GLMs: Validation

Models behaving badly: Part 2!

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Motivation

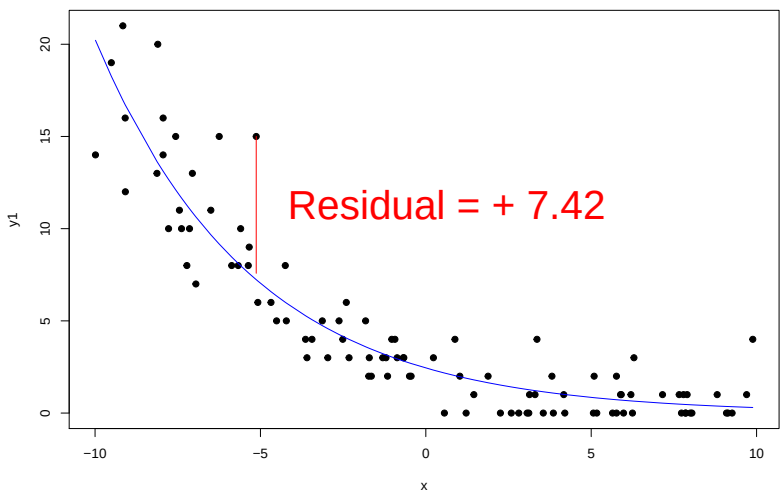
- Are my model results reliable?
  - Residual checks
  - Overdispersion
  - Zero-inflation
- Model selection - which terms should I use?
  - log-likelihood, χ^2 tests, and AIC
  - ML vs REML
- Other things
  - Binomial GLMs with >1 trial
  - Offsets in count models
  - R^2 for GLMs
- Show-and-tell!

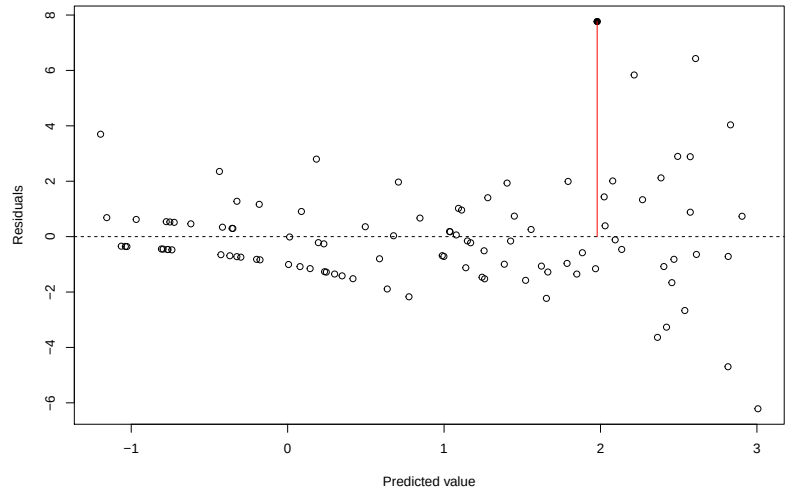
Problem 1: Residual checks

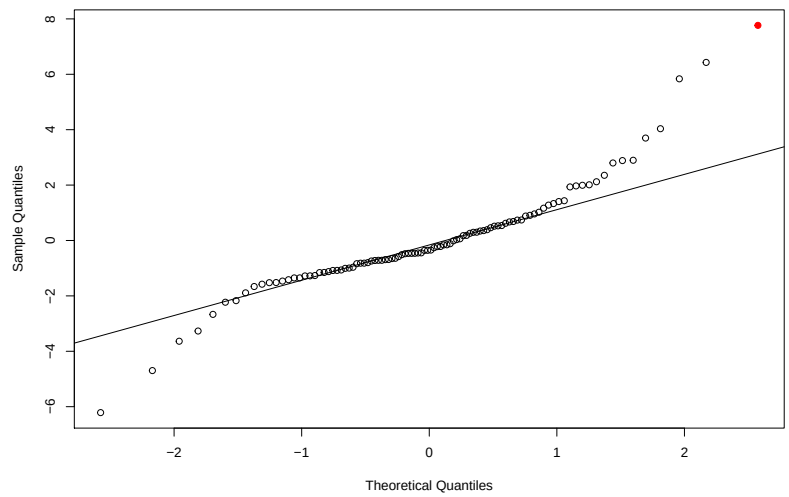
- In LMs, residual checks are used to make sure that:

1. Terms are linearly related
2. Generating process is valid
3. Variance is constant

- "Regular" residuals don't work this way for GLMs!







There are *many* kinds of residuals!

In addition to *response* (regular) residuals there are:

- Working residuals
- Pearson residuals
- **Deviance residuals**

Deviance residuals use *likelihood*:

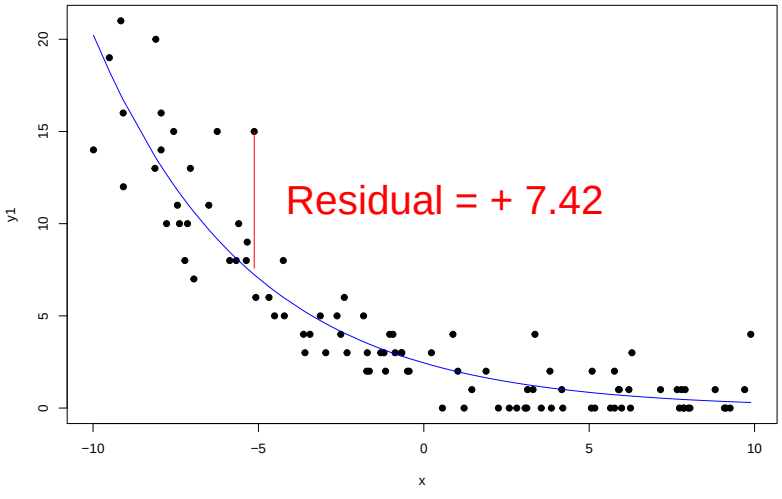
$$r_{dev} = sign(y - \hat{y})\sqrt{2(log(L(y|\theta_s)) - log(L(y|\theta)))}$$

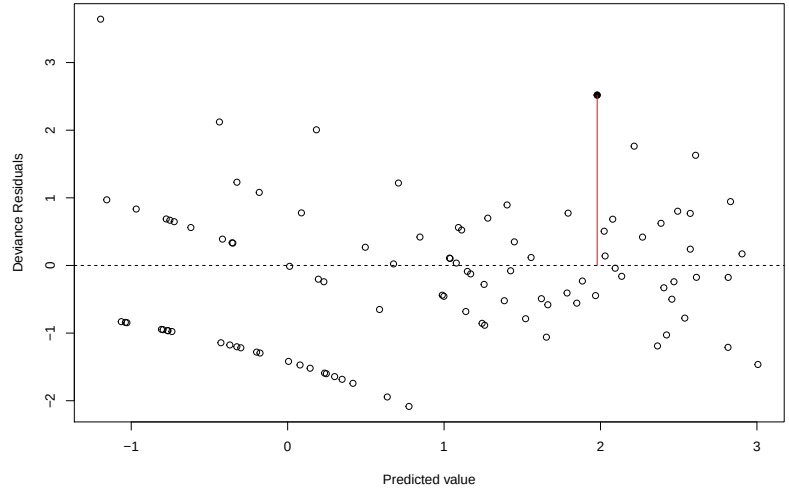
- This may look scary, but R does this all for you!
- These are analogous to regular residuals in LMs
- For more about the different kinds of residuals, see here

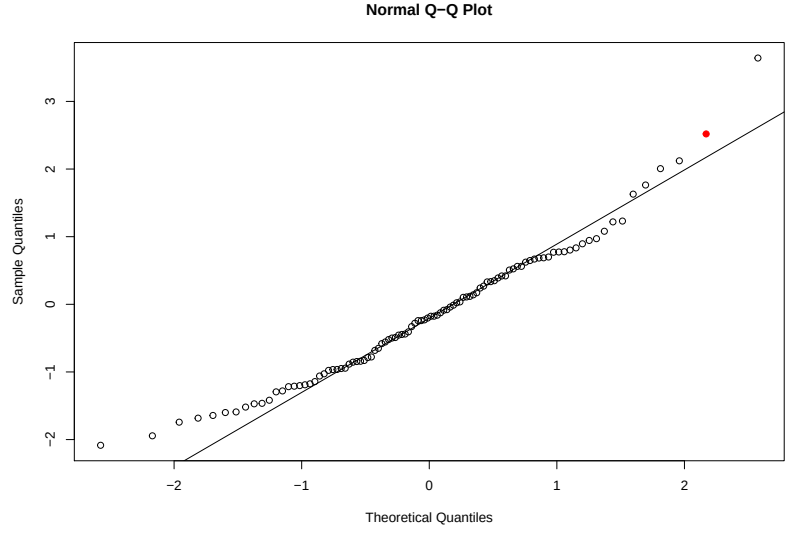
Solution: use deviance residuals for GLMs

Keep in mind:

- Residuals from GLMs will never be as "pretty" as those from LMs
- *Especially* true for:
  - Binomial GLMs
  - Poisson/Negative Binomial GLMs with many zeros

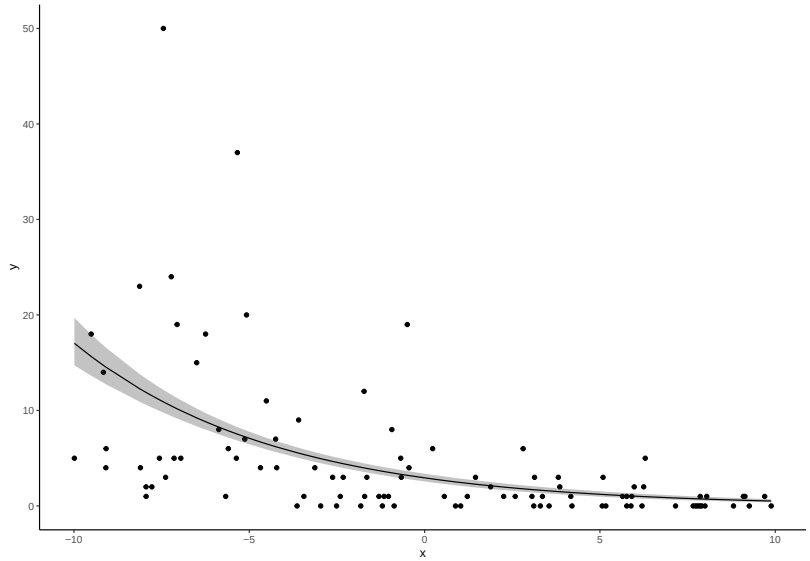






Problem 2: Overdispersion

- Binomial and Poisson families have **no** variance term (e.g. *SD*).
- Sometimes this assumption doesn't work! (Very common for Poisson models)
- Strong overdispersion biases SEs, meaning that p-values are useless



Example: data are much more variable than the predictions from the model

Problem: Overdispersion

```
##
## Call:
## glm(formula = y1 ~ x, family = "poisson", data = d1)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.0843  -0.9460  -0.1897   0.5333   3.6416
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.89455    0.07818   11.44   <2e-16 ***
## x           -0.21145    0.01174  -18.01   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 564.27  on 99  degrees of freedom
## Residual deviance: 106.20  on 98  degrees of freedom
## AIC: 362.01
##
## Number of Fisher Scoring iterations: 5
```

- In Poisson or Binomial models, Residual deviance $\div$ Degrees of Freedom should be ~ 1
- Residual deviance is the sum of all deviance from the model
- This model looks OK ($106.2 \div 98 = 1.08$)

Problem: Overdispersion

```
##
## Call:
## glm(formula = y2 ~ x, family = "poisson", data = d1)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -4.1009  -1.7543  -0.8805   0.4796   8.6102
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  1.07897    0.06871   15.70   <2e-16 ***
## x           -0.17581    0.01069  -16.44   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 851.96  on 99  degrees of freedom
## Residual deviance: 501.98  on 98  degrees of freedom
## AIC: 735.46
##
## Number of Fisher Scoring iterations: 5
```

- This model does **not** look OK ($501.98 \div 98 = 5.12$)
- Generated using Negative Binomial, but fit to Poisson

Causes

Overdispersion can be caused by different things:

- Using the wrong probability distribution
  - e.g. Poisson, but should be Negative Binomial
- Lots of zeros in count data
  - e.g. Very short observation period
- Leaving out an important term
  - e.g. An important *interaction* term was omitted
- Random effects[1] not accounted for
  - e.g. Data collected at different sites, but ignored

[1] Random effects discussed later

Solutions for overdispersion

Try the following (in this order):

1. Consider terms that may have been left out
   1. Fixed effects
   2. Random effects
2. Try distributions that account for overdispersion
   1. Negative Binomial, Beta Binomial, Zero-inflated Poisson[2]
   2. Quasi-binomial[2] and quasi-poisson[2]
   3. Transform counts to presence/absence
3. Lower your expectations, and use a lower critical p-value (e.g. 0.01 instead of 0.05)
4. Design a better study :(

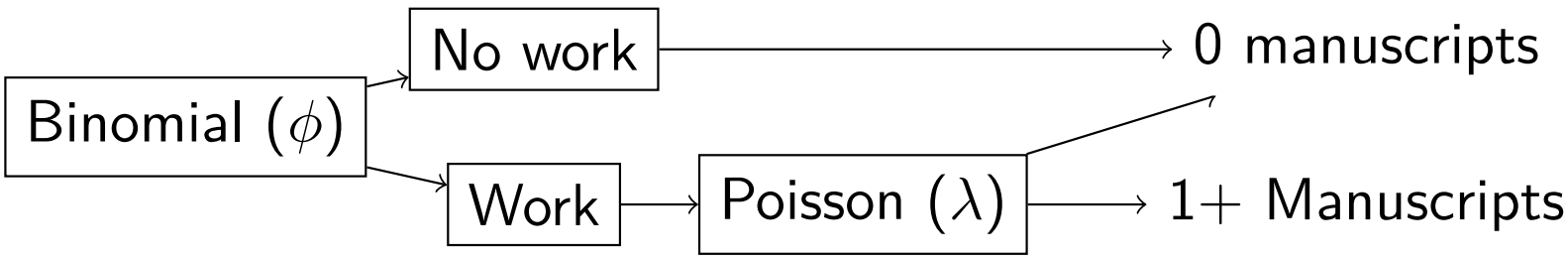
[2] These can be annoying to deal with, so avoid if possible

Zero-inflation: drunk monks

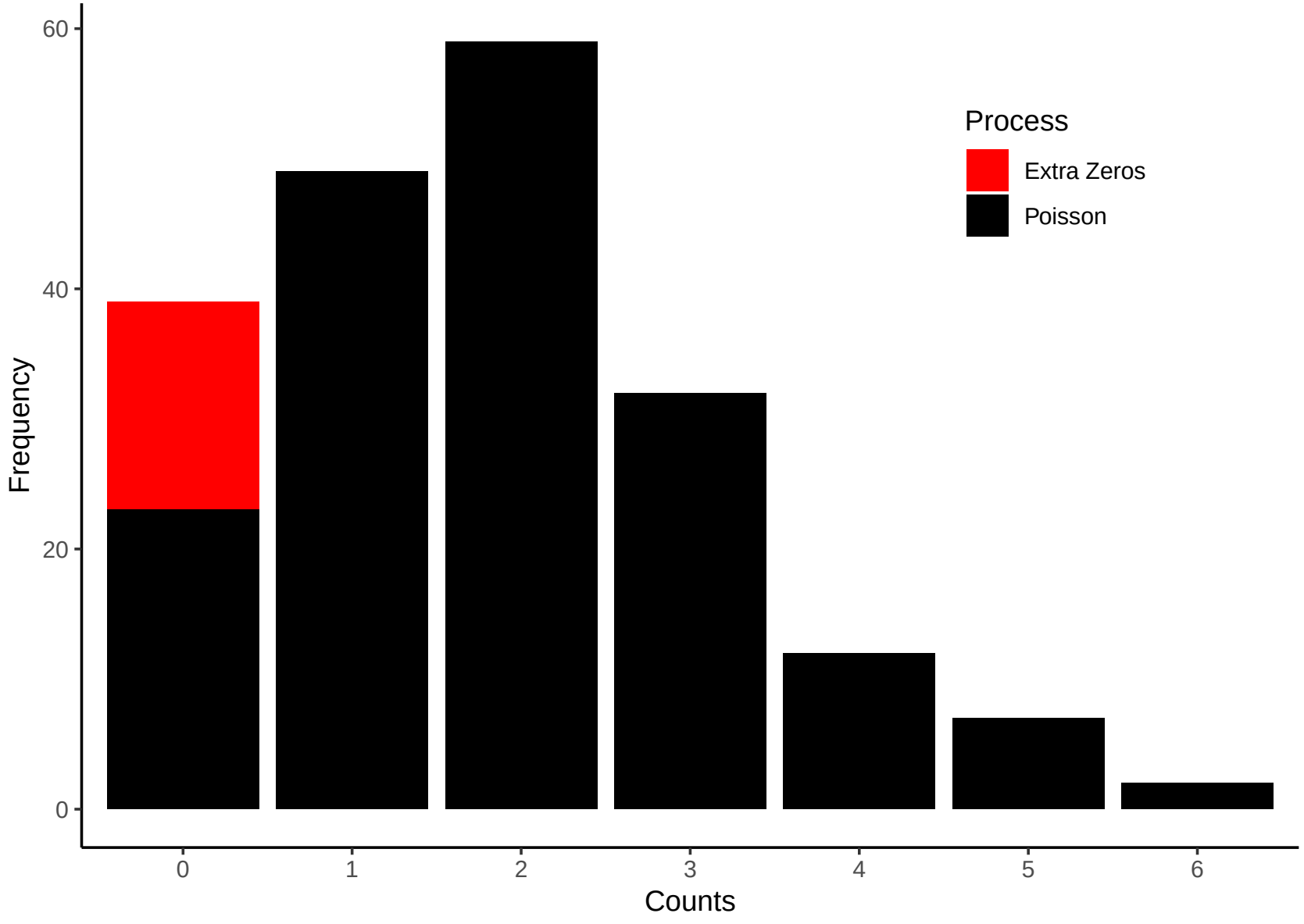
An analogy:

1. Monks at a monastary make copies of manuscripts. Most days they make very few (0 or 1), but occasionally they make many (2-5)
2. Some days they decide to try out the beer that's been brewing in the cellar! No manuscripts get made on those days.
3. The number of manuscripts made (per day) follows a *zero-inflated Poisson distribution*

This is *mixture* of a Poisson and a Binomial:

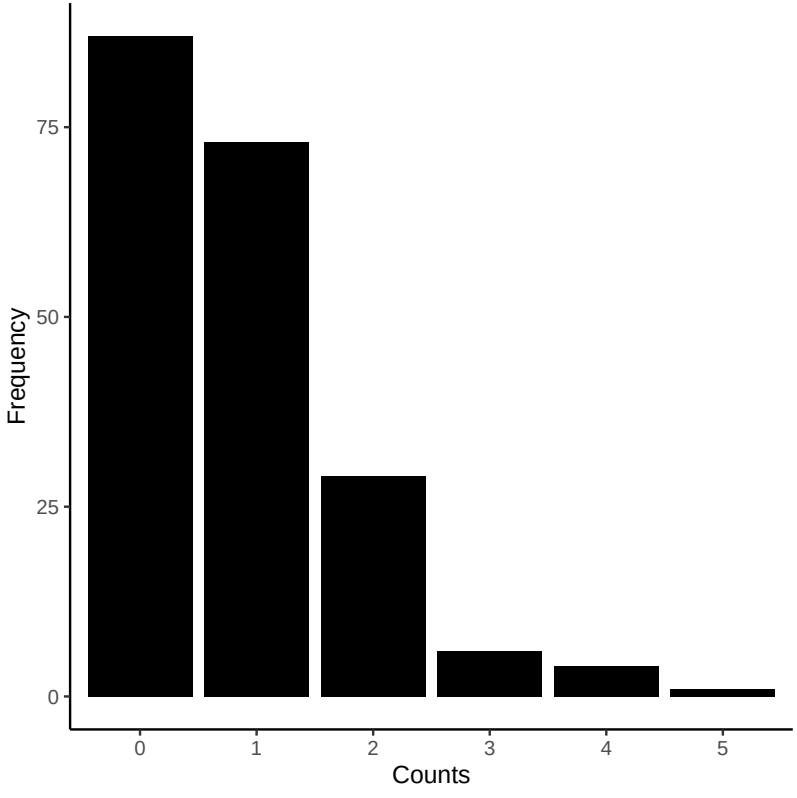


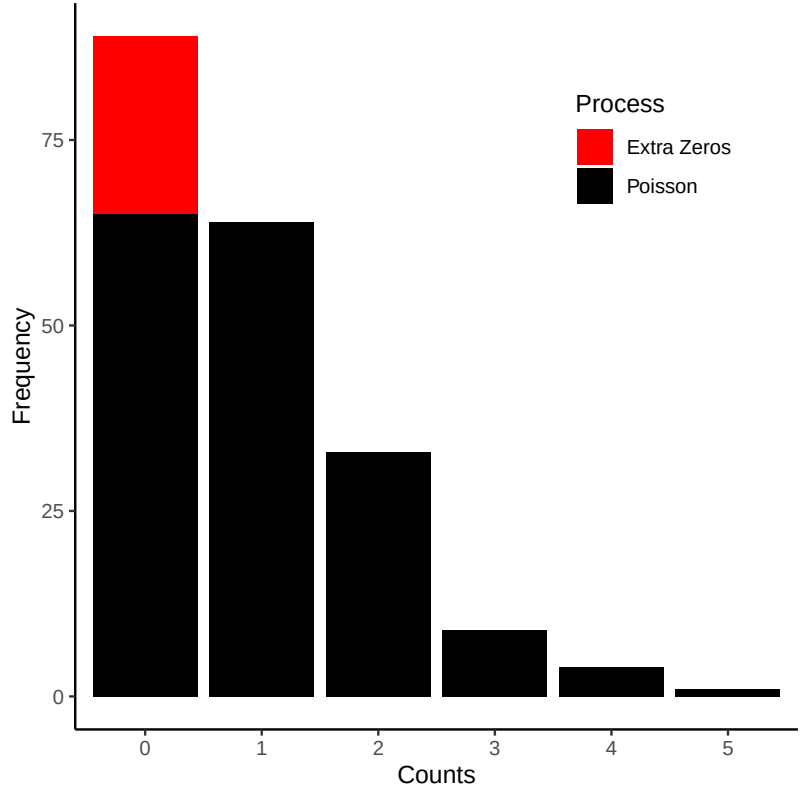
Zero-inflation: graphical model



Problem: hard to fit

- Hard for R to tell the difference between ZIP/ZINB, and a Poisson/NB with a low mean (λ).
- This needs a lot of data in order to work! Consider longer sampling periods in order to reduce zeros





Model selection

How many terms should be in my model?

- Same principle as in regular linear models: **what do you think the process is?**
  - Just because a term is "not significant" doesn't mean it should be dropped out!
  - Just because a term is "significant" doesn't mean it should be left in!
  - I find graphical models very helpful for this (see Lecture 4, p. 17)
  - Avoid selecting models based on R^2. Avoid stargazing[3](hunting for "better" p-values or AIC scores)
- To test whether terms are important in predicting your data (similar to), use *likelihood-ratio tests*
  - `drop1(model,test='Chisq')`
  - AIC tests usually say the same thing as LR tests

[3]"My God, it's full of stars!" -2001, A Space Odyssey

ML vs REML

- Maximum likelihood (ML) estimates of variance (e.g. SD) are always smaller than the actual variance (biased)
- Restricted maximum likelihood (REML) uses a mathematical trick to get around this, but...
- This means that models with different numbers of terms don't have the same REML estimates
- Likelihood between these models technically can't be compared!

Solution:

1. Use ML if comparing between models with different fixed effects, then...
2. Re-fit with REML once you've decided on a model

Other useful things about GLMs!

- Binomial GLMs with >1 trial
- Offsets in count models
- R^2 for GLMs

Binomial GLMs with >1 trial

- If you're measuring single "success/failures", 1s and 0s are used
- If multiple trials occur, R requires counts of successes and failures
- Example: "I counted male and female critters at different sites. Does temperature affect sex ratios?"

```
#Number of females and males are in 2 separate columns in d1
glm(cbind(females,males) ~ temp, family='binomial',data = d1)
```

This will correctly account for different numbers of critters ("trials") at each site

Offsets in count models

- Poisson/NB models assume that counts occur over the same period of time
- Count models use integers only, so you can't just do: *counts* $\div$ *hours*
- Solution: use *offsets* to deal with different observation times
  - Predictor with a slope fixed at 1
- Example: "I counted critters for different lengths of time at each site. Does temperature affect counts?"

```
#hours = observation time at each site, and
#   must be log-transformed before being used in an offset
#
glm(counts ~ offset(log(hours)) + temp, family='poisson',data = d1)
```

This will return estimates that have been scaled to a 1-hour observation time

R-squared for GLMs

- Bad news: there isn't really any good way to get R^2 (explained variance) for non-`lm` models
- OK news: there are many *pseudo*-R^2 measures that are *sort of* like R^2, but nobody really agrees on which one is best
- Good news: ecologists tend to not know or care about this

Solution: pick a single type of R^2 and use that, or omit it completely [4]

- See here, here or here for more info on R^2
- Try `rsquaredglmm()` from `piecewiseSEM` or `r.squaredGLMM()` from `MuMIn`

[4] But be prepared to argue with supervisors, committee members, or reviewers! They will want some kind of measure of how well your model predicted your data.

Show-and-tell!