# GLMs for Count Data

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Psych 6136

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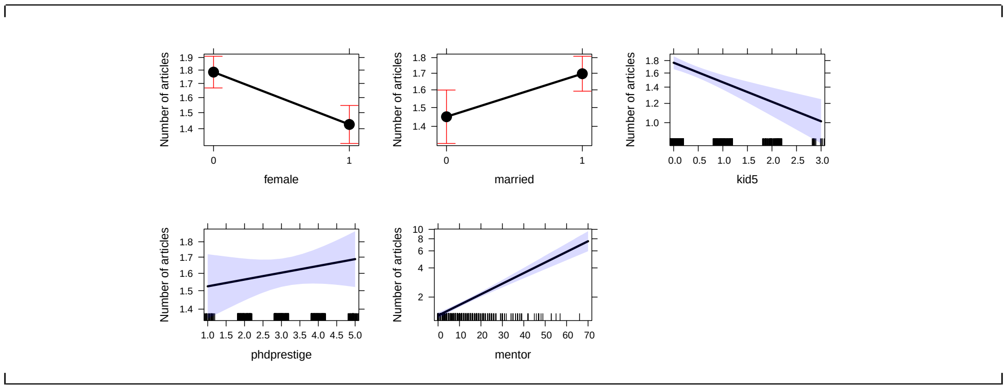



## Outline







## Generalized linear models

We have used generalized linear models (`glm()`) in two contexts so far:

**Loglinear models**

- the outcome variable is the vector of frequencies $\boldsymbol{y}$ in a table cross-classified by factors in a design matrix $\boldsymbol{X}$
- The model is expressed as a linear model for log $\boldsymbol{y}$

$$\log(\boldsymbol{y}) = \boldsymbol{X}\beta$$

- The random (or unexplained) variation is expressed as a Poisson distribution for $\mathcal{E}(\boldsymbol{y} \mid \boldsymbol{X})$





## Generalized linear models

**Logistic regression**

- the outcome variable is a categorical response $\boldsymbol{y}$, with predictors $\boldsymbol{X}$
- The model is expressed as a linear model for the log odds that $y = 1$ vs. $y = 0$.

$$\text{logit}(\boldsymbol{y}) \equiv \log\left[\frac{\Pr(y=1)}{\Pr(y=0)}\right] = \boldsymbol{X}\beta$$

- The random (or unexplained) variation is expressed as a Binomial distribution for $\mathcal{E}(\boldsymbol{y} \mid \boldsymbol{X})$

Hey, aren't these both very like the familiar, classical linear model,

$$\boldsymbol{y} = \boldsymbol{X}\beta + \boldsymbol{\epsilon}, \quad \boldsymbol{\epsilon} \sim \mathcal{N}(0, \sigma^2 \boldsymbol{I}) \quad ?$$

Yes, for some transformation, $g(\boldsymbol{y})$, and with different distributions!

# Generalized linear models

Nelder & Wedderburn (1972) said, "Let there be light!", a general*ized* linear model, encompassing them all, and many more. This has 3 components:

- A random component, specifying the conditional distribution of $\boldsymbol{y}$ given the explanatory variables in $\boldsymbol{X}$, with mean $\mathcal{E}(y_i \mid \boldsymbol{x}_i) = \mu_i$
  - The normal (Gaussian), binomial, and Poisson are already familiar
  - But, these are all members of an exponential family
  - GLMs now include an even wider family: negative-binomial and others
- The systematic component, a linear function of the predictors called the linear predictor

$$\boldsymbol{\eta} = \boldsymbol{X}\beta \quad \text{or} \quad \eta_i = \beta_0 + \beta_1 X_{i1} + \cdots + \beta_p X_{ip}$$

- An invertible link function, $g(\mu_i) = \eta_i = \boldsymbol{x}_i^\mathsf{T}\beta$ that transforms the expected value of the response to the linear predictor
  - The link function is invertable, so we can go back to the mean function $g^{-1}(\eta_i) = \mu_i$





# Mean functions

Standard GLM link functions and their inverses:

**Table 11.1:** Common link functions and their inverses used in generalized linear models

| Link name | Function: $\eta_i = g(\mu_i)$ | Inverse: $\mu_i = g^{-1}(\eta_i)$ |
|---|---|---|
| identity | $\mu_i$ | $\eta_i$ |
| square-root | $\sqrt{\mu_i}$ | $\eta_i^2$ |
| log | $\log_e(\mu_i)$ | $\exp(\eta_i)$ |
| inverse | $\mu_i^{-1}$ | $\eta_i^{-1}$ |
| inverse-square | $\mu_i^{-2}$ | $\eta_i^{-1/2}$ |
| logit | $\log_e \frac{\mu_i}{1-\mu_i}$ | $\frac{1}{1+\exp(-\eta_i)}$ |
| probit | $\Phi^{-1}(\mu_i)$ | $\Phi(\eta_i)$ |
| log-log | $-\log_e[-\log_e(\mu_i)]$ | $\exp[-\exp(-\eta_i)]$ |
| comp. log-log | $\log_e[-\log_e(1-\mu_i)]$ | $1-\exp[-\exp(\eta_i)]$ |

- The top section recognizes standard transformations often used with traditional linear models
- The bottom section is for binomial data, where $y_i$ represents an observed proportion in $n_i$ trials





# Canonical links and variance functions

- For every distribution family, there is a default, canonical link function
- Each one also specifies the expected relationship between mean and variance

**Table 11.2:** Common distributions in the exponential family used with generalized linear models and their canonical link and variance functions

| Family | Notation | Canonical link | Range of $y$ | Variance function, $\mathcal{V}(\mu \mid \eta)$ |
|---|---|---|---|---|
| Gaussian | $N(\mu, \sigma^2)$ | identity: $\mu$ | $(-\infty, +\infty)$ | $\phi$ |
| Poisson | $\text{Pois}(\mu)$ | $\log_e(\mu)$ | $0, 1, \ldots, \infty$ | $\mu$ |
| Negative-Binomial | $\text{NBin}(\mu, \theta)$ | $\log_e(\mu)$ | $0, 1, \ldots, \infty$ | $\mu + \mu^2/\theta$ |
| Binomial | $\text{Bin}(n, \mu)/n$ | $\text{logit}(\mu)$ | $\{0, 1, \ldots, n\}/n$ | $\mu(1-\mu)/n$ |
| Gamma | $G(\mu, \nu)$ | $\mu^{-1}$ | $(0, +\infty)$ | $\phi\mu^2$ |
| Inverse-Gaussian | $IG(\mu, \nu)$ | $\mu^2$ | $(0, +\infty)$ | $\phi\mu^3$ |





# Variance functions and over-dispersion

- In the classical Gaussian linear model, the conditional variance is constant, $\phi = \sigma_\epsilon^2$.
- For binomial data, the variance function is $\mathcal{V}(\mu_i) = \mu_i(1 - \mu_i)/n_i$, with $\phi$ fixed at 1
- In the Poisson family, $\mathcal{V}(\mu_i) = \mu_i$ and the dispersion parameter is fixed at $\phi = 1$.
- In practice, it is common for count data to exhibit overdispersion, meaning that $\mathcal{V}(\mu_i) > \mu_i$.
- One way to correct for this is to allow the dispersion parameter to be estimated from the data, giving what is called the ***quasi-Poisson*** family, with $\mathcal{V}(\mu_i) = \widehat{\phi}\mu_i$.

# Variance functions and over-dispersion

Overdispersion often results from failures of the assumptions of the model:

- supposedly independent observations may be correlated
- the probability of an event may not be constant, or
- it may vary with unmeasured or unmodeled variables





# ML Estimation

- GLMs are fit by the method of maximum likelihood.
- For the Poisson distribution with mean $\mu$, the probability that the random variable $Y$ takes values $y = 0, 1, 2, \ldots$ is

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

- In the GLM with a log link, the mean, $\mu_i$ depends on the predictors in $\boldsymbol{x}$ through

$$\log_e(\mu_i) = \boldsymbol{x}_i^\mathsf{T} \boldsymbol{\beta}$$

- The log-likelihood function (ignoring a constant) for $n$ independent observations has the form

$$\log_e \mathcal{L}(\boldsymbol{\beta}) = \sum^n \{ y_i \log_e(\mu_i) - \mu_i \}$$

- It can be shown that the maximum likelihood estimators are solutions to the estimating equations,

$$\boldsymbol{X}^\mathsf{T} \boldsymbol{y} = \boldsymbol{X}^\mathsf{T} \boldsymbol{\mu}$$

- The solutions are found by iteratively re-weighted least squares.





# Goodness of fit

- The residual deviance defined as twice the difference between the maximum log-likelihood for the *saturated model* that fits perfectly and maximized log-likelihood for the fitted model.

$$D(\boldsymbol{y}, \widehat{\boldsymbol{\mu}}) \equiv 2[\log_e \mathcal{L}(\boldsymbol{y}; \boldsymbol{y}) - \log_e \mathcal{L}(\boldsymbol{y}; \widehat{\boldsymbol{\mu}})] \ .$$

- For classical (Gaussian) linear models, this is just the residual sum of squares
- For Poisson models with a log link giving $\boldsymbol{\mu} = \exp(\boldsymbol{x}^\mathsf{T} \boldsymbol{\beta})$, the deviance takes the form

$$D(\boldsymbol{y}, \widehat{\boldsymbol{\mu}}) = 2 \sum_{i=1}^n \left[ y_i \log_e \left( \frac{y_i}{\widehat{\mu}_i} \right) - (y_i - \widehat{\mu}_i) \right] \ .$$

- For a GLM with $p$ parameters, both the Pearson and residual deviance statistics follow approximate $\chi^2_{n-p}$ distributions with $n - p$ degrees of freedom.





# GLMs for count data

- Typicaly, these are fit using: `glm( y   x1 + x2 + x3, family=poisson, data=mydata)`
- As in other linear models, the predictors $x_j$ can be discrete factors, quantitative variables, and so forth.
- This fixes the dispersion parameter $\phi$ to 1, assuming that the count variable `y` conditional on `x1`, `x2`, ... is Poisson distributed.
- It is possible to fit a quasi Poisson model, allowing $\phi$ to be estimated from the data. Specify: `family=quasipoisson`. This allows the variance to be proportional to the mean,

$$\mathcal{V}(y_i \,|\, \eta_i) = \phi \mu_i$$

- Another possibility is the negative-binomial model, which has

$$\mathcal{V}(y_i \,|\, \eta_i) = \mu_i + \mu_i^2 / \theta$$

# Example: Publications of PhD Candidates

Example 3.24 in DDAR gives data on the number of publications by PhD candidates in biochemistry in the last 3 years of study

```
data("PhdPubs", package = "vcdExtra")
table(PhdPubs$articles)

##
##   0   1   2   3   4   5   6   7   8   9  10  11  12  16  19
## 275 246 178  84  67  27  17  12   1   2   1   1   2   1   1
```

- Predictors are: gender, marital status, number of young children, prestige of the doctoral department, and number of publications by the student's mentor.





# Example: Publications of PhD Candidates

- Initially, ignore the predictors.
- For the Poisson, equivalent to an intercept-only model:
  `glm(articles ~ 1, data=PhdPubs, family="poisson")`

As a quick check on the Poisson assumption:

```
with(PhdPubs, c(mean=mean(articles),
                var=var(articles),
                ratio=var(articles)/mean(articles)))

##   mean    var  ratio
## 1.6929 3.7097 2.1914
```

The assumption that mean = variance could be met when we add predictors.

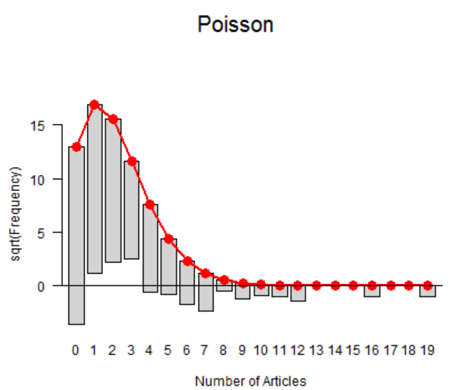


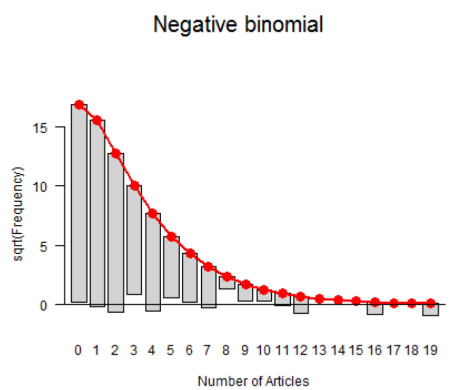


# Example: Publications of PhD Candidates

First, look at rootograms:

```
plot(goodfit(PhdPubs$articles), xlab = "Number of Articles",
     main = "Poisson")
plot(goodfit(PhdPubs$articles, type = "nbinomial"),
     xlab = "Number of Articles", main = "Negative binomial")
```




One reason the Poisson doesn't fit: excess 0s (some never published?)





# Fitting the Poisson model

Fit the model with all main effects:

```
# predictors: female, married, kid5, phdprestige, mentor
phd.pois  <- glm(articles ~ ., data=PhdPubs, family=poisson)
Anova(phd.pois)

## Analysis of Deviance Table (Type II tests)
##
## Response: articles
##             LR Chisq Df Pr(>Chisq)
## female          17.1  1    3.6e-05 ***
## married          6.6  1       0.01 *
## kid5            22.1  1    2.6e-06 ***
## phdprestige      1.0  1       0.32
## mentor         126.8  1    < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Only `phdprestige` is NS; it does no harm to keep it, for now.

# Interpreting coefficients

$\beta_j$ is the increment in log (articles) for a 1 unit change in $x_j$; $\exp(\beta_j)$ is the multiple of articles:

```
round(cbind(beta = coef(phd.pois),
            expbeta = exp(coef(phd.pois)),
            pct = 100 * (exp(coef(phd.pois)) - 1)), 3)

##                beta expbeta     pct
## (Intercept)   0.266   1.304  30.425
## female1      -0.224   0.799 -20.102
## married1      0.157   1.170  17.037
## kid5         -0.185   0.831 -16.882
## phdprestige   0.025   1.026   2.570
## mentor        0.025   1.026   2.555
```

Thus:

- females publish -0.224 fewer log (articles), or 0.8 $\times$ that of males
- married publish 0.157 more log (articles); or 1.17 $\times$ unmarried (17% increase)
- each additional young child decreases this by 0.185; or 0.831 $\times$ articles (16.9% decrease)
- each mentor pub multiplies student pub by 1.026, a 2.6% increase

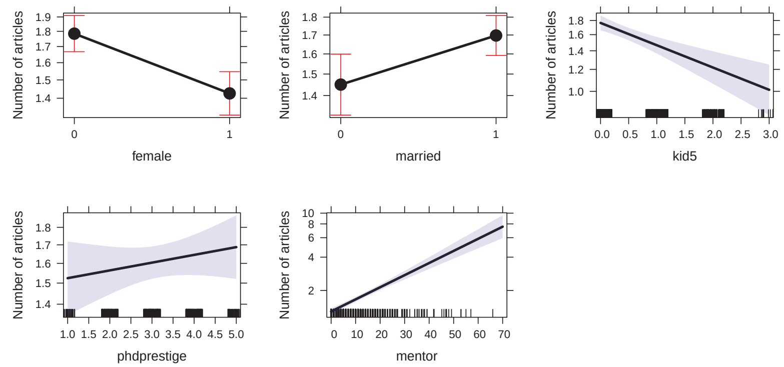




# Effect plots

As usual, we can understand the fitted model from predicted values for the model effects:

```
library(effects); plot(allEffects(phd.pois))
```




These are better visual summaries for a model than a table of coefficients.





# Model diagnostics

Diagnostic tests for count data GLMs are similar to those used for classical linear models

- Test for presence of interactions
  - Fit model(s) with some or all two-way interactions
- Non-linear effects of quantitative predictors?
  - Component-plus-residual plots— `car::crPlot()` are useful here
- Outliers? Influential observations?
  - `car::influencePlot()` is your friend

For count data models, we should also check for over-dispersion. This is similar to homogeneity of variance checks in `lm()`





# Testing for interactions

As a quick check for interactions, fit the model with all two-way terms

```
phd.pois1 <- update(phd.pois, . ~ .^2)
Anova(phd.pois1)

## Analysis of Deviance Table (Type II tests)
##
## Response: articles
##                     LR Chisq Df Pr(>Chisq)
## female                  14.5  1    0.00014 ***
## married                  6.2  1    0.01277 *
## kid5                    19.5  1    9.8e-06 ***
## phdprestige              1.0  1    0.32655
## mentor                 128.1  1    < 2e-16 ***
## female:married           0.3  1    0.60995
## female:kid5              0.1  1    0.72929
## female:phdprestige       0.2  1    0.63574
## female:mentor            0.0  1    0.91260
## married:kid5                  0
## married:phdprestige      1.7  1    0.19153
## married:mentor           1.2  1    0.28203
## kid5:phdprestige         0.2  1    0.68523
## kid5:mentor              2.8  1    0.09290 .
## phdprestige:mentor       3.8  1    0.05094 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

# Compare models I

Compare models: LR tests for nested models (**anova()**), and AIC/BIC (**LRstats()**)

```
anova(phd.pois, phd.pois1, test="Chisq")

## Analysis of Deviance Table
##
## Model 1: articles ~ female + married + kid5 + phdprestige + mentor
## Model 2: articles ~ female + married + kid5 + phdprestige + mentor + fe
##     female:kid5 + female:phdprestige + female:mentor + married:kid5 +
##     married:phdprestige + married:mentor + kid5:phdprestige +
##     kid5:mentor + phdprestige:mentor
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1       909       1634
## 2       900       1618  9     15.2    0.086 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```





# Compare models II

```
LRstats(phd.pois, phd.pois1)

## Likelihood summary table:
##              AIC  BIC LR Chisq  Df Pr(>Chisq)
## phd.pois  3313 3342     1634 909     <2e-16 ***
## phd.pois1 3316 3388     1618 900     <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- There seems to be no reason to include interactions in the model
- We might want to re-visit this, after examining other models for the basic count distribution (quasi-poisson, negative-binomial)

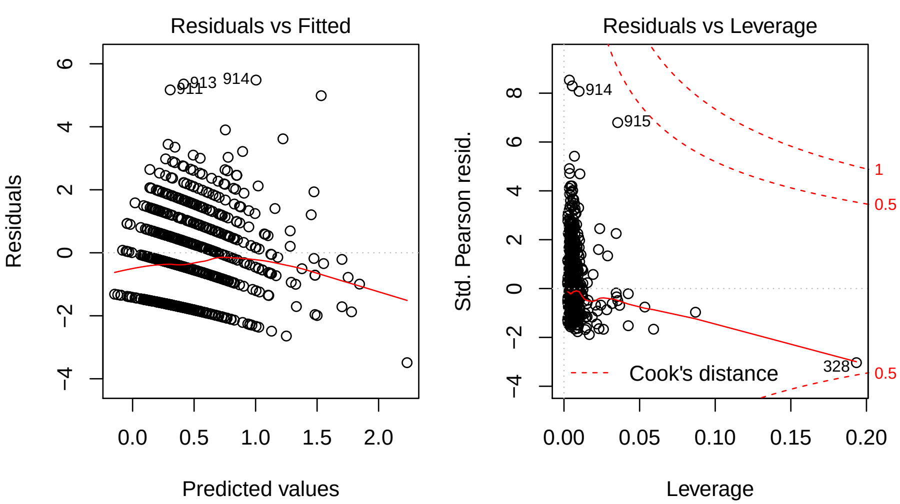




# Basic model plots

Only two of the standard model plots are informative for count data models

```
plot(phd.pois, which=c(1,5))
```







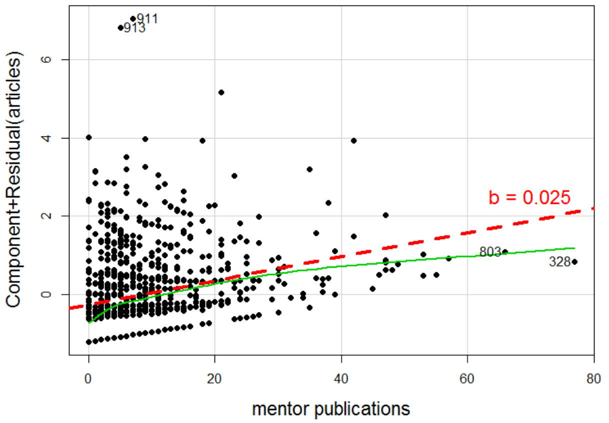

# Nonlinearity diagnostics

- Non-linear relations are difficult to assess in marginal plots, because they don't control (or adjust) for other predictors
- Component-plus-residual plots (also called partial residual plots) can show non-linear relations for numeric predictors
  - These graph the value of $\hat{\beta}_i x_i + \text{residual}_i$ vs. the predictor, $x_i$.
  - In this plot, the slope of the points is the coefficient, $\hat{\beta}_i$ in the full model
  - The residual is $y_i - \hat{y}_i$ in the full model
- A non-parametric (e.g., **loess()**) smooth makes it easy to detect non-linearity

# Nonlinearity diagnostics: car::crPlot()

Is the relationship between articles published by the student and the mentor adequately represented as linear?

```
crPlot(phd.pois, "mentor", pch=16, lwd=4, id.n=2)
```








# Residuals I

Several types of residuals can be defined based on the Pearson and deviance goodness-of-fit measures

- the ***Pearson residual*** is the case-wise contribution to Pearson $\chi^2$

$$r_i^P = \frac{y_i - \widehat{\mu}_i}{\sqrt{\widehat{\mathcal{V}}(y_i)}}$$

- the ***deviance residual*** is the signed square root of the contribution to the deviance $G^2$

$$r_i^D = \text{sign}(y_i - \widehat{\mu}_i)\sqrt{d_i}$$

- Both of these have standardized forms that correct for conditional variance and leverage, and have approx. $\mathcal{N}(0,1)$ distributions.

$$\widetilde{r}_i^P = \frac{r_i^P}{\sqrt{\widehat{\phi}(1-h_i)}}$$

$$\widetilde{r}_i^D = \frac{r_i^D}{\sqrt{\widehat{\phi}(1-h_i)}}$$





# Residuals II

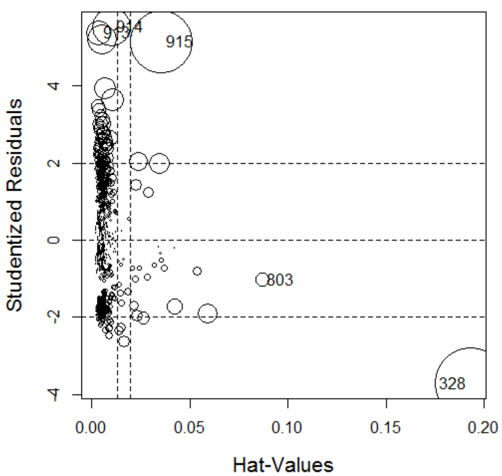
- The most useful is the ***studentized residual*** (or deletion residual), `rstudent()` in R. This estimates the standardized residual resulting from omitting each observation in turn. An approximation is:

$$\widetilde{r}_i^S = \text{sign}(y_i - \widehat{\mu}_i)\sqrt{(1-h_i)(\widetilde{r}_i^D)^2 + h_i(\widetilde{r}_i^P)^2} \ .$$





# Outliers, leverage and influence




```
influencePlot(phd.pois)
```

- Several observations (913–915) stand out with large + residuals
- One observation (328) has a large leverage
- Why are they unusual? Do they affect our conclusions?
- Look back at data & decide what to do!

# Outliers, leverage and influence

At the very least, we should look at these observations in the data:

```
PhdPubs[c(328, 913:915),]

##     articles female married kid5 phdprestige mentor
## 328        1      0       1    1           2     77
## 913       12      0       1    1           2      5
## 914       16      0       1    0           2     21
## 915       19      0       1    0           2     42
```

- case 328: Mentor published 77 papers! Student, only 1
- 913–915: all published $>>$ predicted





# Outlier test

- A formal test for outliers can be based on the studentized residuals, `rstudent(model)`, using the standard normal distribution for *p*-values
- A Bonferroni correction should be applied, because interest focuses on the largest *n* absolute residuals.

For the Poisson model, 4 observations are nominated as large + outliers:

```
outlierTest(phd.pois, cutoff=0.001)

##     rstudent unadjusted p-value Bonferonni p
## 914   5.5423         2.9852e-08   2.7315e-05
## 913   5.3821         7.3617e-08   6.7360e-05
## 911   5.2074         1.9153e-07   1.7525e-04
## 915   5.1504         2.5988e-07   2.3779e-04
```





# Overdispersion

- The Poisson model for counts assumes $\mathcal{V}(\mu_i) = \mu_i$, i.e., the dispersion parameter $\phi = 1$
- But often, the counts exhibit greater variance than the Poisson distribution allows, $\mathcal{V}(\mu_i) > \mu_i$ or $\phi > 1$
  - The observations (counts) may not be independent (clustering)
  - The probability of an "event" may not be constant
  - There may be unmeasured influences, not accounted for in the model
  - These effects are sometimes called "unmodeled heterogeneity"
- The consequences are:
  - Standard errors of the coefficients, $\mathrm{se}(\widehat{\beta}_j)$ are optimistically small
  - Wald tests, $z_j = \widehat{\beta}_j / \mathrm{se}(\widehat{\beta}_j)$, are too large, and thus overly liberal.





# Testing overdispersion

- Statistical tests for overdispersion are described in DDAR §11.3.4.
- They test $H_0 : \mathcal{V}(y) = \mu$, vs. $H_1$ that variance depends on the mean according to some function $f(\mu)$

$$\mathcal{V}(y) = \mu + \alpha \times f(\mu)$$

- This is implemented in `dispersiontest()` in the AER package.
  - If significant, overdispersion should not be ignored
  - Alternatively, you can try fitting a more general model to see what difference it makes.

# Overdispersion: Quasi-poisson models

- Instead, we can fit another version of the model in which the dispersion $\phi$ is a free parameter, estimated along with the other coefficients. That is, the conditional variance is allowed to be

$$\mathcal{V}(y_i \mid \eta_i) = \phi \mu_i$$

- This model is fit with `glm()` using `family=quasipoisson`
  - the estimated coefficients $\widehat{\beta}$ are unchanged
  - the standard errors are multiplied by $\widehat{\phi}^{1/2}$
  - peace, order, and good governance is restored!





# Overdispersion: Quasi-poisson models

- One estimate of the dispersion parameter is the residual deviance divided by degrees of freedom $\widehat{\phi} = D(\boldsymbol{y}, \widehat{\mu})/df$
- The Pearson $\chi^2$ statistic has better statistical properties and is more commonly used

$$\widehat{\phi} = \frac{X_P^2}{n-p} = \sum_{i=1}^{n} \frac{(y_i - \widehat{\mu}_i)^2}{\widehat{\mu}_i} / (n-p) \quad .$$

For the PhdPubs data, these estimates are quite similar: about 80% overdispersion

```
with(phd.pois, deviance / df.residual)

## [1] 1.7971

sum(residuals(phd.pois, type = "pearson")^2) / phd.pois$df.residual

## [1] 1.8304
```





# Fitting the quasi-poisson model

The quasi-Poisson model is can be fit using `glm()` as:

```
phd.qpois <- glm(articles ~ ., data=PhdPubs, family=quasipoisson)
```

The dispersion parameter estimate $\widehat{\phi}$ can be obtained as follows:

```
(phi <- summary(phd.qpois)$dispersion)

## [1] 1.8304
```

This is much better than variance/mean ratio of 2.91 calculated for the marginal distribution ignoring the predictors.



Coefficients unchanged; std. errors multiplied by $\widehat{\phi}^{1/2} = \sqrt{1.83} = 1.35$.

```
summary(phd.qpois)

##
## Call:
## glm(formula = articles ~ ., family = quasipoisson, data = PhdPubs)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -3.488  -1.538  -0.365   0.577   5.483
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.26562    0.13478    1.97  0.04906 *
## female1     -0.22442    0.07384   -3.04  0.00244 **
## married1     0.15732    0.08287    1.90  0.05795 .
## kid5        -0.18491    0.05427   -3.41  0.00069 ***
## phdprestige  0.02538    0.03419    0.74  0.45815
## mentor       0.02523    0.00275    9.19  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasipoisson family taken to be 1.8304)
##
##     Null deviance: 1817.4  on 914  degrees of freedom
## Residual deviance: 1633.6  on 909  degrees of freedom
## AIC: NA
##
## Number of Fisher Scoring iterations: 5
```

# The negative-binomial model

- The negative-binomial model is a different generalization of the Poisson that allows for over-dispersion
- Mathematically, it allows the mean $\mu \mid \boldsymbol{x}_i$ to vary across observations as a gamma distribution with a shape parameter $\theta$.
- The variance function, $\mathcal{V}(y_i) = \mu_i + \mu_i^2/\theta$, allows the variance of $y$ to increase more rapidly than the mean.
- Another parameterization uses $\alpha = 1/\theta$

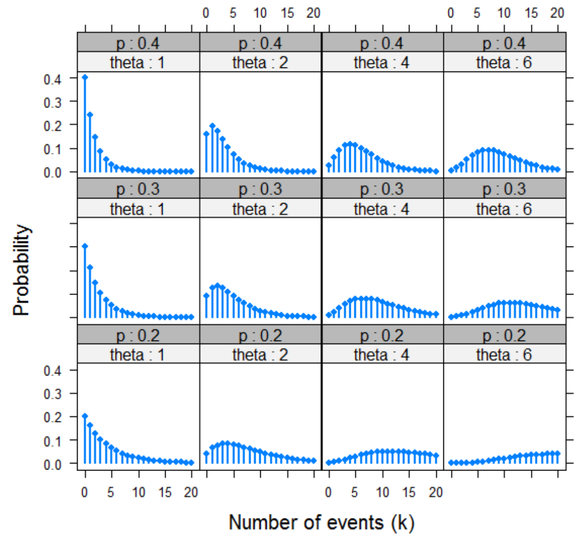
$$\mathcal{V}(y_i) = \mu_i + \mu_i^2/\theta = \mu_i + \alpha\mu_i^2 \ ,$$

- As $\alpha \to 0$, $\mathcal{V}(y_i) \to \mu_i$ and the negative-binomial converges to the Poisson.





# The negative-binomial model




Overdispersion decreases as $\theta$ increases





# The negative-binomial model: Fitting

- For fixed $\theta$, the negative-binomial is another special case of the GLM
- This is handled in the MASS package, with `family=negative.binomial(theta)`
- But most often, $\theta$ is unknown, and must be estimated from the data
- This is implemented in `glm.nb()` in the MASS package.

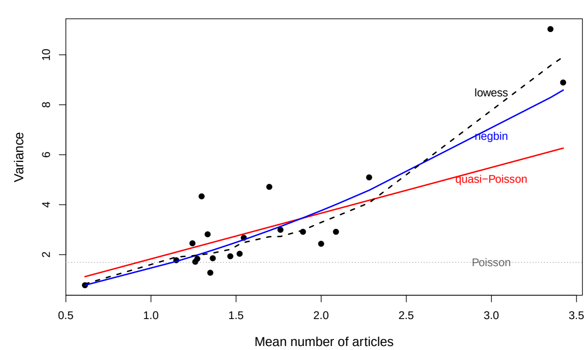
```
library(MASS)
phd.nbin  <- glm.nb(articles ~ ., data=PhdPubs)
```





# Visualizing the mean variance relation

One way to see the difference among models is to plot the variance vs. mean for grouped values of the fitted linear predictor.

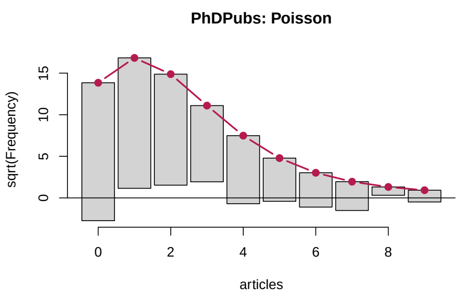


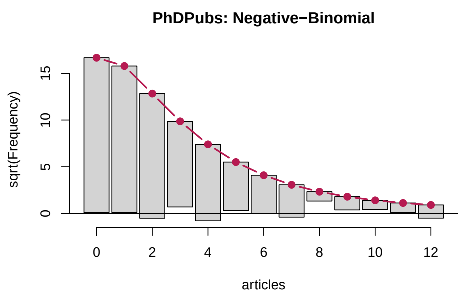

- The smoothed (loess) curve gives the empirical mean–variance relationship
- Also plot the theoretical mean–variance from different models
- For PhdPubs, the data is most similar to the negative-binomial
- The models differ most for those with $> 3$ articles

# Visualizing goodness-of-fit

The countreg package extends the **rootogram()** function to work with fitted models:

```
countreg::rootogram(phd.pois, main="PhDPubs: Poisson")
countreg::rootogram(phd.nbin, main="PhDPubs: Negative-Binomial")
```




The Poisson model shows a systematic, wave-like pattern with excess zeros, too few observed frequencies for counts of 1–3.





# What difference does it make?

The NB is certainly a better fit than the Poisson; the QP cannot be distinguished by standard tests

```
LRstats(phd.pois, phd.qpois, phd.nbin)

## Likelihood summary table:
##             AIC  BIC LR Chisq  Df Pr(>Chisq)
## phd.pois  3313 3342     1634 909     <2e-16 ***
## phd.qpois                    909
## phd.nbin  3135 3169     1004 909      0.015 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Can also compare standard errors of the coefficients:

```
##              pois qpois  nbin
## (Intercept) 0.100 0.135 0.133
## female1     0.055 0.074 0.073
## married1    0.061 0.083 0.082
## kid5        0.040 0.054 0.053
## phdprestige 0.025 0.034 0.034
## mentor      0.002 0.003 0.003
```





# What have we learned?

A summary for an article to this point would use the result of negative-binomial model, from `summary(phd.nbin)`

- The number of articles published by these PhD candidates is most strongly influenced by publications of their mentor
- Increasing young children (`kids5`) results in fewer publications.
- Being married is marginally non-significant— don't interpret
- The prestige of the university doesn't make a difference
- There are still some remaining doubts:
  - Several cases (328, 913–915) appeared unusual in earlier diagnostic plots. Refit without them to see if any conclusions change.
  - The NB model seems to account for the zero counts— students who never published.
  - Is there a better way?





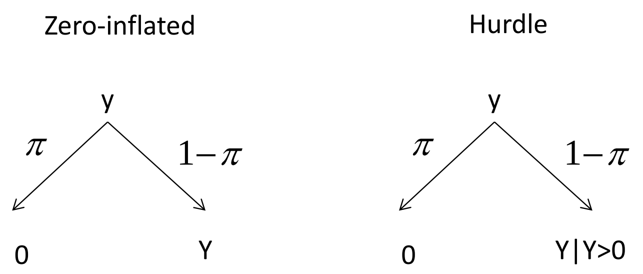
# Excess zero counts

- A common problem in count data models is that many sets of data have more observed zero counts than the (quasi) Poisson or NB models can handle.
  - In the PhdPubs data, 275 of 915 (30%) candidates published zilch, bupkis
  - The expected count of 0 articles in the Poisson model is only 191 (21%)
- Maybe there are two types of students giving zero counts:
  - Those who never intend to publish (non-academic career path?)
  - The rest, who do intend to publish, but have not yet done so
  - This suggests the idea of zero inflation
- An alternative idea is that there is some hurdle to overcome before attaining a positive count, e.g., external pressure from the mentor.

Beyond simply identifying this as a problem of lack-of-fit, understanding the reasons for excess zero counts can contribute to a more complete explanation of the phenomenon of interest.

# Two model types for excess zeros

- ***zero-inflated models***: The responses with $y_i = 0$ arise from a mixture of structural, always 0 values, with $\Pr(y_i = 0) = \pi_i$ and the rest, which are random 0s, with $\Pr(y_i = 0) = 1 - \pi_i$
- ***hurdle models***: One process determines whether $y_i = 0$ with $\Pr(y_i = 0) = \pi_i$. A second process determines the distribution of values of positive counts, $\Pr(y_i \mid y_i > 0)$








# Zero-inflated models

The zero-inflated Poisson (ZIP) model has two components:

- A logistic regression model for membership in the unobserved (latent) class of those for whom $y_i$ is necessarily zero

$$\text{logit}(\pi_i) = \boldsymbol{z}_i^{\mathsf{T}} \boldsymbol{\gamma} = \gamma_0 + \gamma_1 z_{i1} + \gamma_2 z_{i2} + \cdots + \gamma_q z_{iq} \ .$$

- A Poisson model for the other class (e.g., “publishers”), for whom $y_i$ may be 0 or positive.

$$\log_e \ \mu(y_i \mid \boldsymbol{x}_i) = \boldsymbol{x}_i^{\mathsf{T}} \boldsymbol{\beta} = \beta_0 + \beta_1 x_{i1} + \beta_2 x_{i2} + \cdots + \beta_q x_{ip} \ .$$

In applications, the same predictors can be (and often are) used in both models ($\boldsymbol{x} = \boldsymbol{z}$).





# Zero-inflated models

In the ZIP model, the probabilities of observing counts of $y_i = 0$ and $y_i > 0$ are:

$$\begin{aligned} \Pr(y_i = 0 \mid \boldsymbol{x}, \boldsymbol{z}) &= \pi_i + (1 - \pi_i) e^{-\mu_i} \\ \Pr(y_i \mid \boldsymbol{x}, \boldsymbol{z}) &= (1 - \pi_i) \times \left[ \frac{\mu_i{}^{y_i} e^{-\mu_i}}{y_i!} \right], \qquad y_i \geq 0 \ . \end{aligned}$$

The conditional expectation and variance of $y_i$ then are:

$$\begin{aligned} \mathcal{E}(y_i) &= (1 - \pi_i) \, \mu_i \\ \mathcal{V}(y_i) &= (1 - \pi_i) \, \mu_i (1 + \mu_i \pi_i) \ . \end{aligned}$$

When $\pi_i > 0$, the mean of $y$ is always less than $\mu_i$; the variance of $y$ is greater than its mean by a dispersion factor of $(1 + \mu_i \pi_i)$.
The model for the count variable could also be negative-binomial, giving a *zero-inflated negative-binomial* (ZINB) model using $\text{NBin}(\mu, \theta)$





# Zero-inflated data

Generate some random data from $\text{Pois}(3) = \text{ZIP}(3, \pi = 0)$ and $\text{ZIP}(3, \pi = 0.3)$. This uses **`rzipois()`** in the VGAM.

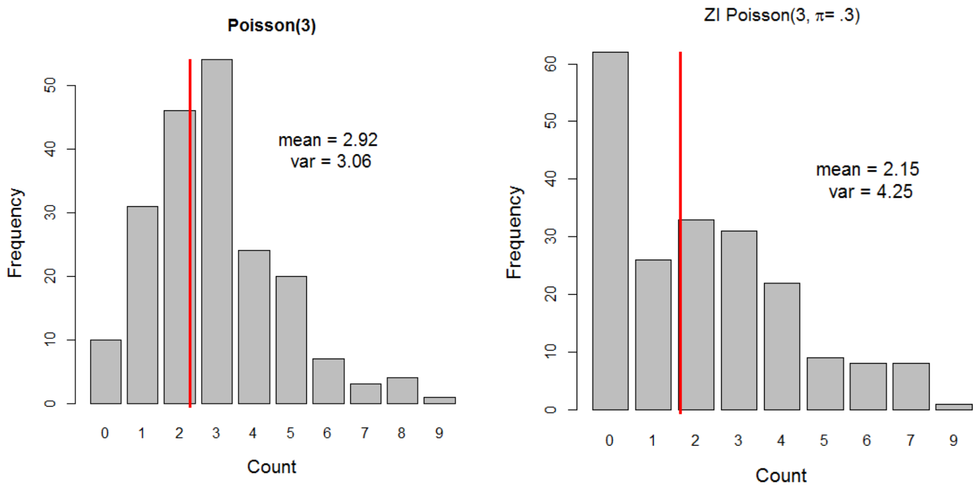
```
library(VGAM)
set.seed(1234)
data1 <- rzipois(200, 3, 0)
data2 <- rzipois(200, 3, .3)
```

Tables of the counts:

```
table(data1)

## data1
##  0  1  2  3  4  5  6  7  8  9
## 10 31 46 54 24 20  7  3  4  1

table(data2)

## data2
##  0  1  2  3  4  5  6  7  9
## 62 26 33 31 22  9  8  8  1
```

# Zero-inflated data

Bar plots of the counts:




The 30% extra zeros decrease the mean and inflate the variance





# Hurdle models

The Hurdle model also has two components:

- A logistic regression model, for the probability that $y_i = 0$ vs. $y_i > 0$

$$\text{logit}\left[\frac{\Pr(y_i = 0)}{\Pr(y_i > 0)}\right] = \boldsymbol{z}_i^{\mathsf{T}} \gamma = \gamma_0 + \gamma_1 z_{i1} + \gamma_2 z_{i2} + \cdots + \gamma_q z_{iq} \ .$$

- A model for the positive counts, taken as a left-truncated Poisson or negative-binomial, excluding the zero counts
- Comparing the ZIP and Hurdle models:
  - In ZIP models, the first (latent) process generates extra zeros (with probability $\pi_i$).
  - In Hurdle models, $y_i = 0$ and $y_i > 0$ are fully observed. The first process generates all the zeros.





# Fitting ZIP and Hurdle models

In R, these models can be fit using the pscl and countreg packages.

countreg is more mature, but is only available on R-Forge, not on CRAN. Use:

```
install.packages("countreg", repos="http://R-Forge.R-project.org")
```

The functions have the following arguments:

```
zeroinfl(formula, data, subset, na.action, weights, offset,
         dist = c("poisson", "negbin", "geometric", "binomial"),
          ...)

hurdle(formula, data, subset, na.action, weights, offset,
         dist = c("poisson", "negbin", "geometric", "binomial"),
          ...)
```

The formula, `y ~ x1 + x2 + ...` uses the same predictors for both models.
Using `y ~ x1 + x2 + ...| z1 + z2 + ...` allows separate predictors for the 0 submodel.

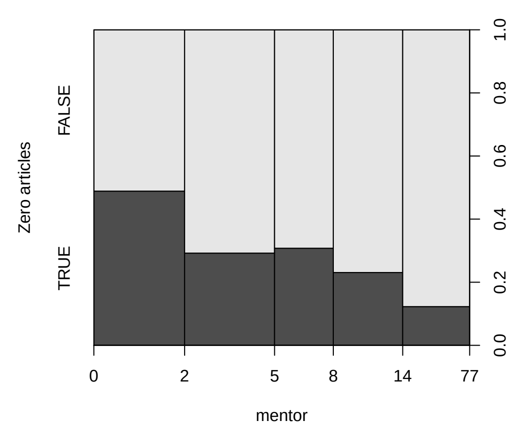




# Visualizing zero counts

It is often useful to plot the data for the binary distinction between $y_i = 0$ vs. $y_i > 0$ as in logistic regression models.

```
plot(factor(articles==0) ~ mentor, data=PhdPubs,
        ylevels=2:1, ylab="Zero articles",
        breaks=quantile(mentor, probs=seq(0,1,.2)), cex.lab=1.25)
```



# Example: Phd Publications

Just to illustrate, we fit all four models, the combinations of (ZI, Hurdle) $\times$ (Poisson, NBin) to the PhdPubs data.

For simplicity, we use all predictors for both the zero model and the non-zero model.

```
library(countreg)
phd.zip <- zeroinfl(articles ~ ., data=PhdPubs, dist="poisson")
phd.znb <- zeroinfl(articles ~ ., data=PhdPubs, dist="negbin")

phd.hp  <- hurdle(articles ~ ., data=PhdPubs, dist="poisson")
phd.hnb <- hurdle(articles ~ ., data=PhdPubs, dist="negbin")
```





# Example: Phd Publications

Compare models, sorting by BIC:

```
LRstats(phd.pois, phd.nbin, phd.zip, phd.znb, phd.hp, phd.hnb,
        sortby="BIC")

## Likelihood summary table:
##            AIC  BIC LR Chisq  Df Pr(>Chisq)
## phd.pois 3313 3342     3301 909     <2e-16 ***
## phd.hp   3235 3292     3211 903     <2e-16 ***
## phd.zip  3234 3291     3210 903     <2e-16 ***
## phd.hnb  3131 3194     3105 902     <2e-16 ***
## phd.znb  3126 3188     3100 902     <2e-16 ***
## phd.nbin 3135 3169     3121 909     <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The standard negative binomial looks best by BIC. Why do you think this is?





Test the coefficients in the ZIP model using **`lmtest::coeftest()`**

```
library(lmtest)
coeftest(phd.zip)

##
## t test of coefficients:
##
##                    Estimate Std. Error t value Pr(>|t|)
## count_(Intercept)  0.59918    0.11861    5.05  5.3e-07 ***
## count_female1     -0.20879    0.06353   -3.29   0.0011 **
## count_married1     0.10623    0.07097    1.50   0.1348
## count_kid5        -0.14271    0.04744   -3.01   0.0027 **
## count_phdprestige  0.00700    0.02981    0.23   0.8145
## count_mentor       0.01785    0.00233    7.65  5.3e-14 ***
## zero_(Intercept)  -0.56332    0.49405   -1.14   0.2545
## zero_female1       0.10816    0.28173    0.38   0.7011
## zero_married1     -0.35558    0.31796   -1.12   0.2637
## zero_kid5          0.21974    0.19658    1.12   0.2639
## zero_phdprestige  -0.00537    0.14118   -0.04   0.9697
## zero_mentor       -0.13313    0.04643   -2.87   0.0042 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Only `mentor` is significant for the zero model!





Re-fit the ZIP and ZNB models using only `mentor` for the zero models:

```
phd.zip1 <- zeroinfl(articles ~ .| mentor, data=PhdPubs, dist="poisson")
phd.znb1 <- zeroinfl(articles ~ .| mentor, data=PhdPubs, dist="negbin")
```

Compare again:

```
LRstats(phd.pois, phd.nbin, phd.zip, phd.znb, phd.hp, phd.hnb,
        phd.zip1, phd.znb1, sortby="BIC")

## Likelihood summary table:
##            AIC  BIC LR Chisq  Df Pr(>Chisq)
## phd.pois 3313 3342     3301 909     <2e-16 ***
## phd.hp   3235 3292     3211 903     <2e-16 ***
## phd.zip  3234 3291     3210 903     <2e-16 ***
## phd.zip1 3227 3266     3211 907     <2e-16 ***
## phd.hnb  3131 3194     3105 902     <2e-16 ***
## phd.znb  3126 3188     3100 902     <2e-16 ***
## phd.nbin 3135 3169     3121 909     <2e-16 ***
## phd.znb1 3124 3168     3106 906     <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Now, the `phd.znb1` model is best by BIC. Why?

# Model interpretation: Coefficients

Ignoring NS coefficients in the revised ZNB model (`phd.znb1`)

```
coef(phd.znb1)[c(1,2,4,6,7,8)]

## count_(Intercept)      count_female1         count_kid5       count_mentor
##          0.357194          -0.211573          -0.167527           0.024057
##  zero_(Intercept)        zero_mentor
##         -0.816912          -0.608024
```

- Count model:

$$\log(\text{articles}) = 0.357 - 0.21 \text{ female} - 0.17 \text{ kids5} + 0.024 \text{ mentor}$$

- Zero model:

$$\text{logit}(\text{articles} = 0) = -0.817 - 0.608 \text{ mentor}$$

Can you describe these in words?

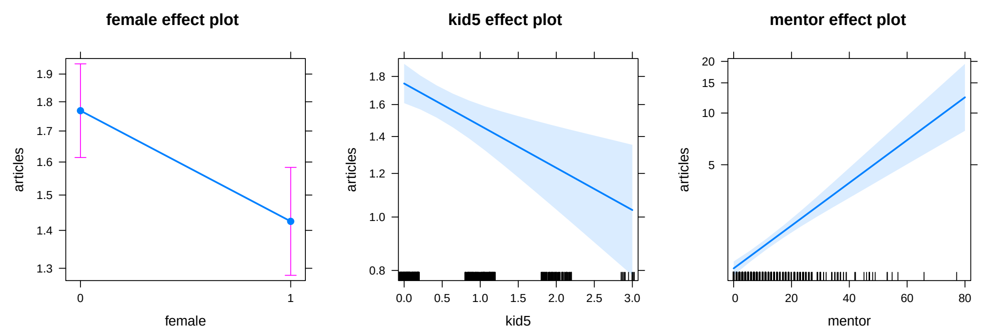




# Model interpretation: Effect plots

- The effects package cannot yet handle zero-inflated or hurdle models.
- But the fitted values don't differ very much among these models
- Here, I use the `phd.nbin` model, and just show the effects for the important terms

```
plot(allEffects(phd.nbin)[c(1,3,5)], rows=1, cols=3)
```



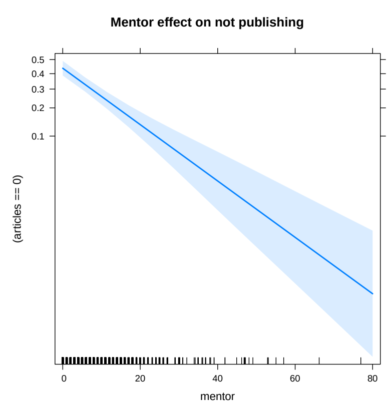





The ZIP sub-model for the zero counts ("did not publish") can also be interpreted visually

- As an approximation, fit a separate logistic model for `articles==0`
- The effect plot for that gives an interpretation of the zero model.

```
phd.zero <- glm((articles==0) ~ mentor, data=PhdPubs, family=binomial)
plot(allEffects(phd.zero), main="Mentor effect on not publishing")
```








# What have we learned?

- The simple Poisson regression model fits very badly
  - Standard errors do not reflect overdispersion
  - Inference about model effects is compromised by overly liberal tests
- The quasi-poisson model corrects for overdispersion.
  - But doesn't account for excess 0s
- The negative-binomial model provides valid tests and fits the 0 counts well.
  - But it doesn't provide any insight into why there are so many 0s
- The ZIP and ZNB models fit well, and account for the 0s.
  - But they lose here on BIC (and AIC) measures, because they have 2× the number of parameters.
  - For simplicity, I have slighted the analogous hurdle models

# What have we learned?

- The revised ZNB model (`phd.znb1`), with only `mentor` predicting 0s, wins on parsimony, and has a simple interpretation.
  - The log odds that a student does not publish decrease by 0.61 for every article published by the mentor
  - Each mentor pub increases student publications by about 2.5%
  - $\Rightarrow$ Encourage or help your supervisor to publish!
  - (Or, choose a high publishing one.)
- For this data set, the main substantive interpretation and predicted effects are similar across models. But details matter!
- In data sets where there are substantive reasons for excess 0s, the ZI and hurdle models provide different explanations.
  - It is not always just a matter of model fit!
  - Hurdle models make the distinction between 0 and $>$ 0 more explicit
  - In ZI models, the interpretation of the mean count is clearer.

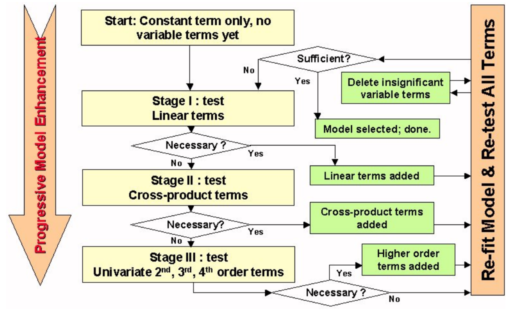


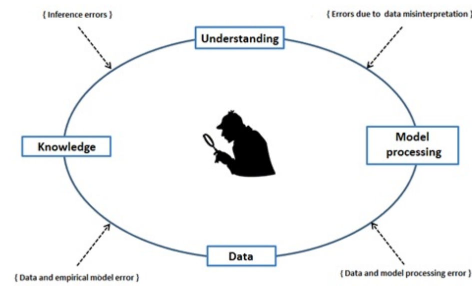


# What have we forgotten?

*"All models are wrong, but some are useful"* — GEP Box

- Model building and model criticism go hand in hand
- But they don't form a linear series of steps, or steps you can put into a flow chart
- Sometimes, you have to go back and re-visit decisions made earlier: Re-think $\rightarrow$ Re-fit $\rightarrow$ Re-interpret








# What I missed

- In the initial model, `phdprestige` was NS; I decided to keep it
- In the check for two way interactions, the interaction `phdprestige:mentor` was borderline ($p = 0.051$)
  - I did a global test for all interactions together.
  - That was NS ($p = 0.08$), so I decided to dismiss them all.
  - (I wanted to keep the model simple, to go on to other topics: overdispersion, models for excess zeros.)





# Back to square two

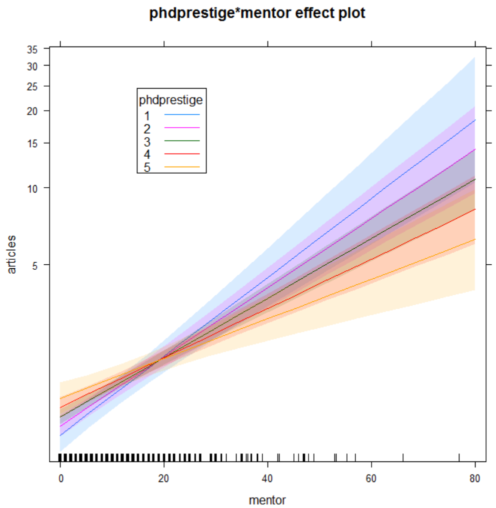
- A question in class made me reconsider the `phdprestige:mentor` interaction
- Perhaps the effect of `mentor` varied with `phdprestige`?

Try this, starting with the negative-binomial model, `phd.nbin`

```
phd.nbin2 <- update(phd.nbin, . ~ . + phdprestige:mentor)
Anova(phd.nbin2)

## Analysis of Deviance Table (Type II tests)
##
## Response: articles
##                    LR Chisq Df Pr(>Chisq)
## female                  9.1  1     0.0026 **
## married                 3.1  1     0.0762 .
## kid5                   10.7  1     0.0011 **
## phdprestige             0.7  1     0.3921
## mentor                 72.8  1     <2e-16 ***
## phdprestige:mentor      5.6  1     0.0179 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

# Visualize the interaction

```
phd.effnb2 <- allEffects(phd.nbin2)
plot(phd.effnb2[4], x.var="mentor", multiline=TRUE, ci.style="bands", ...)
```



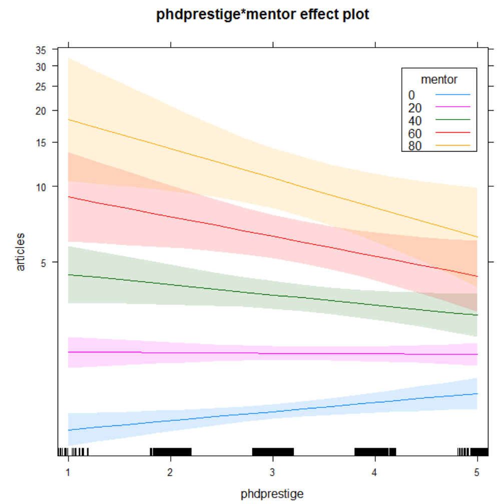

- An effect plot for `phdprestige*mentor` shows the average over other predictors
- This plot, with `mentor` on the X-axis shows that the slope for `mentor` increases with higher prestige of the student's university





# Visualize the interaction— the other way

```
plot(phd.effnb2[4], multiline=TRUE, ci.style="bands", ...)
```




- This plot, with `phdprestige` on the X-axis shows that the slopes change sign depending on the value of `mentor`.
- It explains why the main effect of `phdprestige` is near 0.
- The widths of the confidence bands indicate model uncertainty— they get wider as `mentor` pubs increase, and `phdprestige` differs from average.





# What else is there?

The `PhdPubs` example was rather simple, in that:

- There were only a few predictors
  - Model selection methods could be based on simple `Anova()`s or `coeftest()`s
  - No need for more complex model selection methods, or cross-validation
- Of the quantitative predictors, only `mentor` and `kids5` had important effects
  - The effects of `mentor` and `kids5` were sufficiently linear.
  - No need to try polynomial (`poly(mentor, 2)`) or other non-linear effects
- There turned out to be one important interaction.
  - In Psychology, these are often called moderator effects
  - Interpretation is often based on post-hoc tests of simple slopes or regions of significance
  - Interpretation is usually simplified in effect plots.





# What else is there?

- The response variable, `articles` was measured only once, i.e., there is no longitudinal aspect of the analysis.
  - One extension might track the number of articles published by these students over stages in their career.
  - Longitudinal models are examples of multilevel or hierarchical linear models
  - Well-developed for classical, Gaussian models (`lm()` →`lme4::lmer()` )
  - These models are being extended to GLMs for count data (e.g., `lme4::glmer()` )
- There was only one response variable: `articles`.
  - Another extension might analyse articles published and the number of job interviews upon graduation as a multivariate GLM
  - Yet another, could try to develop a structural equation model (SEM) or path analysis model, with a variable like "hired within one year?" as the ultimate binary outcome.