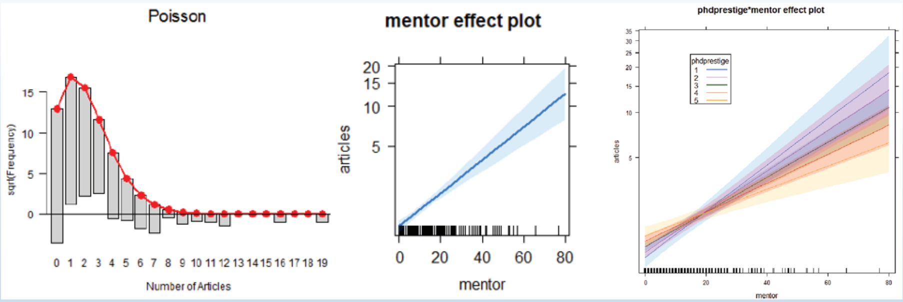

GLMs for Count Data

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Topics

- Generalized linear models
- GLMs for count data
  - Example: PhD publications
- Model diagnostics
  - Interactions
  - Nonlinearity
  - Outliers, leverage & influence
- Overdispersion
  - Quasi-poisson models
  - Negative binomial models
- Excess zeros
  - Zero-inflated models
  - Hurdle models

Count data models: Overview

- Count data models arise when the basic observation is a frequency, $y = 0, 1, 2, \ldots$ of some event and we have some predictors, $x_1, x_2, \ldots$ to help explain them.
  - Typically, these counts ~ Poisson() → "poisson regression"
- Examples:
  - Number of articles published by PhD candidates
    - Predictors: Married?, Female?, Kids < 5?, pubs by mentor
  - Number of parasites in blood samples of Norwegian cod
    - Predictors: Catch area, Year, length of fish
  - Female horseshoe crabs: Number of "satellite" males
    - Predictors: Female weight, color, spine condition, shell width
- Special circumstances
  - Overdispersion: when the variance > mean
  - Zero-counts: When excess 0 counts require an extra model

Generalized linear models

We have used generalized linear models fit with 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,

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

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

Generalized linear models

Nelder & Wedderburn (1972) said, "Let there be light!", a *generalized* 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

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

- 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 $g^{-1}(\eta_i) = \mu_i$

Link functions for the mean

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	μ_i	η_i
square-root	$\sqrt{\mu_i}$	η_i^2
log	$\log_e(\mu_i)$	$\exp(\eta_i)$
inverse	μ_i^{-1}	η_i^{-1}
inverse-square	μ_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 of y_i often used with classical linear models
- The bottom section is for binomial data, where y_i represents an observed count 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 relation between the 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: μ	$(-\infty, +\infty)$	ϕ
Poisson	$\text{Pois}(\mu)$	$\log_e(\mu)$	$0, 1, \dots, \infty$	μ
Negative-Binomial	$\text{NBin}(\mu, \theta)$	$\log_e(\mu)$	$0, 1, \dots, \infty$	$\mu + \mu^2/\theta$
Binomial	$\text{Bin}(n, \mu)/n$	$\text{logit}(\mu)$	$\{0, 1, \dots, n\}/n$	$\mu(1-\mu)/n$
Gamma	$G(\mu, \nu)$	μ^{-1}	$(0, +\infty)$	$\phi\mu^2$
Inverse-Gaussian	$IG(\mu, \nu)$	μ^2	$(0, +\infty)$	$\phi\mu^3$

Variance functions & overdispersion

- In the classical Gaussian linear model, the conditional variance is constant, $\phi = \sigma^2_\epsilon$.
- For binomial data, the variance function is $\mathcal{V}(\mu_i) = \mu_i(1 - \mu_i)/n_i$, with ϕ 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 $\mathcal{V}(\mu_i) = \widehat{\phi}\mu_i$.

What is overdispersion?

Overdispersion often results from failures of 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

Maximum likelihood estimation

- GLMs are fit by the method of maximum likelihood
  - Likelihood ($\mathcal{L}$) = Pr (data | model), as function of model parameters
- For the Poisson distribution with mean μ, the probability that the random variable Y takes the values y = 0, 1, 2, … is

Maximum likelihood estimation

- GLMs are fit by the method of maximum likelihood.
- For the Poisson distribution with mean μ, 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, μ_i depends on the predictors in $\boldsymbol{x}$ through

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

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

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

- 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.

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

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

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

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

GLMs for count data

- Typically, these are fit using

  glm(y ~ x1 + x2 + …, family=poisson, data=mydata)
- As in other linear models, the predictors, x_i, can be discrete factors, quantitative variables, interactions, etc.
- This fixes the dispersion parameter, ϕ to 1, assuming the count variable y | x1, x2, … is Poisson distributed
- It is possible to relax this, and fit a quasi-Poisson model, allowing ϕ to be estimated from the data
  - Specify family=quasipoisson. This allows 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 candiates

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
- number of publications by the student's mentor

Example: Publications of PhD candidates

Initially, ignore the predictors
This is equivalent to an intercept-only Poisson model

```
glm(articles ~ 1, family=poisson, data = PhdPubs)
```

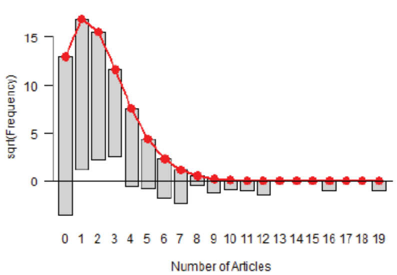
As a check on the Poisson assumption, calculate the mean and variance

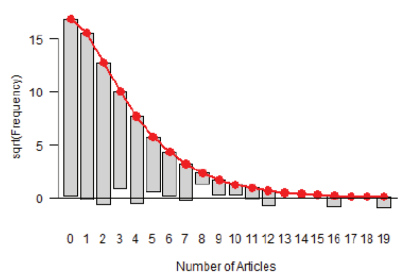
```
> with(PhdPubs, c(mean=mean(articles),
                  var=var(articles),
                  ratio=var(articles)/mean(articles)))
 mean   var ratio
 1.69  3.71  2.19
```

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

First, look at rootograms:

```r
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 Poisso model

Fit the model with all main effects; note the ~ . notation for this

```
> 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

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

```r
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
```

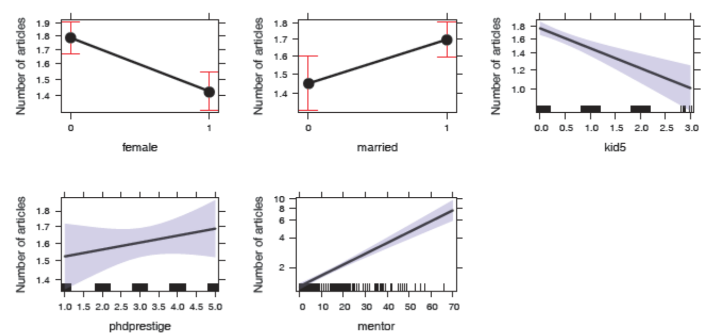
Thus:

- females publish -0.224 fewer log (articles), or 0.8 × that of males
- married publish 0.157 more log (articles); or 1.17 × unmarried (17% increase)
- each additional young child decreases this by 0.185; or 0.831 × 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:

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



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

Model diagnostics

Diagnostic methods 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() is useful here
- Outliers? Influential observations?
  - car::influencePlot() is your friend
- For count data models we should also check for overdispersion
  - Similar to homogeneity of variance checks in lm()

Checking for interactions

As a quick check for interactions, fit a model with all two-way terms, . ~ .^2

```
> 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

The all main effects and all two-way models are nested, so we can compare them with anova()

```
> 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 + 
female:married +
    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
```

→ No evidence that the two-way terms result in a significantly better model

Compare models

We can also compare using AIC/BIC with **vcdExtra::Lrstats()**

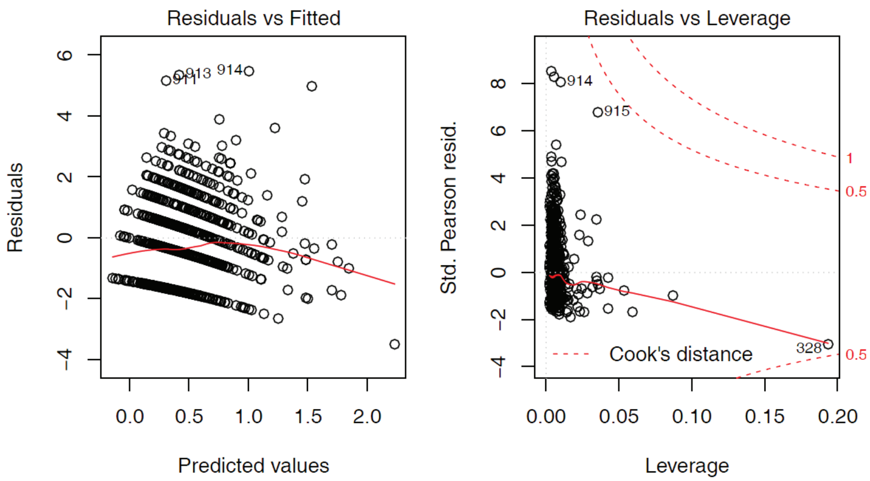
```
> LRstats(phd.pois, phd.pois1)
Likelihood summary table:
             AIC  BIC LR Chisq  Df Pr(>Chisq)
phd.pois   3313 3342     1634 909     <2e-16 ***
phd.pois1 3316 3388     1618 900     <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- There seems to be no reason to include interactions in this model
  - Interactions increase AIC & BIC
- We might want to revisit 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))
```



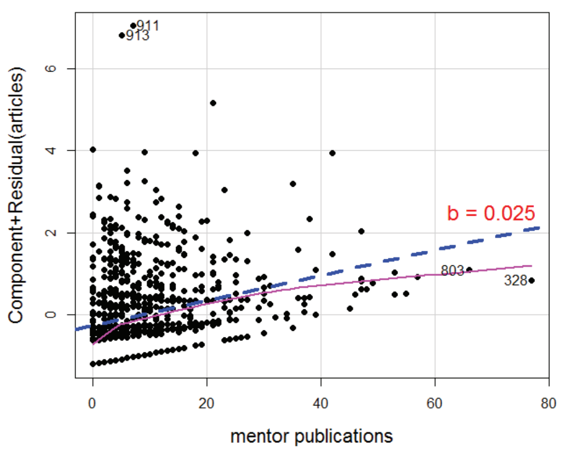
Nonlinearity diagnostics

- Nonlinear 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 nonlinear relations for numeric predictors
  - These graph the value of $\hat{\beta}_i$ xi + 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 $y_i - \widehat{y}_i$ in the full model
- A non-parametric (e.g., loess()) smooth facilitates detecting nonlinearity

Nonlinearity diagnostics: crPlot()

Is the relation between article published by the student and by the mentor adequately represented as linear?

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



The smoothed curve doesn't differ much from the fitted line

A couple of points stand out: 328, 803, 911, 913

Residuals

Residuals contain all the information about how a model doesn't fit, and maybe why

For GLMs, there are several types, based on the Pearson and deviance goodness-of-fit statistics

- the ***Pearson residual*** is the case-wise contribution to Pearson χ^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

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

These are raw residuals, on the scale of the counts themselves

Residuals

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

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

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

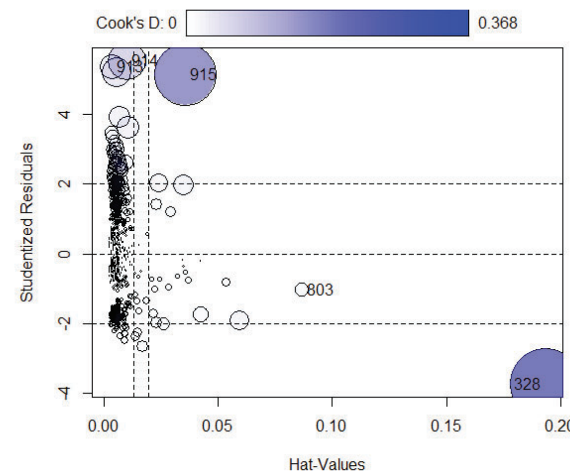
- The most useful is the ***studentized residual*** (or deletion residual), `rstudent()` in R. This estimates the standardized residual resulting from omitting each observation in turn. An approximation is:

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

Don't worry about the formulas, but do know the difference among raw, standardized and studentized residuals

Outliers, leverage & influence

```
influencePlot(phd.pois, id = list(n=2))
```



Influence (CookD) =
Leverage (Hat) x |Residual|

Several cases (913-915) stand out with large + residuals

One observation (328) has a large leverage

Why are they unusual? Do they affect conclusions?

Examine data & decide what to do

Who is influential & why?

At the very least, you should examine these flagged observations in the data

```
> PhdPubs[c(328, 803, 913:915),]
    articles female married kid5 phdprestige mentor
328        1      0       1    1           2     77
803        4      0       1    2           5     66
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
803: High prestige school, mentor published 66; published a bit less than predicted
913-915: Wow! all published >> than 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 this Poisson model, 4 observations are flagged as large + residuals

```
> outlierTest(phd.pois, cutoff = 0.001)
    rstudent unadjusted p-value Bonferroni p
914     5.54           2.99e-08     2.73e-05
913     5.38           7.36e-08     6.74e-05
911     5.21           1.92e-07     1.75e-04
915     5.15           2.60e-07     2.38e-04
```

What to do?
- Delete them & refit?
- Keep them, but report as unusual?
- Fit a better model, hope these will go away?

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, $\text{se}(\widehat{\beta}_j)$ are optimistically small
  - Wald tests, $z_j = \widehat{\beta}_j / \text{se}(\widehat{\beta}_j)$, are too large, and thus overly liberal.

Testing overdispersion

- Statistical tests for overdispersion test H_0: Var(y) = μ vs. the alternative

$$H_1: \text{Var}(y) = \mu + ? \times f(\mu)$$

- Implemented in **`AER::dispersiontest()`**
  - If significant, overdispersion should not be ignored
  - You can try fitting a more general model
    - Quasi-poisson
    - Negative-binomial

Quasi-poisson models

- The quasi-poisson model allows the dispersion, ϕ, to be a free parameter, estimates with other coefficients
- The conditional variance is allowed to be a multiple of the mean

$$\text{Var}(y_i \mid \eta_i) = \phi\, \mu_i$$

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

Quasi-poisson models

- A simple estimate of the dispersion parameter is the residual deviance divided by degrees of freedom $\phi = D(y, \mu) / df$
- A Pearson χ^2 statistic has better statistical properties & is more commonly used

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

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

```
> with(phd.pois, deviance/df.residual)
[1] 1.8

> sum(residuals(phd.pois, type = "pearson")^2)/phd.pois$df.residual
[1] 1.83
```

Fitting the quasi-poisson model

You can fit the quasi-poisson model using glm()

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

The estimate of the dispersion parameter is calculated by the summary() method. You can get it as follows:

```
> (phi <- summary(phd.qpois)$dispersion)
[1] 1.83
```

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 1.83)

    Null deviance: 1817.4  on 914  degrees of freedom
Residual deviance: 1633.6  on 909  degrees of freedom
AIC: NA
```

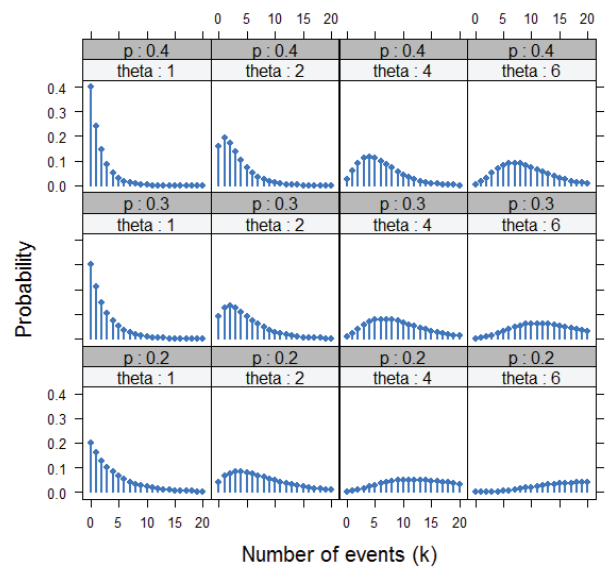

The negative-binomial model

- 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 θ.
- 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



Negative-binomial distributions for varying p & θ

Overdispersion decreases as θ increases

Fitting the negative-binomial

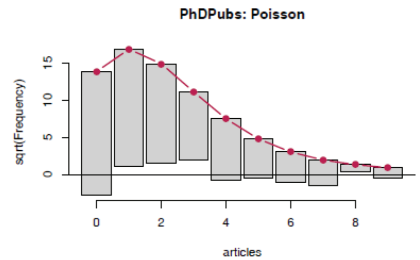
- For fixed θ, the negative-binomial is another special case of the GLM
- This is handled in the MASS package, with `family=negative.binomial(theta)`
- But most often, θ is unknown, and must be estimated from the data
- This is implemented in `glm.nb()` in the MASS package.

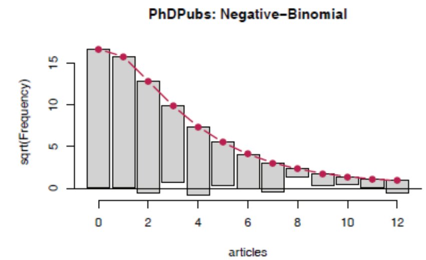
```
> library(MASS)
> unlist(summary(phd.nbin)[c("theta", "SE.theta")])
  theta SE.theta
  2.267    0.272
```


Visualizing goodness-of-fit

The countreg package extends rootogram() 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.

Comparing models: 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
```

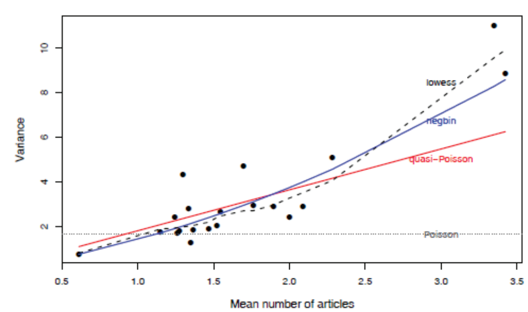
We can also compare coefficients and their standard errors for these models

```
              pois  qpois   nbin
(Intercept)  0.266  0.266  0.213
female1     -0.224 -0.224 -0.216
married1     0.157  0.157  0.153
kid5        -0.185 -0.185 -0.176
phdprestige  0.025  0.025  0.029
mentor       0.025  0.025  0.029
```

```
              pois  qpois   nbin
(Intercept) 0.0996 0.1348 0.1327
female1     0.0546 0.0738 0.0726
married1    0.0613 0.0829 0.0819
kid5        0.0401 0.0543 0.0528
phdprestige 0.0253 0.0342 0.0343
mentor      0.0020 0.0027 0.0032
```


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

What have we learned?

A summary to this point should use the result of the negative-binomial model

```
> lmtest::coeftest(phd.nbin)
z test of coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  0.21295    0.13274    1.60  0.10866
female1     -0.21625    0.07259   -2.98  0.00289 **
married1     0.15279    0.08194    1.86  0.06224 .
kid5        -0.17634    0.05279   -3.34  0.00084 ***
phdprestige  0.02934    0.03427    0.86  0.39192
mentor       0.02868    0.00324    8.86  < 2e-16 ***
```

For interpretation, examine the coefficients, β, e^{β} and % change

```
> round(cbind(beta = coef(phd.nbin),
              expbeta = exp(coef(phd.nbin)),
              pct = 100 * (exp(coef(phd.nbin)) - 1)), 3)
              beta expbeta    pct
(Intercept)  0.213   1.237  23.73
female1     -0.216   0.806 -19.45
married1     0.153   1.165  16.51
kid5        -0.176   0.838 -16.17
phdprestige  0.029   1.030   2.98
mentor       0.029   1.029   2.91
```


What have we learned?

The number of articles published by PhD candidates:

- Most strongly predicted by mentor pubs, but with a modest effect. On average, each mentor pub increases PhD articles by 2.9%
- Next, increasing young children (kids5) results in fewer publications. On average, each additional kid reduces PhD articles by 16%
- Being married is marginally NS, but intriguing. Our estimate shows married candidates publish 16.5% more articles than non-married.
- Perhaps surprisingly, the prestige of the PhD institution has no significant effect in this purely main-effect model. Yet, a unit change in phdprestige is estimated as a 3% increase in PhD articles
- Yet, we still have doubts:
  - Several cases (328, 913-915) appeared unusual in diagnostic plots. Should we refit w/o them to see if conclusions change?
  - The NB model might not be the best way to account for the zero counts – students who never published
  - Is there a better way?

Excess zero counts

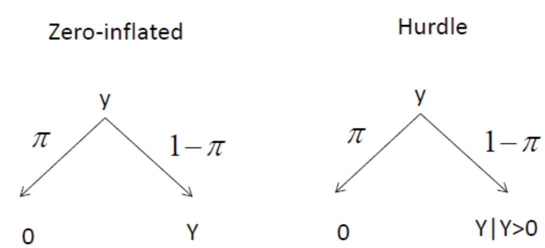
- A common problem in count data models is that many sets of data have more observed zero counts than the (quasi) Poisson or NB models can handle.
  - In the PhdPubs data, 275 of 915 (30%) candidates published zilch, bupkis
  - The expected count of 0 articles in the Poisson model is only 191 (21%)
- 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.

Models for excess zeros

Two types of models, with different mechanisms for zero counts

- ***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

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

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

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

In application, the same predictors can be (and often are) used in both models (**x** = **z**)

Zero-inflated models

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

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

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 μ_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 $\text{NBin}(\mu, \theta)$

Exploring zero-inflated data

A little insight can be gained by generating random data from Poisson & zero-inflated analog. The example uses VGAM::rzipois()
Pois(μ=3) = ZIP(μ=3, π=0)
vs. ZIP(μ=3, π=.3)

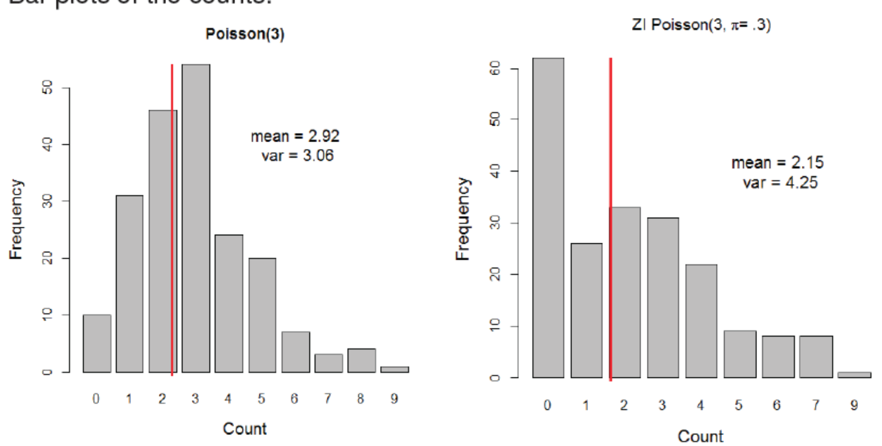
```
> set.seed(1234)
> data1 <- VGAM::rzipois(200, 3, 0)
> data2 <- VGAM::rzipois(200, 3, .3)
```

The tables of counts show far more zeros in data2

```
> 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
```


Exploring zero-inflated data

Bar plots of the counts:



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

Hurdle models

The Hurdle model has 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 π_i).
  - In Hurdle models, $y_i = 0$ and $y_i > 0$ are fully observed. The first process generates all the zeros.

Fitting ZIP & 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:

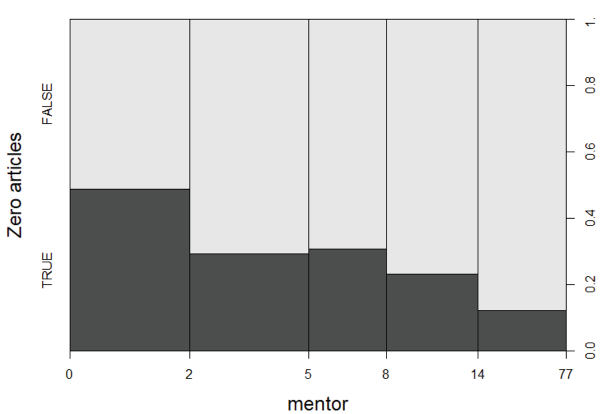
```
zeroinfl(formula, data, subset, na.action, weights, offset,
         dist = c("poisson", "negbin", "geometric", "binomial"),
          ...)

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=1:2, ylab="Zero articles",
       breaks=quantile(mentor, probs=seq(0,1,.2)))
```



As expected, zero counts decrease with mentor pubs

NB: this gives a spineplot

Fitting models

To illustrate, we fit all four models, the combinations of (ZI, hurdle) × (poisson, nbin) to the phdpubs data.

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

```
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")
```

Comparing models

Compare the 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 3313.3 3342.3   3301.3 909  < 2.2e-16 ***
phd.hp   3234.5 3292.4   3210.5 903  < 2.2e-16 ***
phd.zip  3233.5 3291.3   3209.5 903  < 2.2e-16 ***
phd.hnb  3130.9 3193.5   3104.9 902  < 2.2e-16 ***
phd.znb  3125.8 3188.4   3099.8 902  < 2.2e-16 ***
phd.nbin 3135.4 3169.1   3121.4 909  < 2.2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The standard negative binomial model looks best by BIC.
Why do you think this is? (Hint: look at the residual df)

Nevertheless, it is useful to examine the coefficients in the ZIP model

```
> 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 in the ZIP model

Let's refit 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 models 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 looks best by BIC. Let's stick with this.

Model interpretation: Coefficients

Ignoring the 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
           0.3572           -0.2116           -0.1675            0.0241
 zero_(Intercept)       zero_mentor
          -0.8169           -0.6080
```

- 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: Coefficients

Often easier to interpret exp(β)

```
> exp(coef(phd.znb1)[c(1,2,4,6,7,8)])
count_(Intercept)     count_female1        count_kid5      count_mentor
           1.429             0.809             0.846             1.024
 zero_(Intercept)       zero_mentor
           0.442             0.544
```

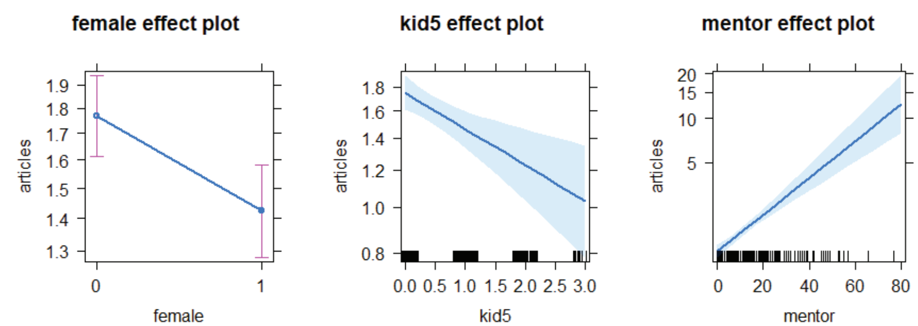
Female: Women publish .21 fewer log articles, .81 times that of men (20% decrease)
Kids5: Each additional kid<5 → .17 fewer log articles, a 15% decrease
Mentor: Each additional mentor article → .024 more PhD log pubs (2.4% increase)

Count model: Each additional mentor article decreases log odds PhDpubs = 0 by 0.608, a 45% decrease

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

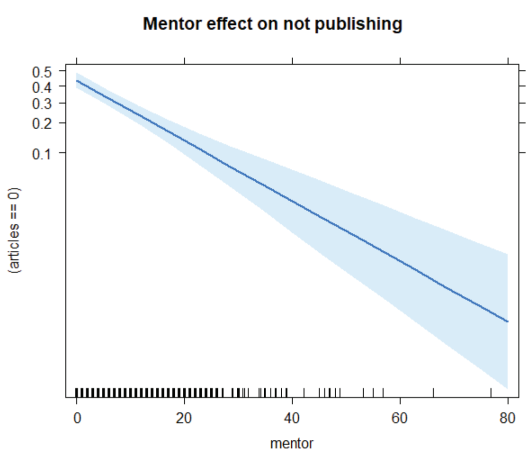
```
plot(allEffects(phd.nbin)[c(1,3,5)], rows=1, cols=3)
```



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

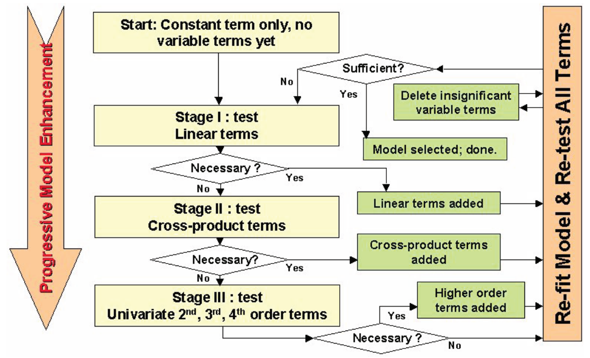
What have we learned?

- 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

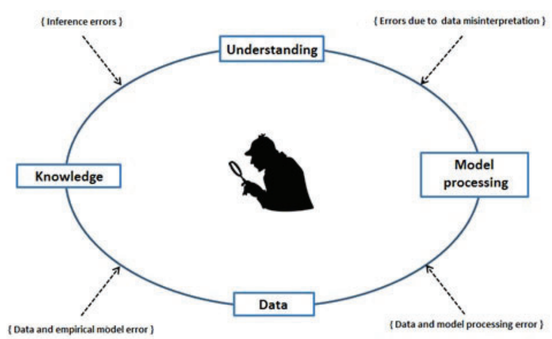
- Model building and model criticism go hand in hand
- But they don't form a linear series of steps you can put into a flow chart



What have we forgotten?

- Sometimes, you have to go back and revisit 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
  - This was NS (p = 0.08), so I decided to dismiss them all
  - (I wanted to keep he model simple, to go on to other topics: overdispersion, models for excess zeros)

Back to square TWO

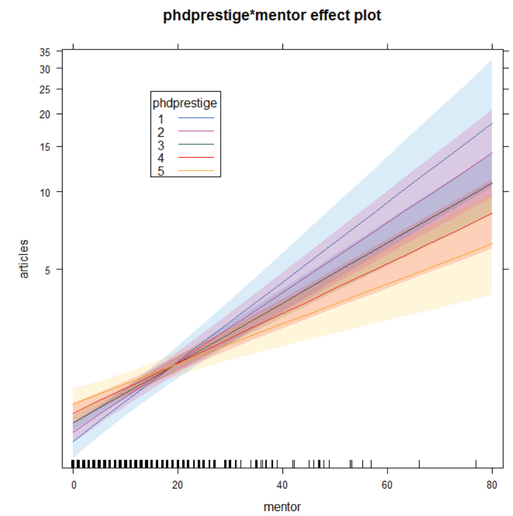
- A question in a former class made me reconsider the phdprestige:mentor interaction
- Perhaps, the effect of mentor varied with phdprestige?

Try this, starting with the negative-binomial, `phd.nbin` (`update()` is your friend)

```
> 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

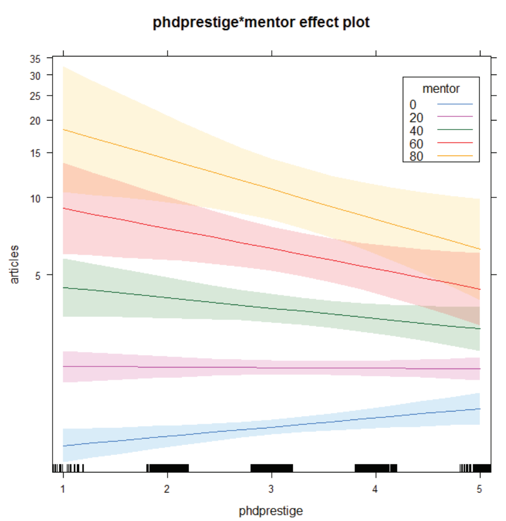
```
phd.effnb2 <- allEffects(phd.nbin2)
plot(phd.effnb2[4], x.var="mentor", multiline=TRUE, ci.style="bands", ...)
```



- 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

```
phd.effnb2 <- allEffects(phd.nbin2)
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.

Back to square ONE

Aren't we done yet?

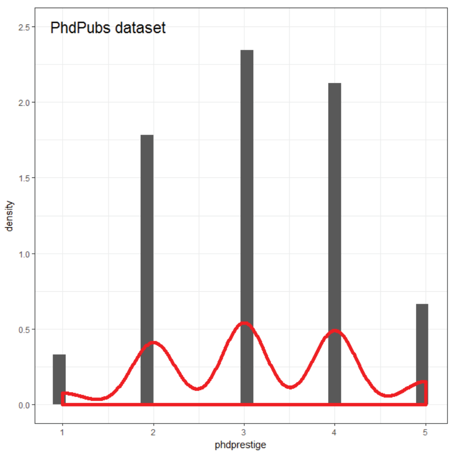
"All data are wrong, but some are useful – Sitsofe Tsagbey et al. TAS, 2017

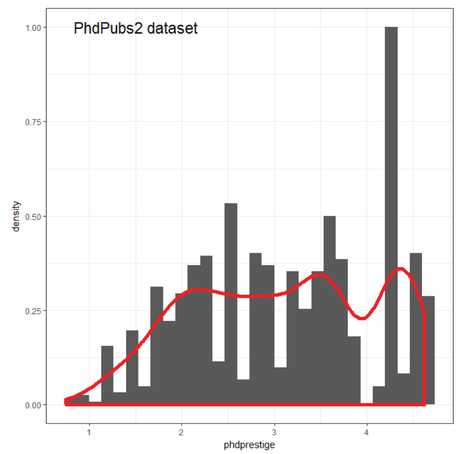
- A nagging doubt: what is the coding for phdprestige?
  - Email from Scott Long: "the higher the number, the more prestigious the program"
  - "PS: The data I used did not categorize the continuous phd scale into discrete categories"
- Found the original Stata data set:

```
library(foreign)
PhdPubs2 <-
     read.dta("http://www.stata-press.com/data/lf2/couart2.dta")
```

Compare distributions

Histograms with smoothed density estimate of the two versions of `phdprestige`
They are very different!





What to do?

Re-run the analysis with the new data set, PhdPubs2

- This could be called a sensitivity analysis – does the new data alter conclusions?
- Q: Are the results of the phd.nbin2 and phd.znb2 models about the same. A: YES!
- Q: Is the interaction of phdprestige:mentor about the same. A: YES!
- Q: Does the effect plot look about the same? A: YES!

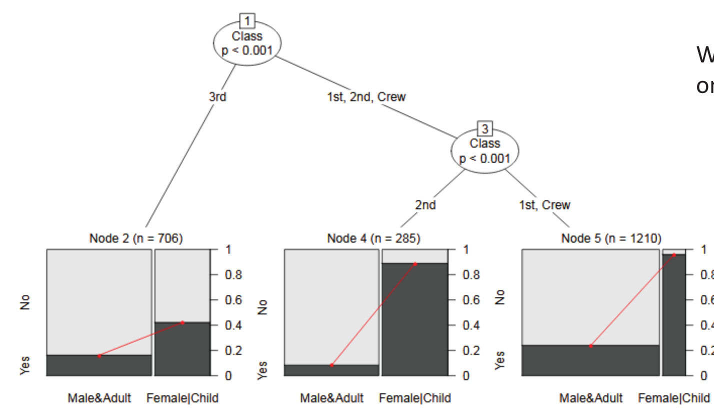
What else is there?

The PhdPubs example was rather simple

- There were only a few predictors
  - Model selection methods could be based on simple Anova(), coeftest(), LRstats()
  - No need for more complex model selection methods or cross-validation
- Of the quantitative predictors, only mentor & kid5 had important effects
  - The effects of these were sufficiently linear
  - No need to try non-linear effects (poly(mentor,2), ns(mentor,2))
- There turned out to be one important interaction
  - In Psychology, these are called "moderator" effects
  - Interpretation often based on post-hoc tests of simple slopes
  - Interpretation is usually simplified in effect plots

Other methods: Recursive partitioning

- Recursive partitioning, or regression trees are often an attractive alternative to linear models
  - Interactions are handled by partitioning the ranges of variables
  - Or, models can be fit to subsets of the data defined by recursive partitioning



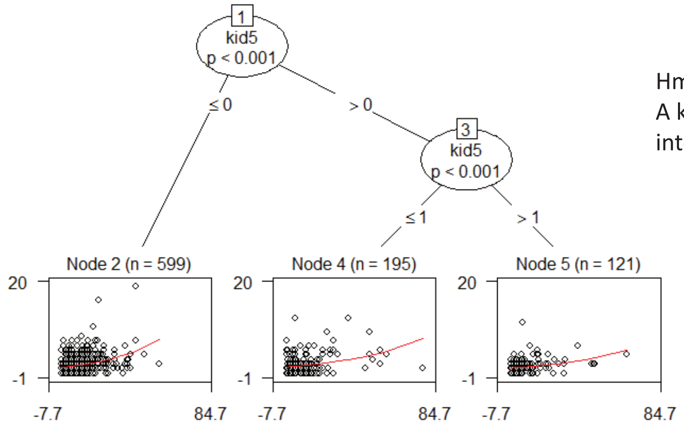
Who survived on the *Titanic*?

Logistic regression tree fit to the Titanic data with partykit::glmtree()

Other methods: Recursive partitioning

Could there be a simpler or different model for the PhdPubs data?

```
library(partykit)
phd.tree <- glmtree(articles ~ mentor| female+married+kid5+phdprestige,
                    data=PhdPubs, family=poisson)
plot(phd.tree)
```



Hmm?
A kid5:mentor interaction?

Summary

- GLMs introduce a wide class of models for count data, starting from log(**μ**) = **X** **β**, **μ**|**X** ~ Poisson
  - Overdispersion → quasi-poisson, negative binomial
- Excess zero counts introduce new ideas & methods
  - ZIP model: structural model for the 0s
  - Hurdle model: random model for 0s, 2nd model for Y>0
- In all this, we rely on data & model plots for understanding