Count Response

STAT 526
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Basic Poisson Regression
(Faraway Ch. 3)

Poisson Distribution

- Y: Counts of events that occur randomly over fixed interval of time or space
  - No upper limit for the number of events
  - Approximates $Binomial(n, \pi)$ distribution when n is large and π is small. Then $\lambda = n\pi$.
  - Approaches Normality as λ increases

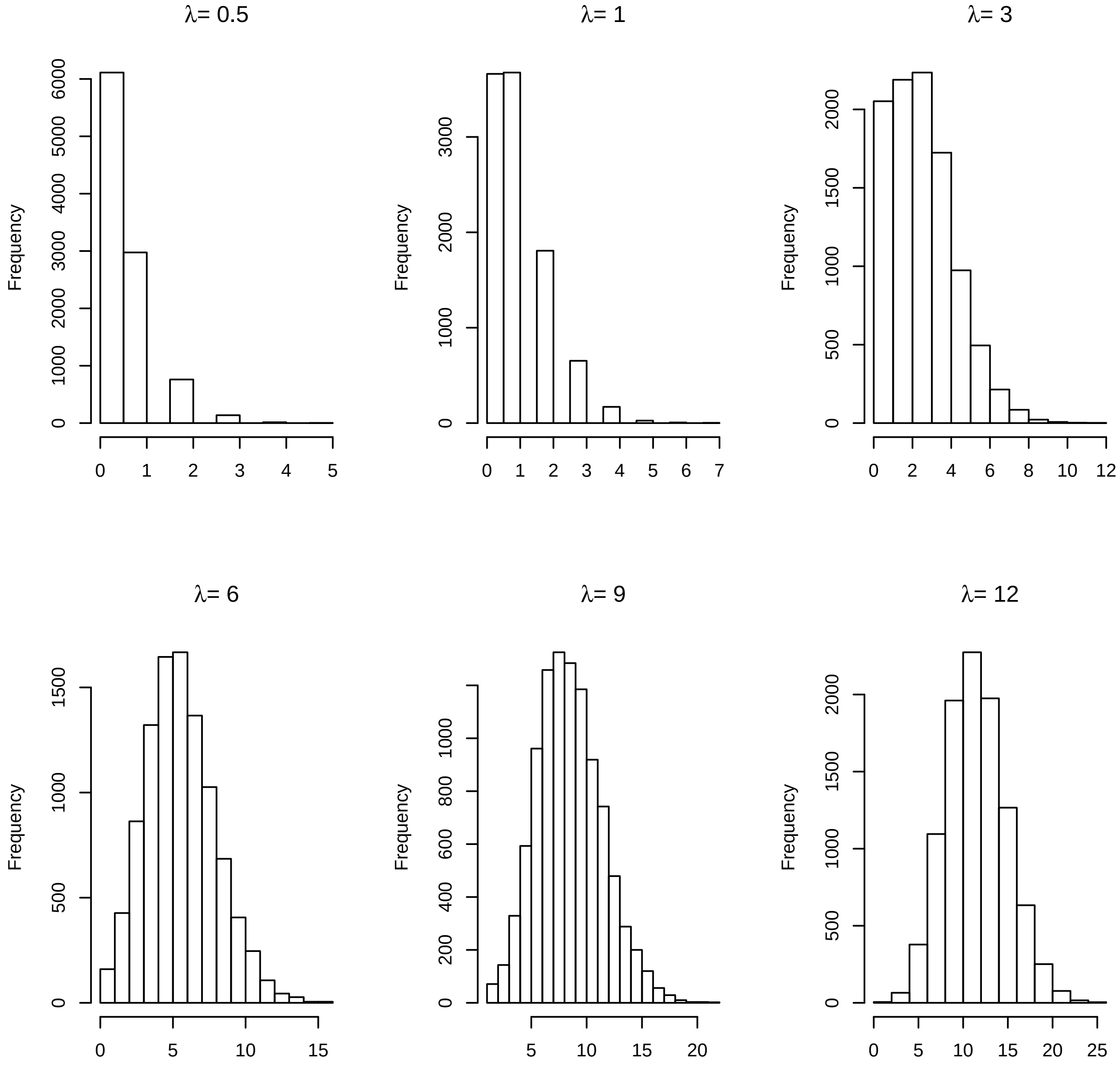
- $P\{Y = y\} = \frac{e^{-\lambda}\lambda^y}{y!}, \ y = 1, \ldots$

- $E\{Y\} = Var\{Y\} = \lambda$

- If $Y_i \overset{ind}{\sim} Poisson(\lambda_i), \ i = 1, \ldots,$

  then $\sum\limits_i Y_i \sim Poisson(\sum\limits_i \lambda_i)$

Poisson(λ) for various λ



Poisson Regression

- Model

$$\begin{aligned} Y_i &\overset{ind}{\sim} Poisson(\lambda_i), \text{ where} \\ & log\lambda_i = \mathbf{X}_i'\beta \ (= \eta,\ link) \end{aligned}$$

  – $\beta_j =$ difference in log E{Y} following a unit change in predictor X_j, while the others are constant

- Log-likelihood

$$\begin{aligned} l(\beta) &= log \prod_{i=1}^{n} \left[\frac{\lambda_i^{y_i} e^{-\lambda_i}}{y_i!} \right] = \sum_{i=1}^{n} (y_i log\lambda_i - \lambda_i - log\, y_i!) \\ &= \sum_{i=1}^{n} \left(y_i \, \mathbf{X}_i'\beta - exp\, \mathbf{X}_i'\beta \right) + constant \end{aligned}$$

- Pearson X^2

$$X^2 = \sum_{i=1}^{n} \frac{(y_i - \widehat{\lambda}_i)^2}{\widehat{\lambda}_i}$$

- Deviance

$$D = 2 \sum_{i=1}^{n} \left(y_i log \frac{y_i}{\widehat{\lambda}_i} - (y_i - \widehat{\lambda}_i) \right)$$

  – Different numeric values of deviance for grouped and ungrouped data

Inference About Individual β_j: Wald Test

- Same as for Binomial response
- Test $H_0: \ \beta_j = 0$ versus $H_a: \ \beta_j \neq 0$.
- Test statistic $z^* = \frac{b_j - 0}{s\{b_j\}}$
- **Approximate** variance $s^2\{\mathbf{b}\}$

$$s^2\{\mathbf{b}\} = \left(\left[- \frac{\partial^2 \log_e L(\beta)}{\partial \beta_j \partial \beta_{j'}} \right]_{\beta = \mathbf{b}} \right)^{-1}$$

- **Approximate** distribution of z
  - $z^* \sim \mathcal{N}(0, 1)$. Alternatively, $(z^*)^2 \sim \chi^2_1$
  - reject H_0 if $|z^*| > z^{1-\alpha/2}$
  - CI for β_j: $b_j \pm z^{1-\alpha/2} s\{b_j\}$

Example: Galapagos Plants (Faraway Ch. 3)

- Study the number of plant species on 30 Galapagos islands as function of geographic variables

```
library(faraway)
data(gala)
?gala

# faraway does not use the 2nd predictor,
# so we'll remove it too.
gala <- gala[, -2]
head(gala)
```

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

Model with all the predictors

```
> fit1 <- glm(Species~., family=poisson, data=gala)
> summary(fit1)

Call:
glm(formula = Species ~ ., family = poisson, data = gala)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-8.2752  -4.4966  -0.9443   1.9168  10.1849

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  3.155e+00  5.175e-02  60.963  < 2e-16 ***
Area        -5.799e-04  2.627e-05 -22.074  < 2e-16 ***
Elevation    3.541e-03  8.741e-05  40.507  < 2e-16 ***
Nearest      8.826e-03  1.821e-03   4.846 1.26e-06 ***
Scruz       -5.709e-03  6.256e-04  -9.126  < 2e-16 ***
Adjacent    -6.630e-04  2.933e-05 -22.608  < 2e-16 ***
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1   1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 3510.73  on 29  degrees of freedom
Residual deviance:  716.85  on 24  degrees of freedom
AIC: 889.68
```

Model Diagnostics (Faraway Sec. 6.4)

Goodness of Fit Tests

- Residual Deviance
  - Test H_0 : our model vs H_a: saturated model
  - Distribution poorly approximated by χ^2

```
> pchisq(fit1$deviance,
    fit1$df.residual,lower.tail=FALSE)
[1] 7.073157e-136  # reject H0
```

- Pearson X^2
  - Test H_0 : our model vs H_a: saturated model
  - Distribution better approximated by χ^2

```
> pchisq( sum(residuals(fit1, type="pearson")^2 ),
    fit1$df.residual, lower.tail=FALSE)
[1] 2.18719e-145  # reject H0
```

- Better approximation of χ^2 when Poisson approaches Normal
- Can look more into model diagnostics to find possible reasons for poor fit

Model Diagnostics: Residual Plots

- Response residuals $r_i = y_i - \widehat{\lambda}_i$
  - Of limited use: variance is function of the expected value

- Pearson residuals $r_{i,P} = \frac{y_i - \widehat{\lambda}_i}{\sqrt{\widehat{\lambda}_i}}$
  - $\sum_i r_{i,P}^2 = X^2$
  - Account for differences in variance

- Deviance residuals

  $$r_{i,D} = sign(y_i - \widehat{\lambda}_i) \left[2(y_i \, log \, \frac{y_i}{\widehat{\lambda}_i} - (y_i - \widehat{\lambda}_i)) \right]^{1/2}$$

  - Defined by analogy with Pearson residuals
  - Define $d_i = 2(y_i \, log \, \frac{y_i}{\widehat{\lambda}_i} - (y_i - \widehat{\lambda}_i))$, such that

    $\sum_i r_{i,D}^2 = \sum_i d_i = Deviance$
  - Account for differences in variance

Residual Plots (Next Slide)

(a) As in linear regression, can plot response residuals r_i vs $\widehat{E\{Y_i\}} = \hat{\lambda}_i$

```
plot(residuals(fit1, type="response") ~
    predict(fit1, type="response"),
    xlab=expression(hat(lambda)),
    ylab="Response residuals", main="(a)")
abline(h=0)
```

- Of limited use:
  Variance is function of the expected value;
  Most predicted expected values are small

(b) Plot response residuals r_i vs link $\hat{\eta} = X\hat{\beta}$

```
plot(residuals(fit1, type="response") ~
    predict(fit1, type="link"),
    xlab=expression(paste(hat(eta), " = X", hat(beta))),
    ylab="Response residuals", main="(b)")
abline(h=0)
```

- The points on x axis are better separated
  Variance still function of the expected value

Residual Plots (Next Slide)

(c) Plot deviance residuals $r_{i,D}$ vs link $\widehat{\eta} = X\widehat{\beta}$

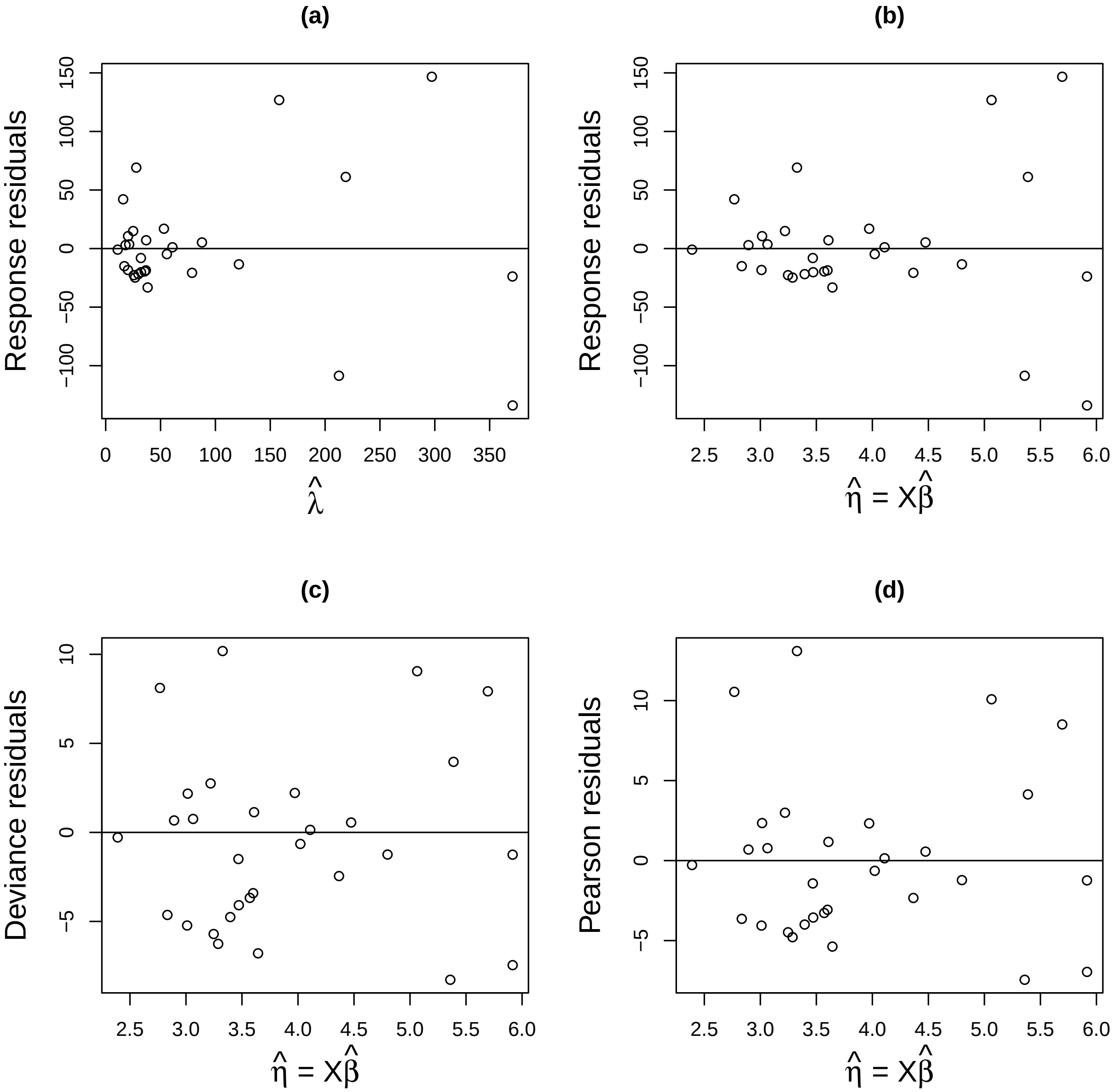
```
plot(residuals(fit1) ~
    predict(fit1, type="link"),
    xlab=expression(paste(hat(eta), " = X", hat(beta))),
    ylab="Deviance residuals", main="(c)")
abline(h=0)
```

(d) Plot Pearson residuals $r_{i,P}$ vs link $\widehat{\eta} = X\widehat{\beta}$

```
plot(residuals(fit1, type="pearson") ~
    predict(fit1, type="link"),
    xlab=expression(paste(hat(eta), " = X", hat(beta))),
    ylab="Pearson residuals", main="(d)")
abline(h=0)
```

- Interpretation of (c) and (d):
  - Y axis accounts for differences in variance
  - X axis better separates the predicted values
  - Systematic nonlinear relationship → lack of fit
    - * No apparent problems for this dataset
  - Large/nonconstant variance → violations of the assumed Poisson distribution
    - * Potential overdispersion

Residual Plots



- No obvious problematic trends in (c) or (d)

Model Diagnostics: Functional Form of Predictors

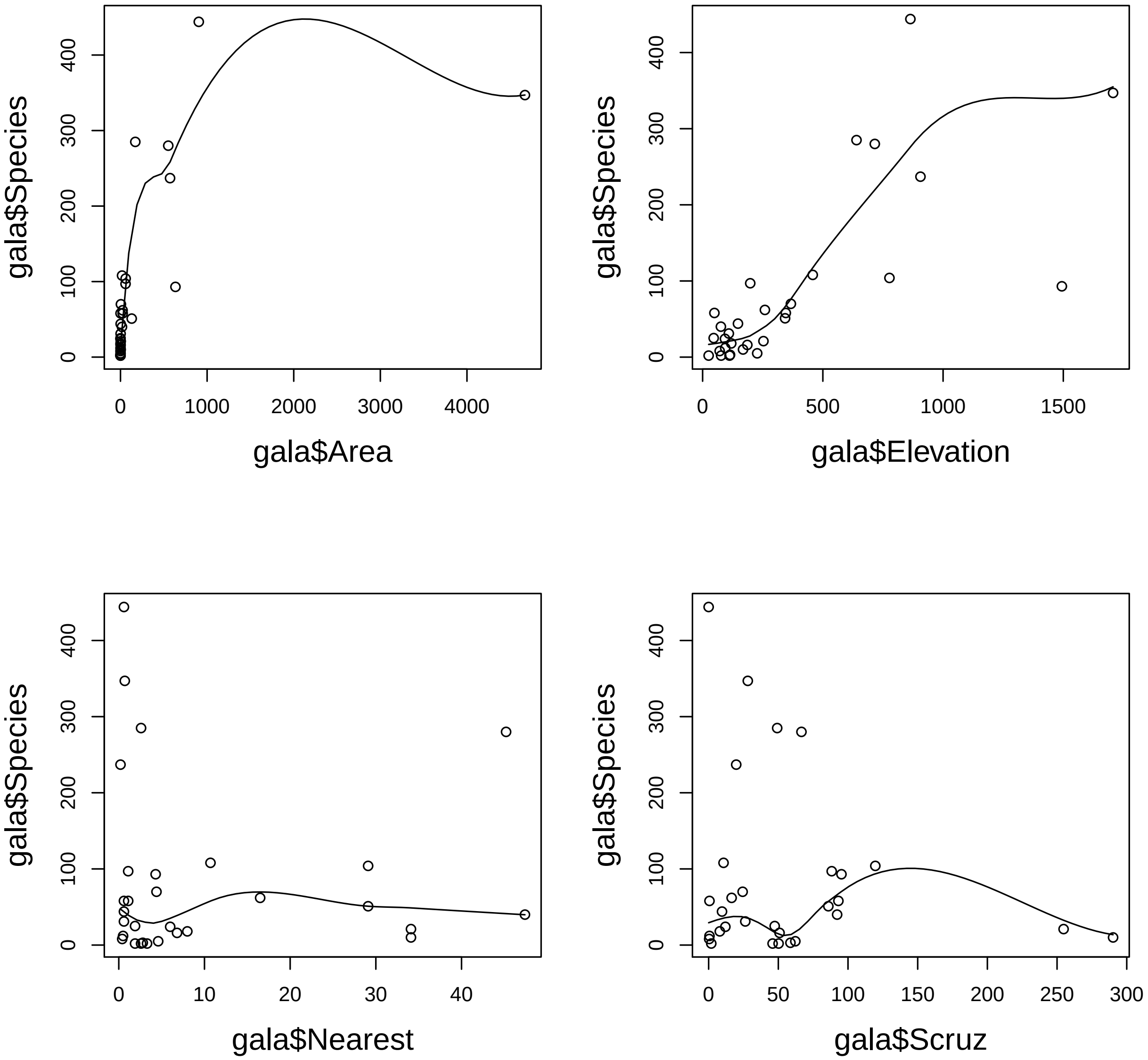
- As in linear regression, can plot Y against each predictor X_j

```
scatter.smooth(gala$Area, gala$Species)
scatter.smooth(gala$Elevation, gala$Species)
scatter.smooth(gala$Nearest, gala$Species)
scatter.smooth(gala$Scruz, gala$Species)
```

- The plots are of limited use, and may not show clear trends:
  - Lower response conts are more frequents
  - $Var\{Y\} = E\{Y\} \rightarrow$ large Y are unreliable

- Transformations can be helpful
  - Look for transformations for predictors even if there is no obvious problems in residual plots

Plotting Y vs X_j



- Most predictors indicate some non-linearity

Consider $log(Area)$

(a) $Area$ vs $Species$

```
plot(gala$Area, gala$Species, main="(a)")
```

(b) Use $log(Area)$

```
scatter.smooth(log(gala$Area), gala$Species,
    main="(b)")
```

(c) Account for the log link:
$log(Area)$ vs $Species$

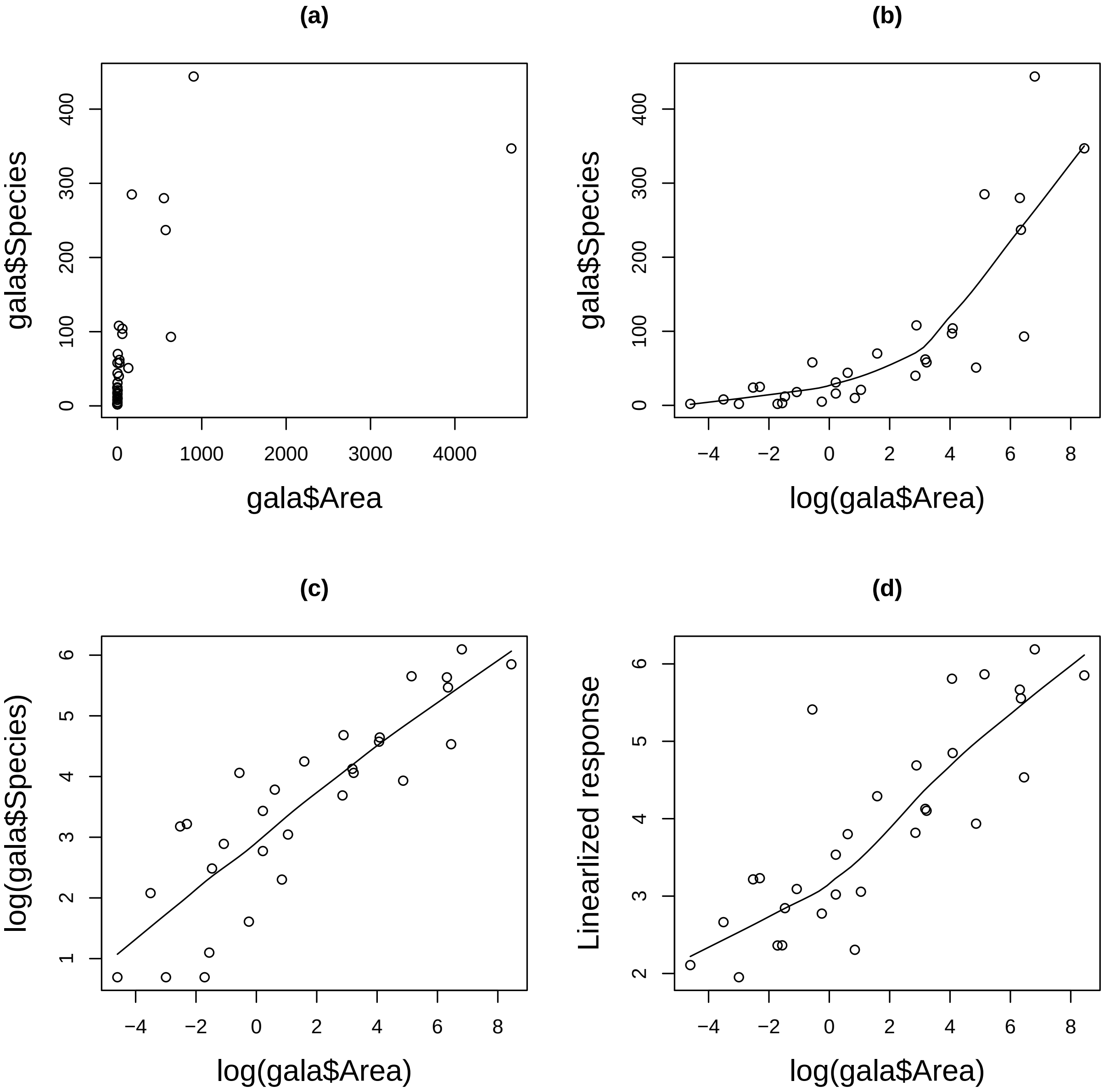
```
scatter.smooth(log(gala$Area), log(gala$Species),
    main="(c)")
```

(d) Faraway suggests plotting linearized response:
$Z_i = \mathbf{X}_i'\widehat{\beta} + (Y_i - \widehat{\lambda})/\widehat{\lambda}$

```
lambda<- predict(fit1, type="response")
z <- predict(fit1) + (gala$Species-lambda)/lambda
scatter.smooth(log(gala$Area), z,
    ylab="Linearlized response", main="(d)")
```

- log and the linearized response are similar

Consider $log(Area)$



- Log transformation appears appropriate

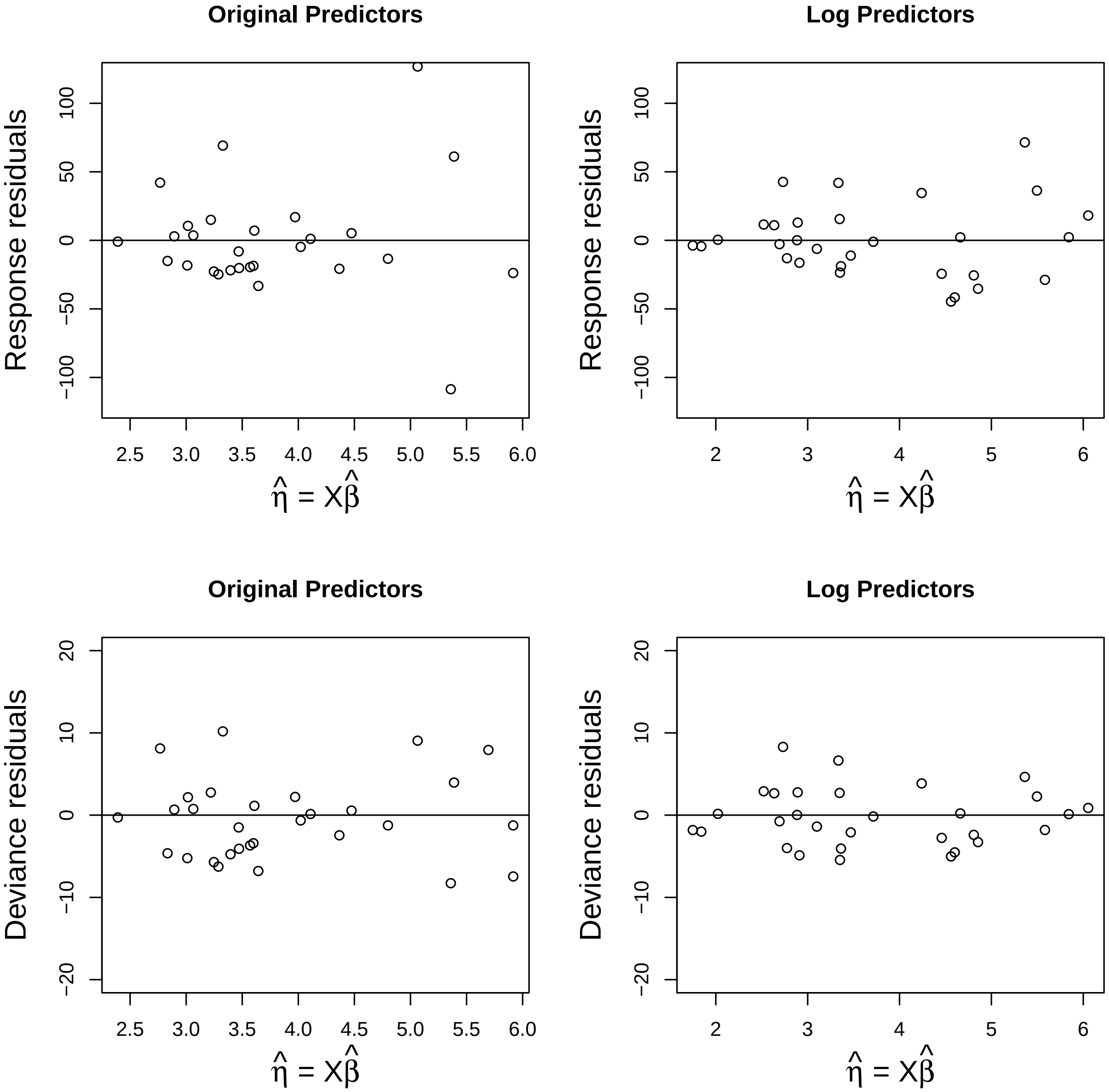
Residuals of Original and Log-Transformed Predictors

- Apply log transform to all predictors

```
>fit2 <- glm(Species~ log(Area)+log(Elevation)+
    log(Nearest)+log(Scruz+0.1)+log(Adjacent),
    family=poisson, data=gala)

>anova(fit1, fit2)

Analysis of Deviance Table
Model 1: Species ~ Area + Elevation +
    Nearest + Scruz + Adjacent
Model 2: Species ~ log(Area) + log(Elevation) +
    log(Nearest) + log(Scruz + 0.1) + log(Adjacent)

  Resid. Df Resid. Dev Df Deviance
1        24     716.85
2        24     359.12  0   357.72
```

  - obtain a substantial reduction in deviance
  - the model with all the transformed predictors yields a better overall fit
  - Next: visualize the change in plots of response and deviance residuals

Residuals of Original and Log-Transformed Predictors



- More compact residuals after the transform

Model Diagnostics: Partial Residuals and Link

(a) Partial contribution of a predictor:
Plot $Z_i - \mathbf{X}_i'\widehat{\beta} + X_{ij}\widehat{\beta}_j$ vs X_j

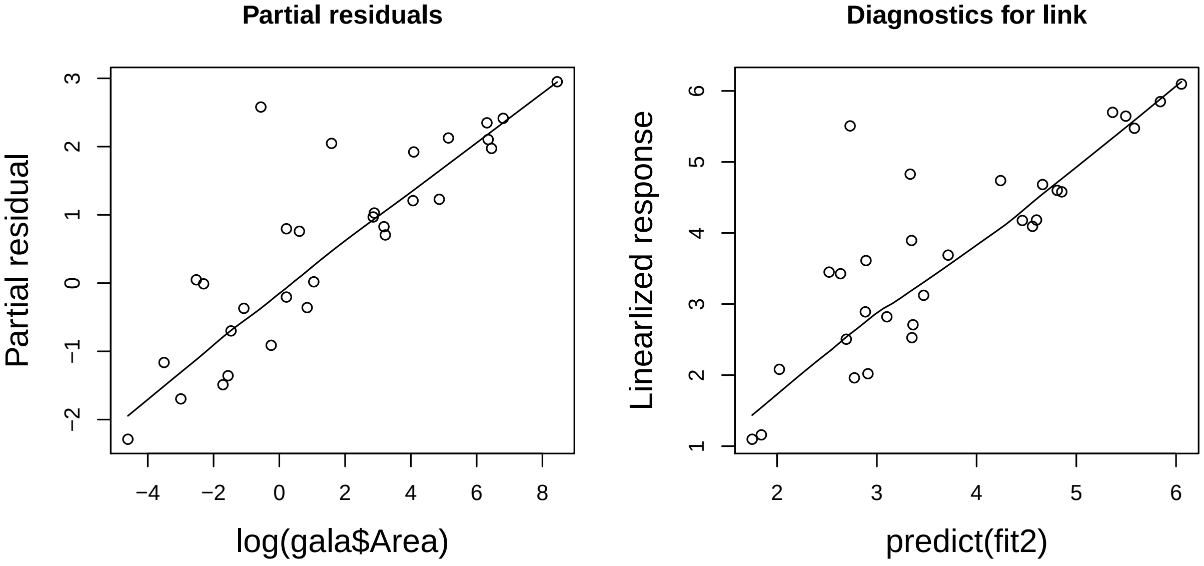
```
lambda <- predict(fit2, type="response")
u <- (gala$Species-lambda)/lambda +
    coef(fit2)[2]*log(gala$Area)
scatter.smooth(log(gala$Area), u,
    ylab="Partial residual", main="Partial residuals")
```

(b) Choice of link function:
Plot Z_i vs $\mathbf{X}_i'\widehat{\beta}$

```
z <- predict(fit2) + (gala$Species-lambda)/lambda
scatter.smooth(predict(fit2), z,
    ylab="Linearlized response",
    main="Diagnostics for link")
```

- No major problems in this dataset
  - Points roughly forming straight lines indicate no gross departures from the assumptions
  - Possible two outliers

Model Diagnostics: Partial Residuals and Link



- No major problems in this dataset
  - Points roughly forming straight lines indicate no gross departures from the assumptions
  - Two potential outliers

Model Diagnostics: Outliers

- Same concepts as in linear and logistic regression

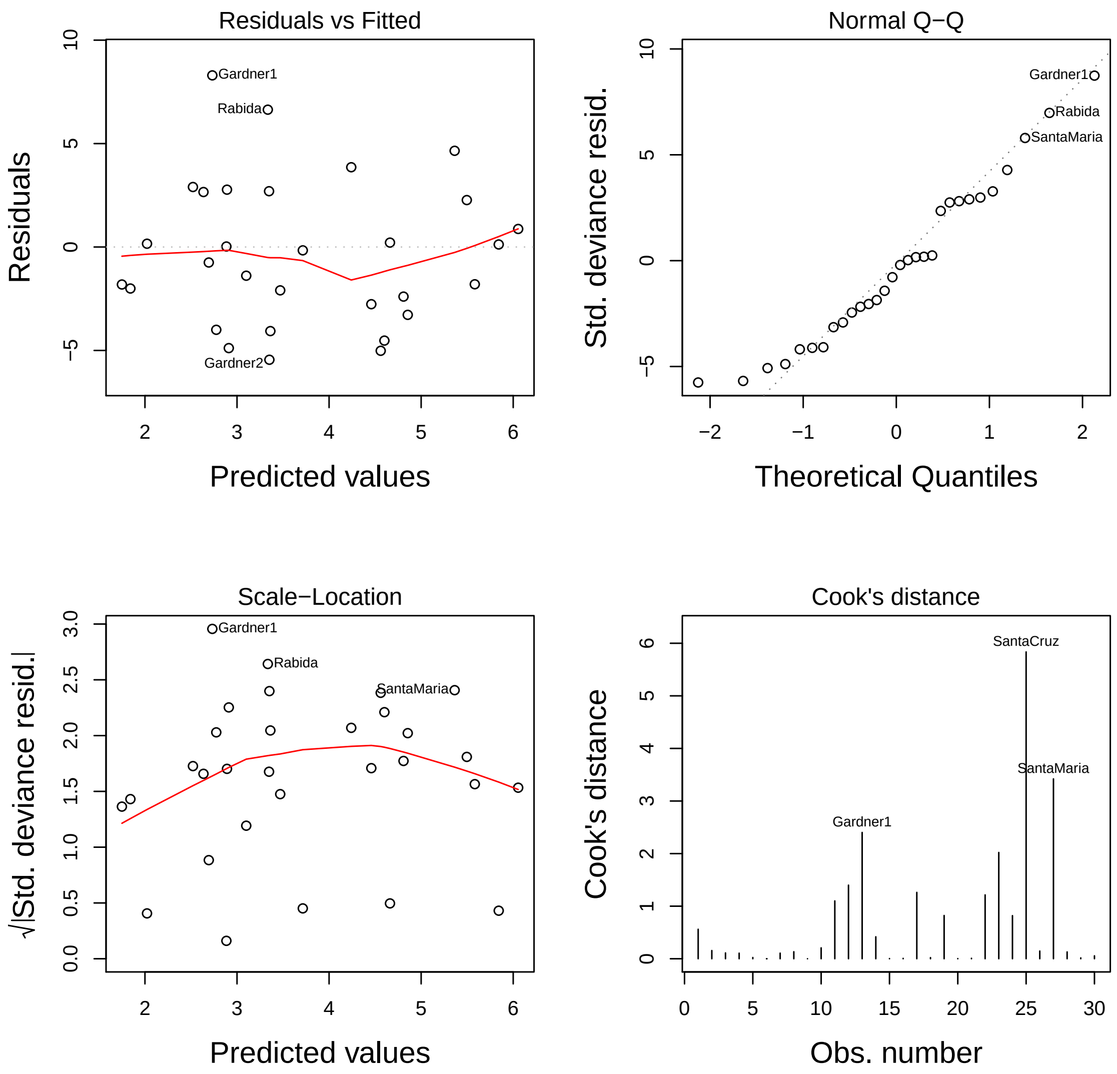
- Automated plots in R (next slide)

```
for (i in 1:4)
    plot(fit2, which=i)
```

- Manual plots in R (following slide)

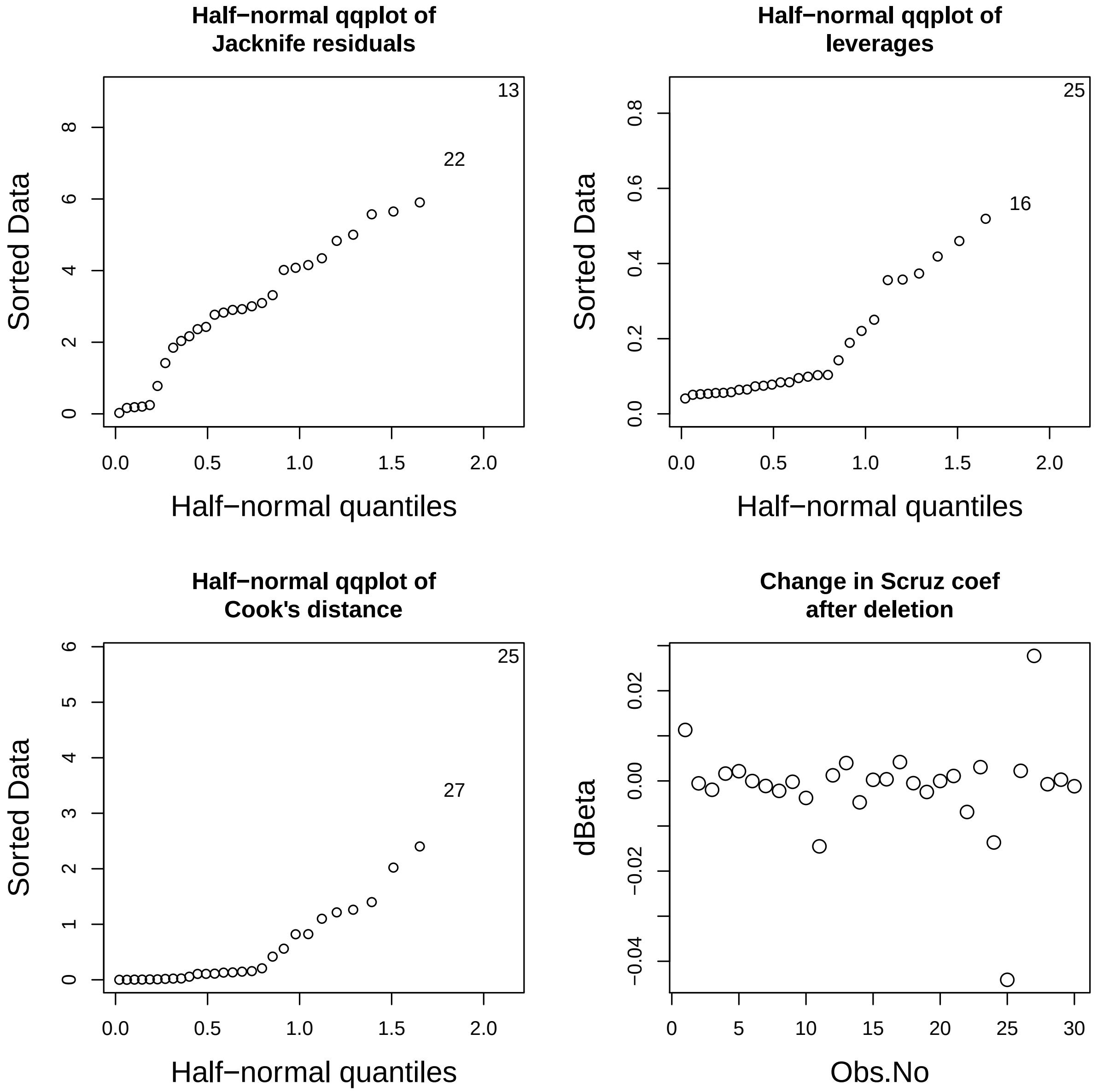
```
halfnorm( rstudent(fit2),
    main="Half-normal qqplot of Jacknife residuals")

halfnorm( influence(fit2)$hat,
    main="Half-normal qqplot of leverages")

halfnorm( cooks.distance(fit2),
    main="Half-normal qqplot of Cook’s distance")

plot( influence(fit2)$coef[,5], xlab="Obs.No",
    ylab="dBeta",
    main="Change in Scruz coef after deletion")
```

Diagnostics: Outliers



- 'Residuals' = deviance residuals;
'Predicted values' = $\mathbf{X}_i'\widehat{\beta}$;
'Std. deviance resid' = $r_{SD} = \frac{r_D}{\sqrt{\widehat{\phi}(1-h_{ii})}}$ (p. 124);
'Cook's distance' (p. 125).

Diagnostics: Outliers



- #25= 'Scruz'. The influence can be due to adding 0.1 at the log transform.

Overdispersion
(Faraway Ch. 3)

Overdispersion

- Suppose $Y \sim Poisson(\lambda)$
  - as for Binomial response, overdispersion arises in case of hierarchical or clustered observations

- Suppose λ itself is a r.v. with $E\{\lambda\} = \theta$.
  - $E\{Y\} = E\{E\{Y|\lambda\}\} = \theta$
  - $Var\{Y\} = E\{Var\{Y|\lambda\}\} + Var\{E\{Y|\lambda\}\}$

    $= \theta + Var\{\lambda\} > \theta$

- Quasipoisson distribution
  - $E\{Y\} = \lambda$
  - $Var\{Y\} = \phi\lambda$
  - Can estimate $\widehat{\phi}$: $\widehat{\phi} = \frac{1}{n-p}X^2 = \frac{1}{n-p}\sum_{i=1}^{n}\frac{(y_i-\widehat{\lambda}_i)^2}{\widehat{\lambda}_i}$

- Comparing nested models in presence of overdispersion:
  - Test H_0 : reduced model vs H_a : full model
  - $F = \frac{(D_0-D_1)/(df_0-df_1)}{\widehat{\phi}_1} \overset{approx.}{\sim} F(df_0 - df_1, df_1)$

Example: Galapagos Plants

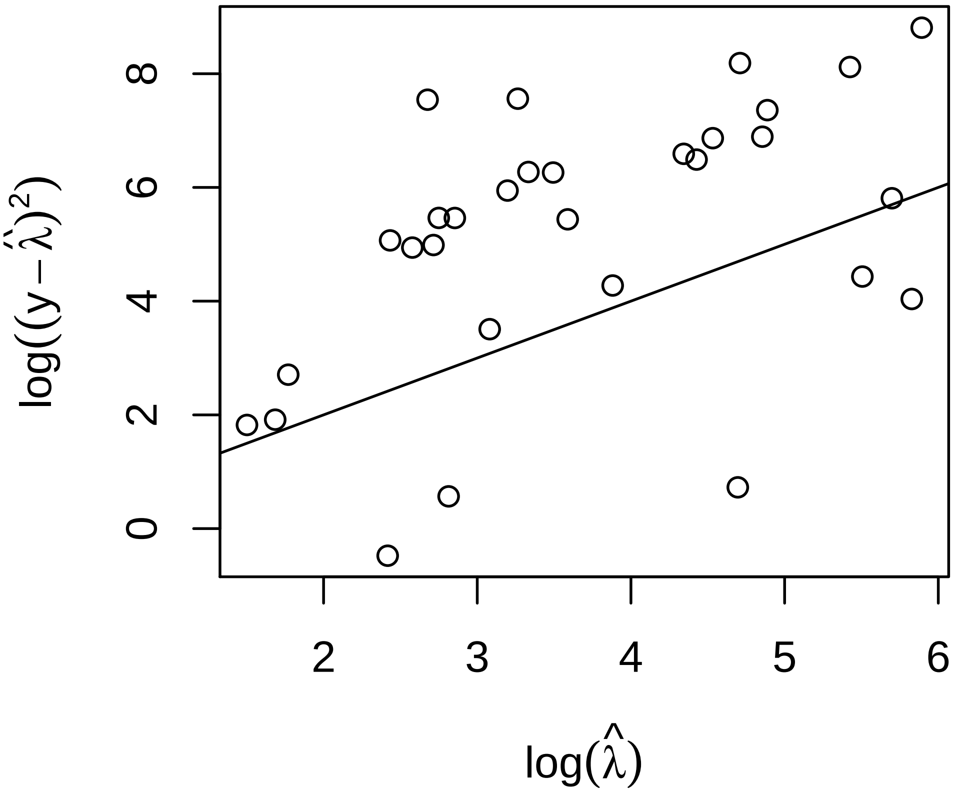
- Fit a simplified model with 2 predictors

```
> fit3 <- glm(Species~ log(Area)+log(Adjacent),
    family=poisson, data=gala)

Coefficients:
               Estimate Std. Error z value Pr(>|z|)
(Intercept)    3.276683   0.044132   74.25   <2e-16 ***
log(Area)      0.375029   0.008023   46.74   <2e-16 ***
log(Adjacent) -0.095747   0.006118  -15.65   <2e-16 ***
...
(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 3510.73  on 29  degrees of freedom
Residual deviance:  395.54  on 27  degrees of freedom
AIC: 562.37
```

- Log-log plot of mean vs variance (next slide)

```
lambda <- predict(fit3, type="response")
plot(log(lambda),
    log((gala$Species -lambda)^2),
    xlab=expression(hat(lambda)),
    ylab=expression((y - hat(lambda))^2))
abline(0,1)
```

Diagnostics: Overdispersion



- X axis: $log(\widehat{E\{Y\}})$ of each observation
- Y axis: $log(\widehat{Var\{Y\}})$ of each observation
- The variance is increasing with the mean
- The variance is larger than the mean
  → indicates overdispersion

Account for Overdispersion

- Estimate the dispersion parameter

```
> sum(residuals(fit3, type="pearson")^2) / fit3$df.res
[1] 16.52745   # >> 1, i.e. overdispersion present
```

- Quasipoisson model

```
> summary( glm(Species~ log(Area)+log(Adjacent),
    family=quasipoisson, data=gala) )

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)    3.27668    0.17942   18.26  < 2e-16 ***
log(Area)      0.37503    0.03262   11.50 6.56e-12 ***
log(Adjacent) -0.09575    0.02487   -3.85 0.000658 ***
...

(Dispersion parameter for quasipoisson family taken
    to be 16.52745)

    Null deviance: 3510.73  on 29  degrees of freedom
Residual deviance:  395.54  on 27  degrees of freedom
AIC: NA
```

- Same parameters, larger SE, weaker significance

Rate Models
(Faraway Ch. 3)

Motivation

- Each Y_i can represent a different interval in space or time
  - # of crimes in cities of different size
  - # of customers served by workers who work different hours
  - # cars running red light in different intersections

- Modeling Y_i as Poisson response is often more appropriate than Binomial
  - counts can be small as compared to the total (crimes)
  - the total may not be a count
    (workers, intersections)

- Goal: express a common effect of covariates on all Y_i, while accounting for differences in 'exposure'
  - 'exposure' needs to be a defined variable

Formulation

- Model Y_i as

$$\begin{aligned} Y_i \overset{ind}{\sim} & \; Poisson(\lambda_i),\; \lambda_i = exposure_i \, e^{\mathbf{x}_i'\beta}, \\ & i.e.\; log(\lambda_i) = log(exposure_i) + \mathbf{x}_i'\beta \end{aligned}$$

- The model is equivalent to using *exposure* as a predictor with the coefficient=1
  - *exposure* is often called an *offset* in this context

Example: Gamma Radiation (Faraway Sec. 3.2)

- Effect of gamma radiation on the numbers of chromosomal abnormalities (`ca`) in cells

- Different number of cells (`cells`, in hundreds) exposed to a dose and a rate of radiation

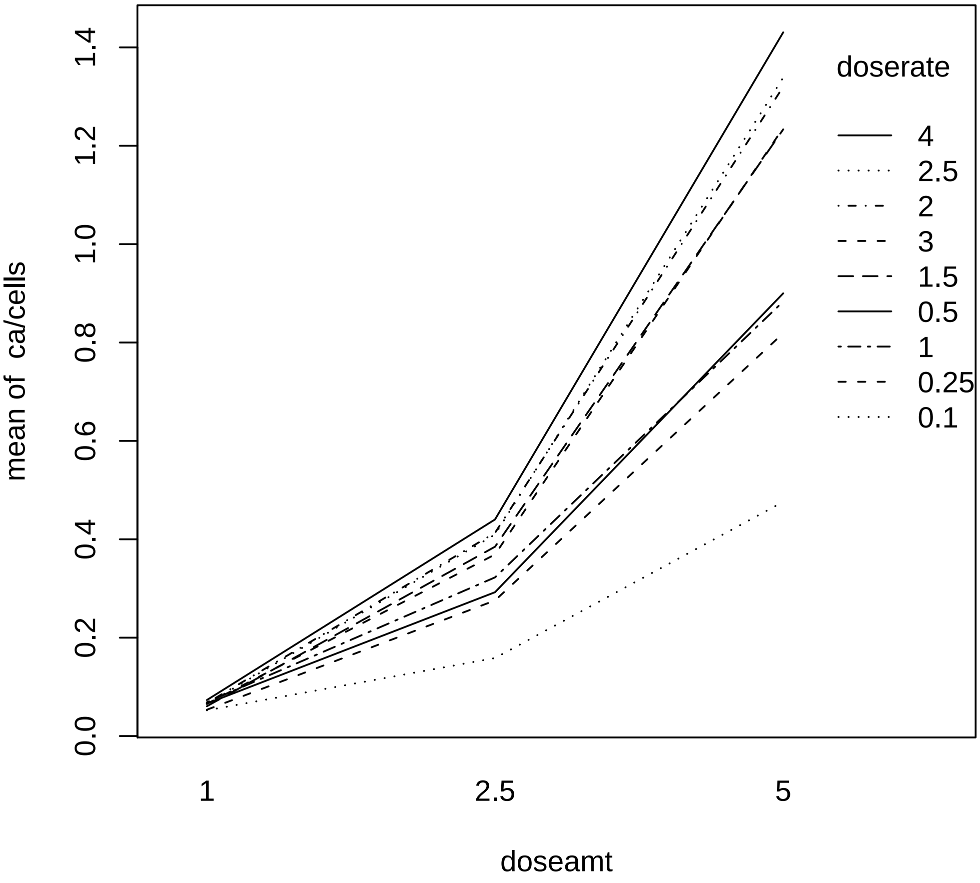
- `cells` can be viewed as 'exposure' variable

```
library(faraway)
data(dicentric)
?dicentric

> head(dicentric)
  cells  ca doseamt doserate
1   478  25       1     0.10
2  1907 102       1     0.25
3  2258 149       1     0.50
4  2329 160       1     1.00
5  1238  75       1     1.50
6  1491 100       1     2.00
```

Visualize the data

- Interaction plot: proportion of cells with abnormality
  - The effect of dose rate is multiplicative

```
> with(dicentric,
    interaction.plot(doseamt, doserate, ca/cells))
```



Model Without Offset

```
> # indicate that 'dose' is categorical:
> dicentric$doseF <- factor(dicentric$doseamt)

> # the total number of cells as an independent predictor
> fit4 <- glm(ca ˜ log(cells) + log(doserate)*doseF,
     family=poisson, data=dicentric)

...
Coefficients:
                      Estimate Std. Error z value Pr(>|z|)
(Intercept)           -2.76534    0.38116  -7.255 4.02e-13 ***
log(cells)             1.00252    0.05137  19.517  < 2e-16 ***
log(doserate)          0.07200    0.03547   2.030 0.042403 *
doseF2.5               1.62984    0.10273  15.866  < 2e-16 ***
doseF5                 2.76673    0.12287  22.517  < 2e-16 ***
log(doserate):doseF2.5 0.16111    0.04837   3.331 0.000866 ***
log(doserate):doseF5   0.19316    0.04299   4.493 7.03e-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: 211.15
```

- The coefficient of log(cells) is close to 1, and the offset is appropriate

Model With Offset

```
> fit5 <- glm(ca ~ offset(log(cells)) + log(doserate)*doseF,
    family=poisson, data=dicentric)

...
Coefficients:
                      Estimate Std. Error z value Pr(>|z|)
(Intercept)           -2.74671    0.03426 -80.165  < 2e-16 ***
log(doserate)          0.07178    0.03518   2.041 0.041299 *
doseF2.5               1.62542    0.04946  32.863  < 2e-16 ***
doseF5                 2.76109    0.04349  63.491  < 2e-16 ***
log(doserate):doseF2.5 0.16122    0.04830   3.338 0.000844 ***
log(doserate):doseF5   0.19350    0.04243   4.561  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: 209.16
```

- The coefficients did not change much from the previous model.

- Good residual deviance, no evidence of overdispersion.

Grouped vs Ungrouped Data

- Since $Y_i \overset{ind}{\sim} Poisson(\lambda_i),\ i = 1, \ldots,$
  $\rightarrow \sum_i Y_i \sim Poisson(\sum_i \lambda_i)$,
  we can model aggregate data
  - as in Binomial or Multinomial response, log-likelihood only involves sums of y_i with same covariate patterns
  - e.g. add total cells and counts of abnormalities for entries with same `doseamt` and `doserate`

- Rate models: individual vs grouped
  - different deviances
  - same parameter estimates
  - same comparison of nested models

- Models with no offset: indiv. vs grouped
  - different deviances
  - same parameters except intercept
  - same comparison of nested models

Allowing for Extra Variation:

Negative Binomial
(Faraway Sec. 3.3)

Negative Binomial: Distribution

- Independent trials with $P\{success\} = p$
  - $Z=$ the number of trials until kth success
  - $Z \sim NB(p,k),\ Z = k, k+1, \ldots$

- Probability distribution
  - $P\{Z = z\} = \left(\begin{array}{c} z-1 \\ k-1 \end{array} \right) p^k (a-p)^{z-k}$
  - $E\{Z\} = \frac{k}{p}$
  - $Var\{Z\} = \frac{k(1-p)}{p^2}$

- Obtained as the marginal distribution of $Y|\lambda \sim Poisson(\lambda)$ where $\lambda \sim G(k, \alpha)$
  - $P\{Y = y\} = \frac{1}{y!} \lambda^y e^{-\lambda},\ Y = 0, 1, \ldots$
  - $f(\lambda) = \frac{\alpha^k}{\Gamma(k)} \lambda^{k-1} e^{-\alpha\lambda},\ \lambda > 0$

Negative Binomial: Genesis

- Suppose $Y|\lambda \sim Poisson(\lambda)$, $\lambda \sim G(k, \alpha)$
  - Joint distribution of Y and λ:

$$p(Y = y,\, \lambda) = \frac{\alpha^k}{\Gamma(k)\, y!} \lambda^{y+k-1} e^{-(\alpha+1)\lambda}$$

  - Marginal distribution of Y (by integrating λ):

$$\begin{aligned} p(Y = y) &= \frac{\alpha^k}{\Gamma(k)\, y!} \int_0^\infty \lambda^{y+k-1} e^{-(\alpha+1)\lambda} d\lambda \\ &= \frac{\alpha^k}{\Gamma(k)\, y!} \frac{\Gamma(y+k)}{(\alpha+1)^{y+k}} \\ &= \frac{\Gamma(y+k)}{\Gamma(k)\Gamma(y+1)} \left(\frac{\alpha}{\alpha+1}\right)^k \left(\frac{1}{\alpha+1}\right)^y \\ &= \frac{(y+k-1)!}{(k-1)!y!} \left(\frac{\alpha}{\alpha+1}\right)^k \left(\frac{1}{\alpha+1}\right)^y \\ &= \left(\begin{array}{c} y+k-1 \\ k-1 \end{array}\right) \left(\frac{\alpha}{\alpha+1}\right)^k \left(\frac{1}{\alpha+1}\right)^y \end{aligned}$$

- $\Rightarrow\ Z = Y + k \sim NB(\frac{\alpha}{\alpha+1}\ ,\ k),\ Y = 0, 1, \ldots$

Negative Binomial: Model

- $Y+k \sim NB(\frac{\alpha}{\alpha+1}\ ,\ k),\ Y=0,1,\ldots$
  - $E\{Y\}=E\{Y+k\}-k=\frac{k}{\alpha/(\alpha+1)}-k=\frac{k}{\alpha}\ (\overset{denote}{=}\ \mu)$
  - $Var\{Y\}=Var\{Y+k\}=\frac{k(1-\alpha/(\alpha+1))}{\alpha^2/(\alpha+1)^2}=\frac{k}{\alpha}+\frac{k}{\alpha^2}$ $=\mu+\mu^2/k$ (= Poisson variance + extra component)

- Log-likelihood of $y_1,\ldots,y_n$

$$\sum_{i=1}^{n}\left(y_i\,log\frac{1}{\alpha_i+1}+k\,log\frac{\alpha_i}{\alpha_i+1}\right)+constant$$

$$\overset{k/\alpha=\mu}{=}\quad\sum_{i=1}^{n}\left(y_i\,log\frac{\mu_i}{k+\mu_i}+k\,log\frac{1}{k+\mu_i}\right)+constant$$

  - Can model $log\,\frac{\mu_i}{k+\mu_i}=\mathbf{x}_i'\beta$

- k is usually assumed same for all y_i
  - fixed *a priori*, or estimated from the data
  - assumes constant coefficient of variation of λ: $\sqrt{Var\{\lambda\}}/E\{\lambda\}=1/\sqrt{k}$

Example: Galapagos Plants

- Negative Binomial in an instance of the Exponential Family of distributions when k is fixed
- Fix k, use `glm`.

```
> fit.nb <- glm(Species~ log(Area)+log(Adjacent),
    family=negative.binomial(1), data=gala)

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)    3.27257    0.15304  21.384  < 2e-16 ***
log(Area)      0.35100    0.03773   9.304 6.52e-10 ***
log(Adjacent) -0.03204    0.04015  -0.798    0.432
...

(Dispersion parameter for Negative Binomial(1) family
    taken to be 0.4650222)

    Null deviance: 54.069  on 29  degrees of freedom
Residual deviance: 13.965  on 27  degrees of freedom
AIC: 292.97
```

Example: Galapagos Plants

- Use `glm.nb`, and estimate k from data

```
> fit.nb1 <- glm.nb(Species~ log(Area)+log(Adjacent),
    data=gala)

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)    3.27777    0.14495  22.613   <2e-16 ***
log(Area)      0.34973    0.03541   9.875   <2e-16 ***
log(Adjacent) -0.03316    0.03737  -0.887    0.375
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1   1

(Dispersion parameter for Negative Binomial(2.6196)
    family taken to be 1)

    Null deviance: 134.240  on 29  degrees of freedom
Residual deviance:  32.741  on 27  degrees of freedom
AIC: 284.99

              Theta:  2.620
          Std. Err.:  0.753
```

- Not a big difference in model fit in this example