lambda(t, M)dtdM\right]$$

  under the assumption that the joint instantaneous rate is distributed exponential (see the figure!)

- What we need now is a posterior distribution for $\boldsymbol{\mu} = (a, b, p, c)$ conditional on the mainshock.

Multivariate Application: the Predicting Earthquake Aftershocks (cont.)

- Start with some (regionalized) data, calculate posteriors with a Bayesian gaussian model and update as new data (earthquakes) occur.
- Multivariate priors:

$$\boldsymbol{\mu}|\boldsymbol{\Sigma} \sim \mathcal{N}_k\left(\mathbf{m}, \frac{\boldsymbol{\Sigma}}{n_0}\right), \qquad \boldsymbol{\Sigma}^{-1} \sim \mathcal{W}(\alpha, \boldsymbol{\beta}),$$

  where n_0/n measures our belief in the representativeness prior data.
- This produces posteriors:

$$\hat{\boldsymbol{\mu}}|\boldsymbol{\Sigma} \sim \mathcal{N}_k\left(\frac{n_0\mathbf{m} + n\bar{\mathbf{x}}}{n_0 + n}, \frac{\boldsymbol{\Sigma}}{n_0 + n}\right)$$

$$\widehat{\boldsymbol{\Sigma}^{-1}} \sim \mathcal{W}_k\left(\alpha + n, \boldsymbol{\beta}^{-1} + S^2 + \frac{n_0 n}{n_0 + n}(\bar{x} - \mathbf{m})(\bar{x} - \mathbf{m})'\right).$$

Multivariate Application: the Predicting Earthquake Aftershocks (cont.)

- Some information to build "Generic California" priors:
  - 62 aftershock sequences with $M_{\text{mainshock}} \geq 5$, occurring from 1933 to 1987 in California (exclusive of two unusual events),
  - Omori's Law parameters (a, p) from $M_{\text{mainshock}} - M_{\text{aftershock}} \geq 3$,
  - b from $M_{\text{mainshock}} - M_{\text{aftershock}} \geq 2$,
  - c picked to get maximum distinction between mainshock "coda" and aftershocks using post-1970 data.
- Reasenberg and Jones (1989) assume $\boldsymbol{\Sigma}^{-1}$ is diagonal and produce normal priors with means:

$$\bar{a} = -1.67, \quad \bar{b} = 0.91, \quad \bar{p} = 1.08, \quad c = 0.05$$

($\sigma_a = 0.0.7$, $\sigma_b = 0.02$, $\sigma_p = 0.03$, c deterministic).

Multivariate Application: the Predicting Earthquake Aftershocks (cont.)

- Data taken from real-time sequence of aftershocks for two excluded events:
  - ▷ Coalinga (1983), $M_{\text{mainshock}} = 6.5$
  - ▷ Whittier-Narrows (1987), $M_{\text{mainshock}} = 5.9$

  and updated *during* aftershock times.
- Thus probabilities are Bayesianly improved during risk period for an event greater than the mainshock.
- Updating the "Generic California" priors with the conjugate-normal Bayesian model gives any desired set of probabilities over a period of time after the mainshock by integrating some region of the posterior.

Probability of $M_{\text{aftershock}} > M_{\text{mainshock}} - 1$

Within	**Time After Mainshock, Coalinga**								
$t_2 - t_1$	15 min.	6 hrs.	12 hrs.	1 day	3 days	7 days	15 days	30 days	60 days
1 Day	0.330	0.176	0.125	0.081	0.033	0.015	0.007	0.003	0.002
3 Days	0.413	0.265	0.209	0.153	0.077	0.039	0.020	0.010	0.005
7 Days	0.467	0.330	0.276	0.218	0.129	0.074	0.040	0.022	0.011
30 Days	0.545	0.427	0.378	0.324	0.234	0.165	0.109	0.069	0.039
60 Days	0.577	0.466	0.420	0.370	0.283	0.214	0.154	0.105	0.066

Within	**Time After Mainshock, Whittier-Narrows**								
$t_2 - t_1$	15 min.	6 hrs.	12 hrs.	1 day	3 days	7 days	15 days	30 days	60 days
1 Day	0.393	0.141	0.084	0.044	0.012	0.004	0.001	0.000	0.000
3 Days	0.431	0.185	0.123	0.074	0.026	0.010	0.004	0.001	0.000
7 Days	0.488	0.208	0.146	0.095	0.040	0.017	0.007	0.003	0.001
30 Days	0.465	0.232	0.171	0.120	0.062	0.034	0.017	0.009	0.004
60 Days	0.470	0.238	0.178	0.127	0.069	0.040	0.023	0.012	0.006

Example for Whitter-Narrows, if the main shock happened within the last 15 minutes then the probablity of a serious aftershoock in the next 24 hours is 0.393.