

Generalized Linear Models

“The trouble with normal is that it always gets worse”

Samuel Robinson, Ph.D.

Sept 29, 2023

Part 1: The exponential family

Outline

- Meet (some of) the exponential family!



Christmas gifts for the nerds in your life

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 - Normal



Christmas gifts for the nerds in your life

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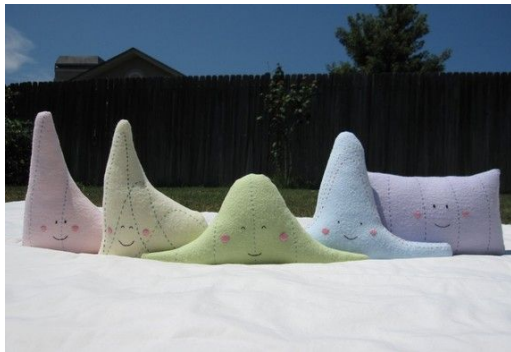
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Christmas gifts for the nerds in your life

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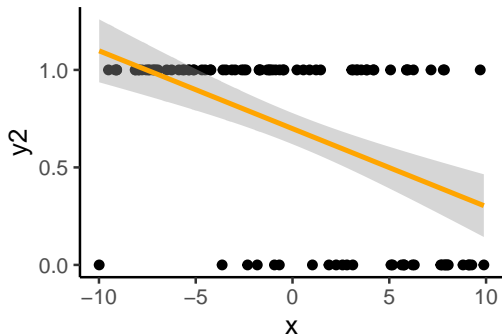
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- “Play time”

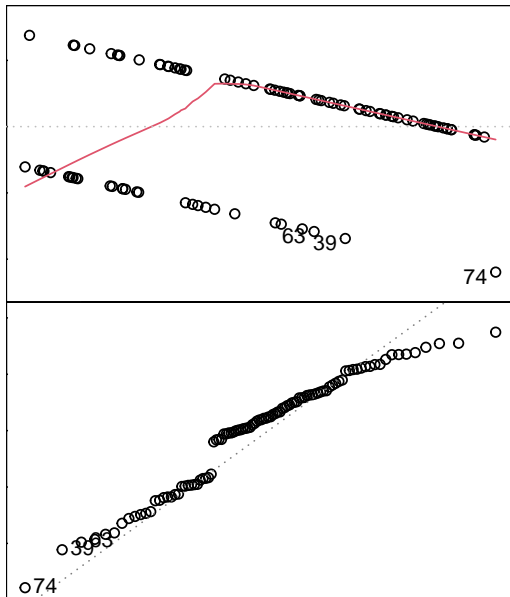


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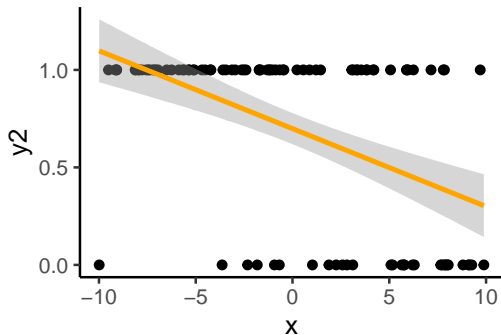
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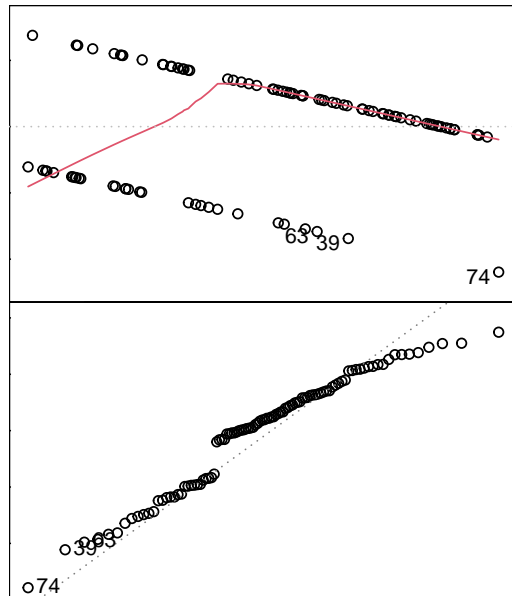
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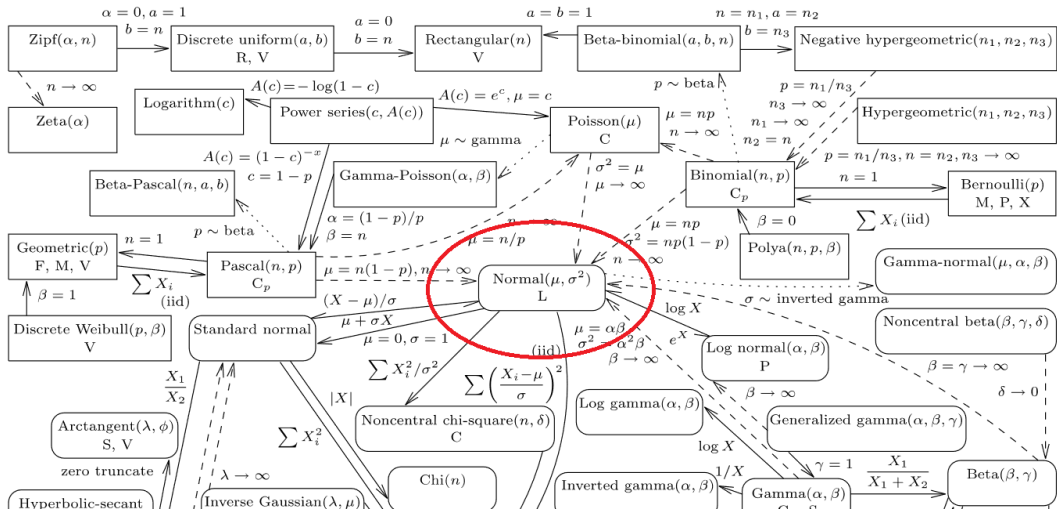
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- Some types of data can never be transformed to make the residuals normal
- Solution: **use the distribution that generates the data!**

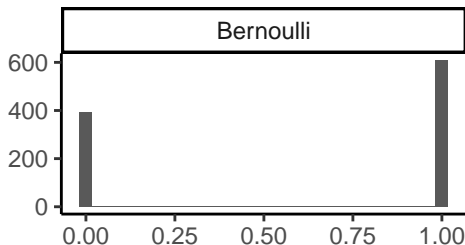
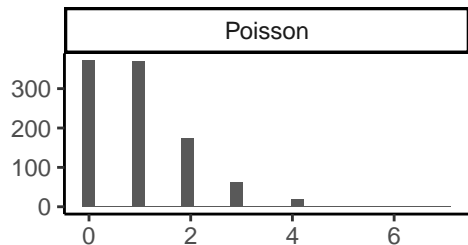
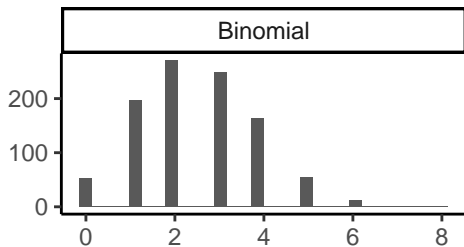
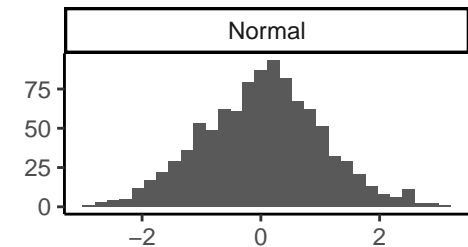


But how do I know which distribution to use?



And if thou gaze long into an abyss, the abyss will also gaze into thee - F. Nietzsche

Let's take a look at some *common* ones!

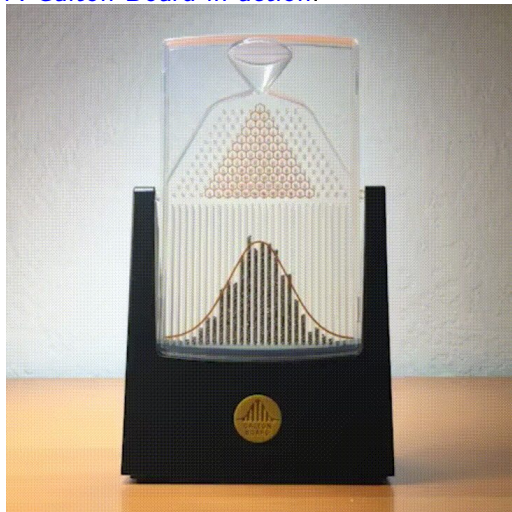


Time to meet the Exponential family!

The Normal Distribution (aka *Gaussian*)

- Imagine many random $+$ and $-$ numbers added together

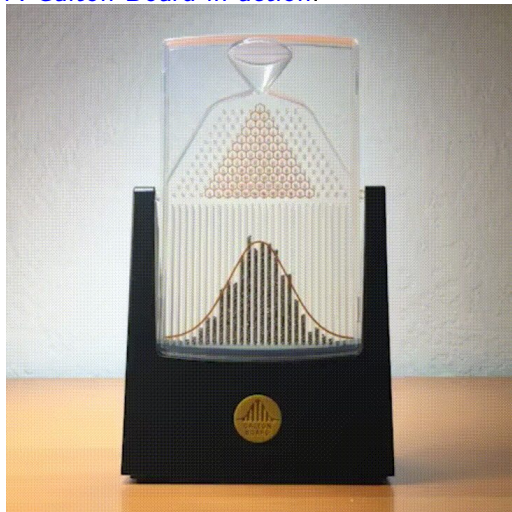
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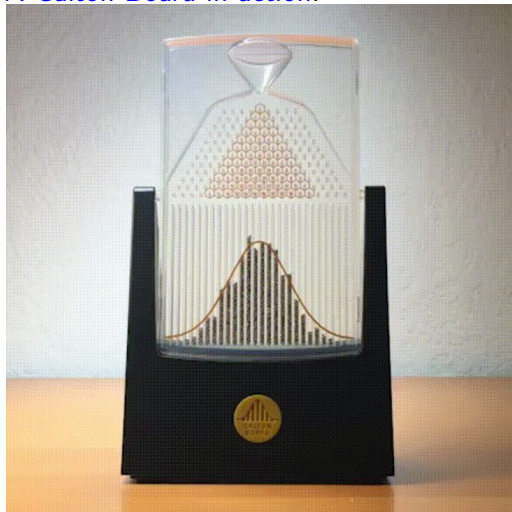
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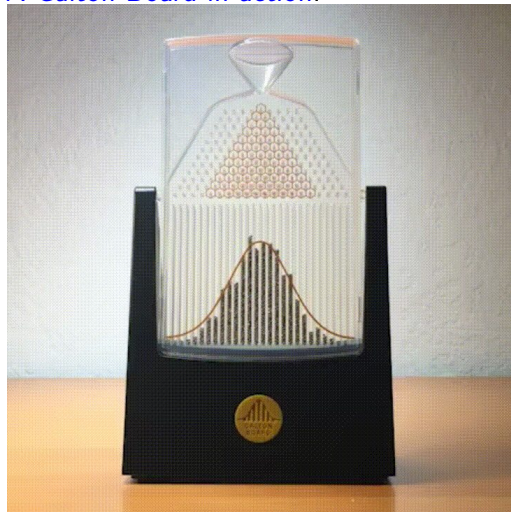
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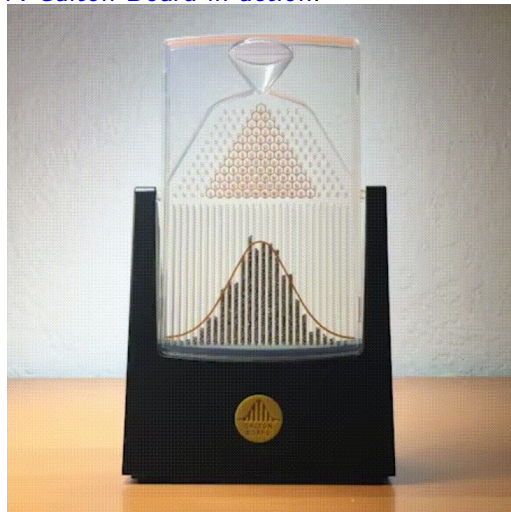
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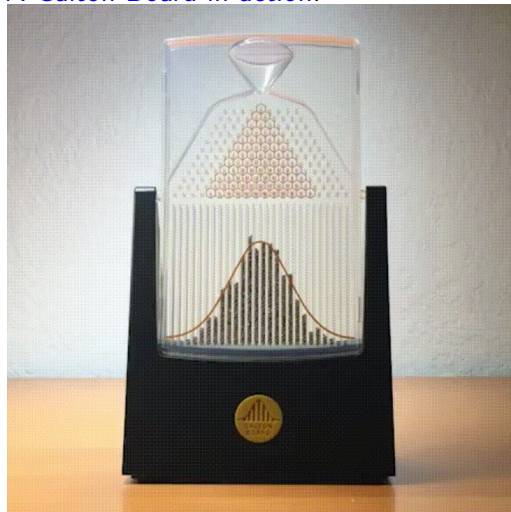
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 - e.g. Height is driven by many sets of genes

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The Normal Distribution - scary math!

- 2 parameters: mean (μ) and standard deviation (σ)

$$p(x|\mu, \sigma) = \frac{1}{\sigma\sqrt{2\pi}} e^{-\frac{1}{2}\left(\frac{x-\mu}{\sigma}\right)^2}$$

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Example: what is the probability of getting a 4, if the mean is 5 and SD is 1?

$$p(4|5, 1) = \frac{1}{1\sqrt{2\pi}} e^{-\frac{1}{2}\left(\frac{4-5}{1}\right)^2} \\ = \sim 0.24$$

In R, this is easy:

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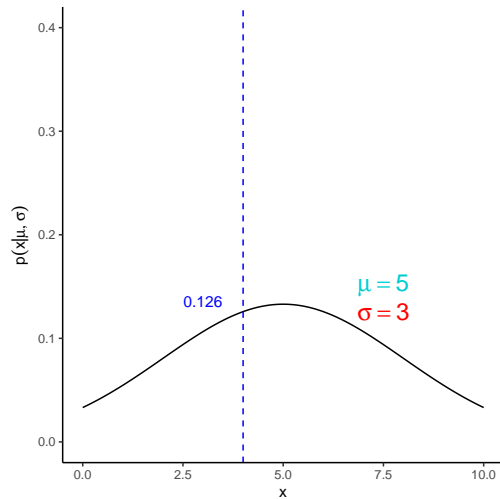
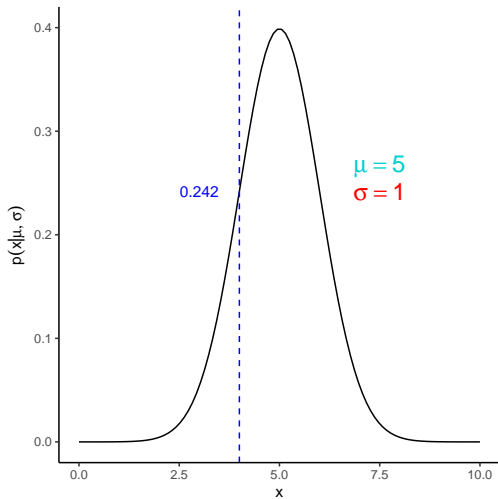
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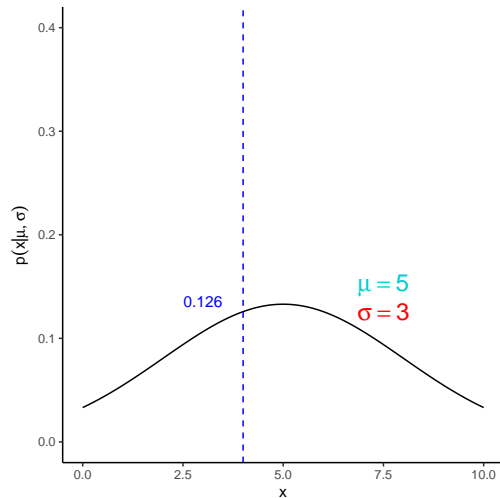
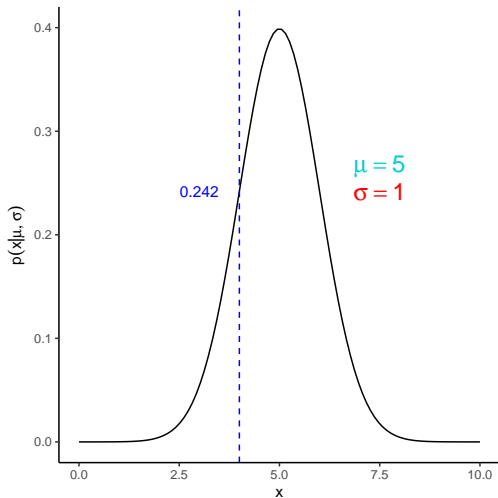
```
#d stands for "density"  
dnorm(x=4, mean=5, sd=1)  
## [1] 0.2419707
```

The Normal Distribution



- Probability of x changes with μ and σ

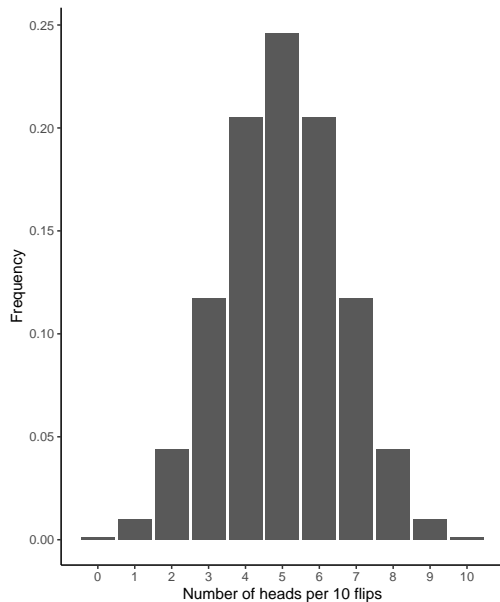
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- Left: $\sigma = 1$, Right: $\sigma = 3$

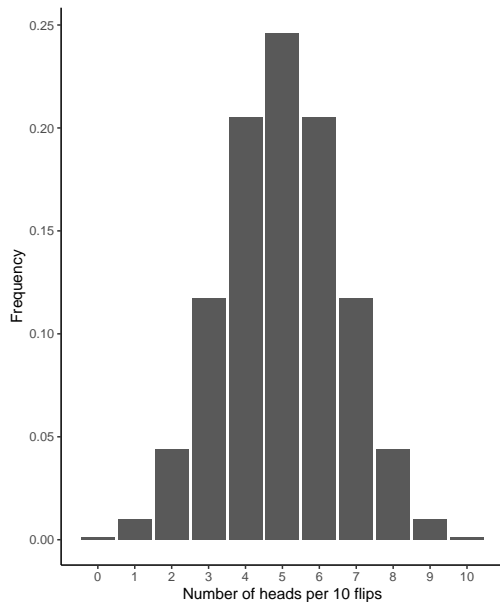
The Binomial Distribution

- Imagine you have 10 coins, and you flip them all



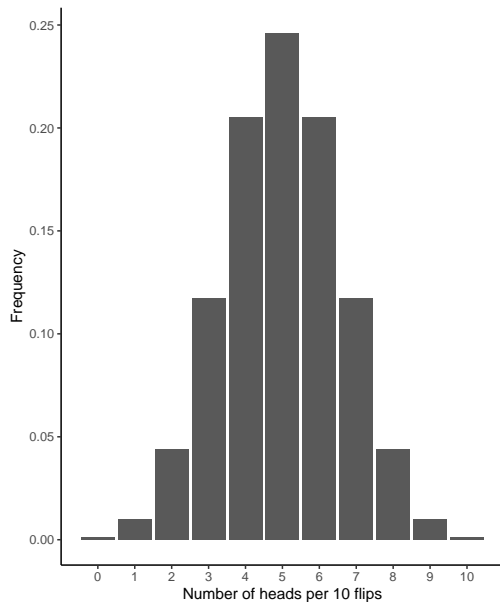
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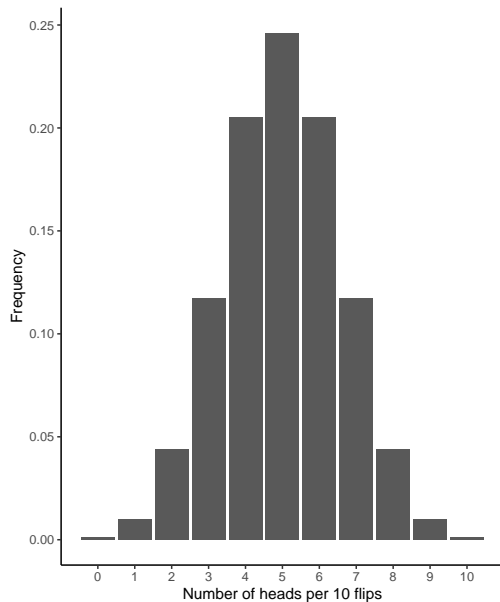
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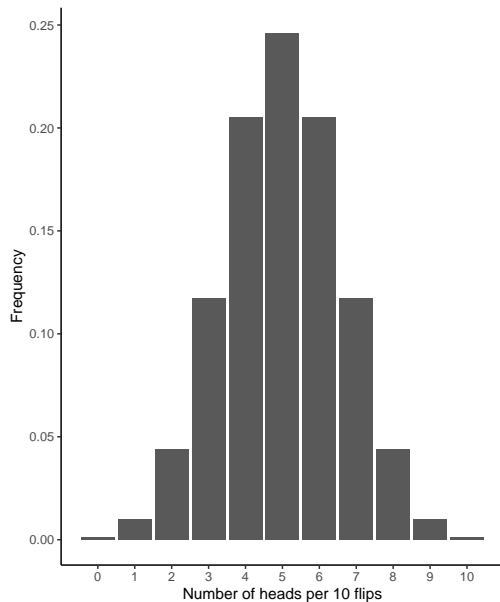
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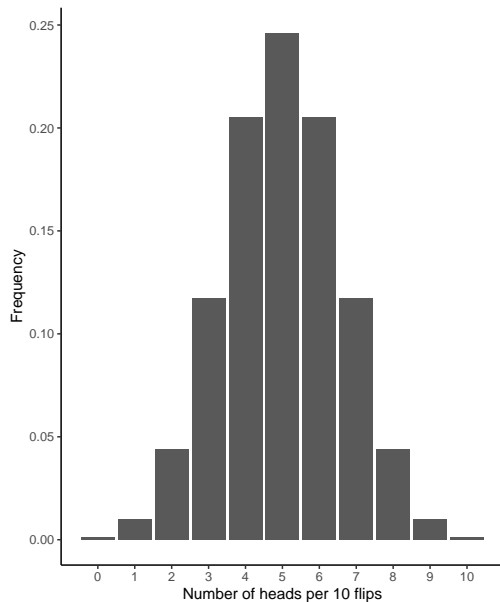
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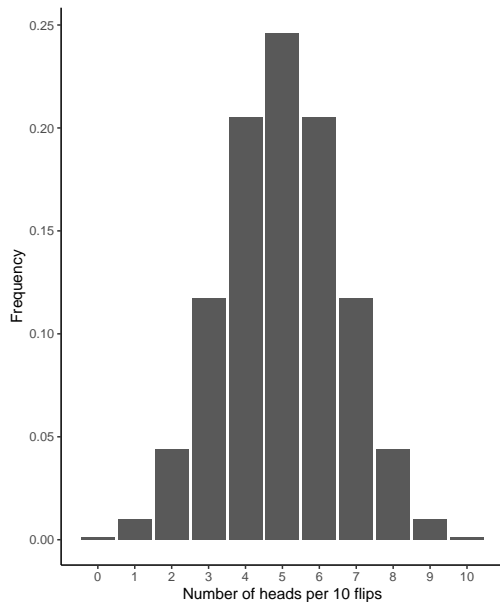
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- If $N = 1$, this is called a *Bernoulli trial*



The Binomial Distribution - scary math!

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$$p(x|\phi, N) = \binom{N}{x} \phi^x (1 - \phi)^{N-x}$$

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Example: what is the probability of getting 4 successes, if ϕ is 0.25 and N is 15?

$$p(4|0.25, 15) = \binom{15}{4} 0.25^4 (1 - 0.25)^{15-4} \\ = \sim 0.23$$

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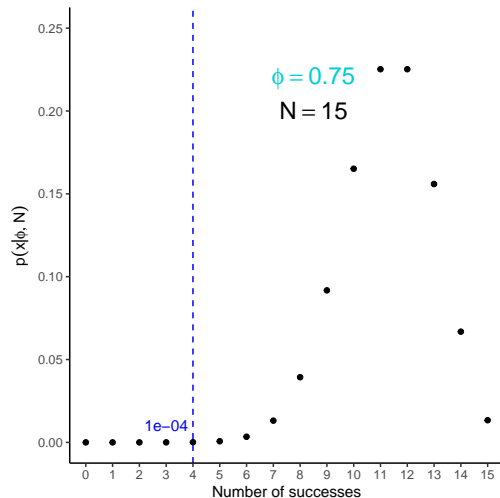
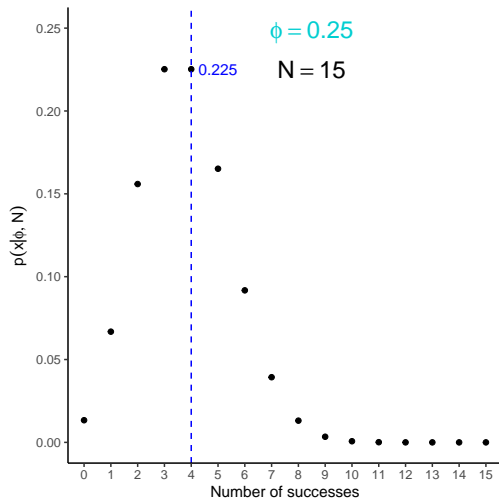
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In R, this is easy:

```
dbinom(x=4, size=15, prob=0.25)
```

```
## [1] 0.2251991
```

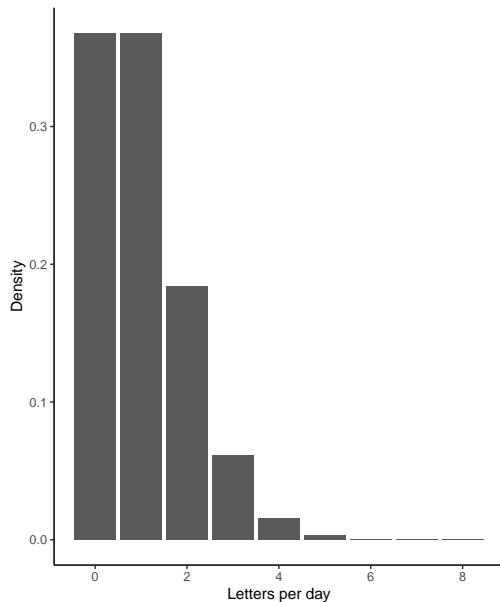
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- Probability of x “successes” changes with ϕ and N

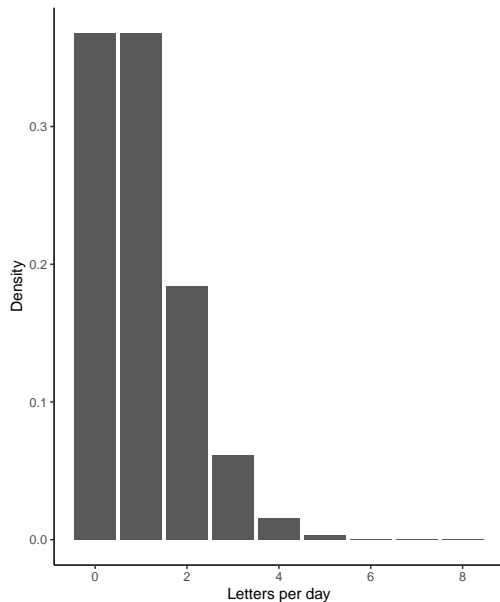
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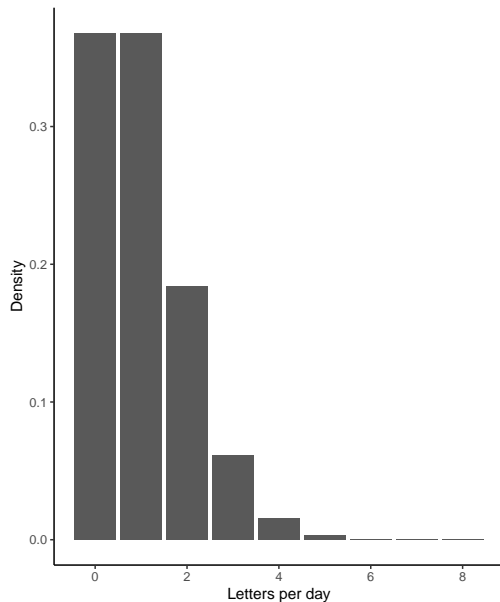
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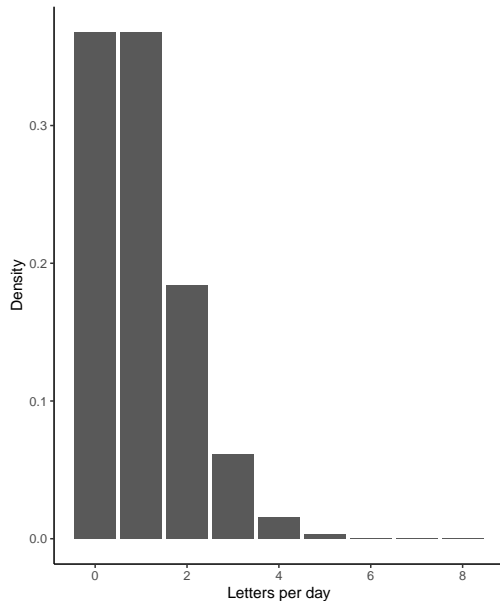
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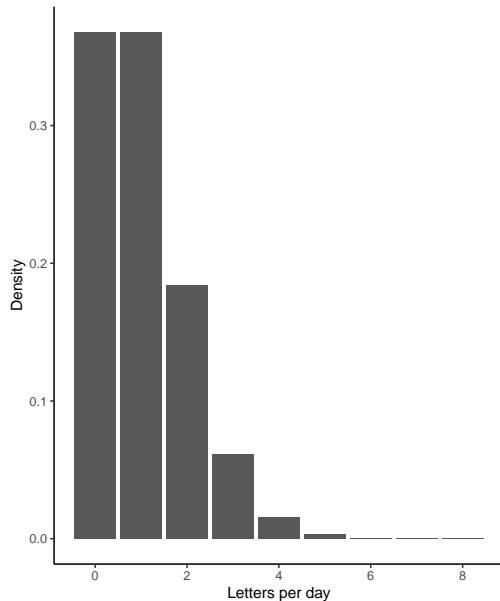
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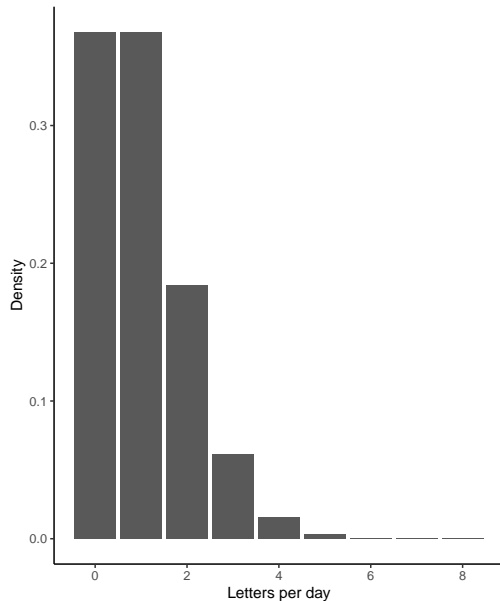
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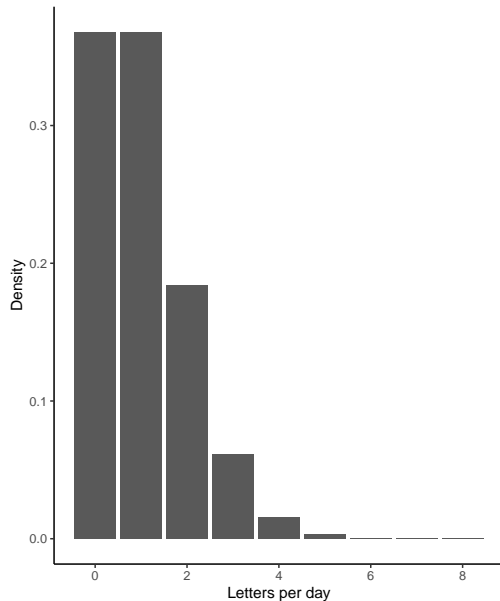
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- Equivalent to Binomial distribution, where N is unknown



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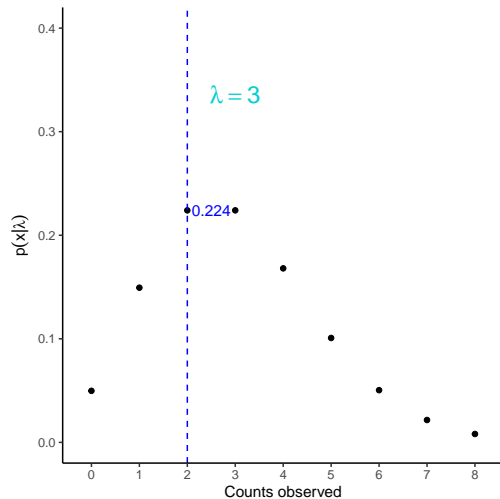
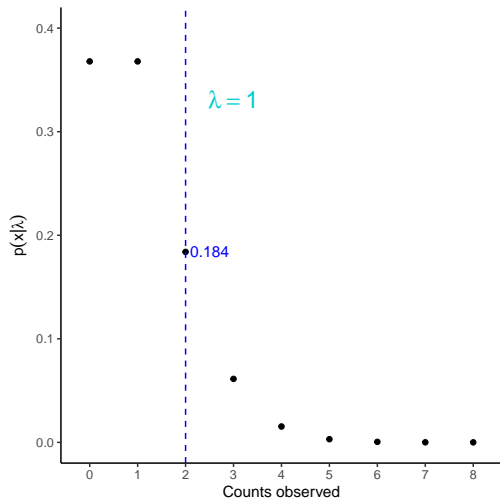
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In R, this is easy:

```
dpois(x=2,lambda=1)
```

```
## [1] 0.1839397
```

The Poisson Distribution



- Probability of x counts changes with λ

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 - *Beta Binomial* and *Negative Binomial* distributions

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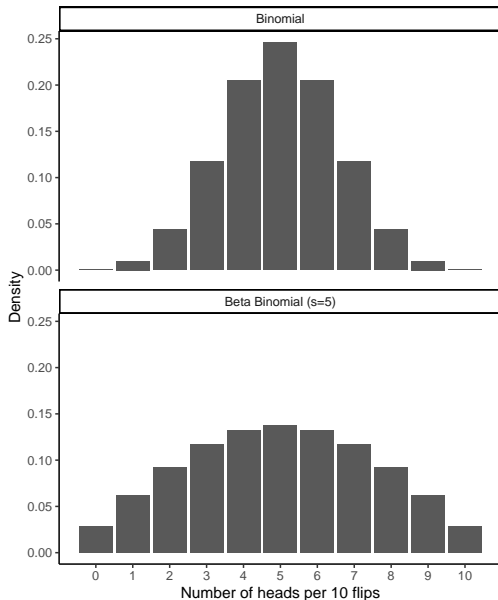
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#Extra distributions

```
library(rmutil)
```

```
dbetabinom(x,m=phi,size=N,s=5)
```



The Negative Binomial Distribution

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- Negative Binomial is similar to a Poisson, but can have longer tails

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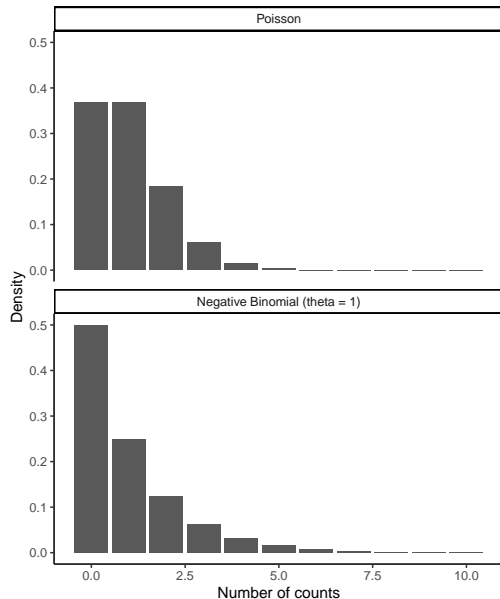
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```
#size = theta parameter  
dnbinom(x,mu,size=1)
```



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These are by *no means* the only useful distributions, but are fairly common

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 - `rbinom(n, size, prob)` or `rbetabinom(n,size,m,s)`

Part 2: Maximum likelihood and GLMs

Outline

- Maximum likelihood

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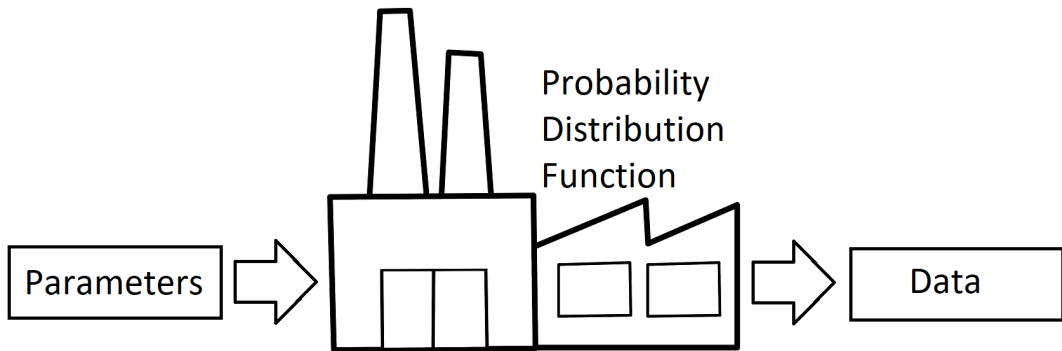
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 - Predictors \rightarrow Linear model

How is our data made?

Making data can be thought of as a *factory*

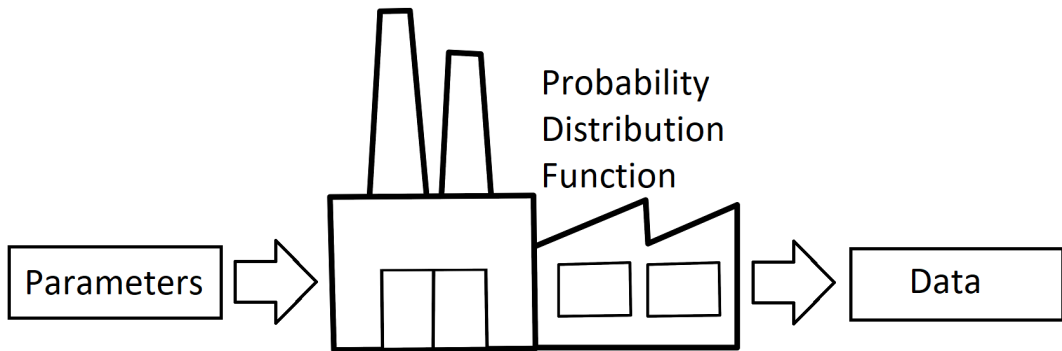
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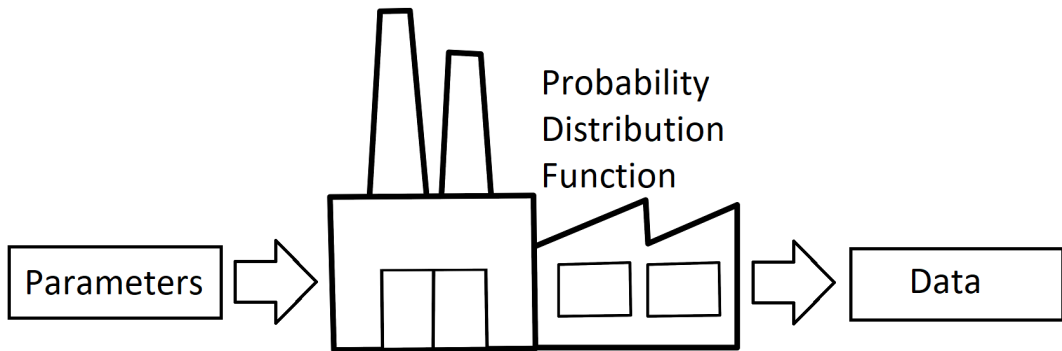
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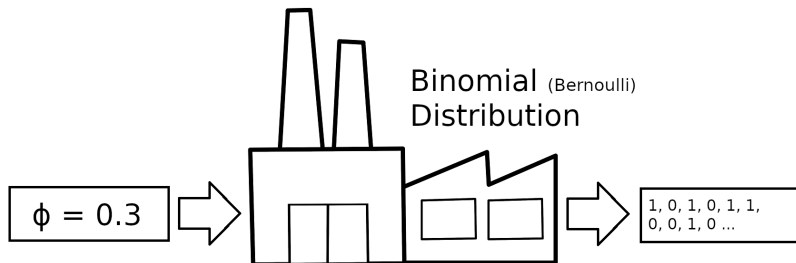
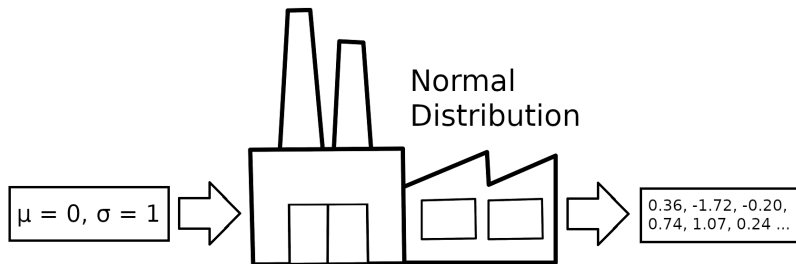
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- Process: **probability function**
- Output: **data** (things made by the process)

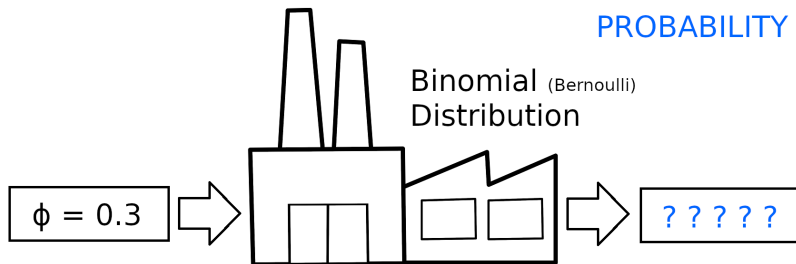


Examples

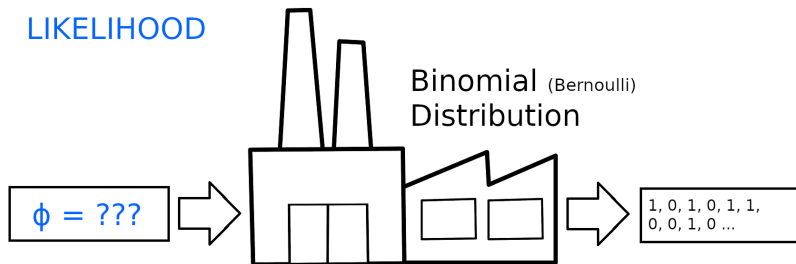


Likelihood vs Probability

PROBABILITY



LIKELIHOOD



Likelihood vs Probability (cont.)

Probability and likelihood both use the same PDF

- “I know that $\phi = 0.3$. What is the chance of getting 2 heads and a tail?”

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dbinom(1,1,0.3)*dbinom(1,1,0.3)*dbinom(0,1,0.3)
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```
## [1] 0.063
```

Since we're (mostly) collecting data and trying to guess parameters from it, are we dealing with *probability* or *likelihood*?

Likelihood vs Probability (cont.)

Let's see how *likelihood* changes with different values of ϕ :

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#phi = 0.3  
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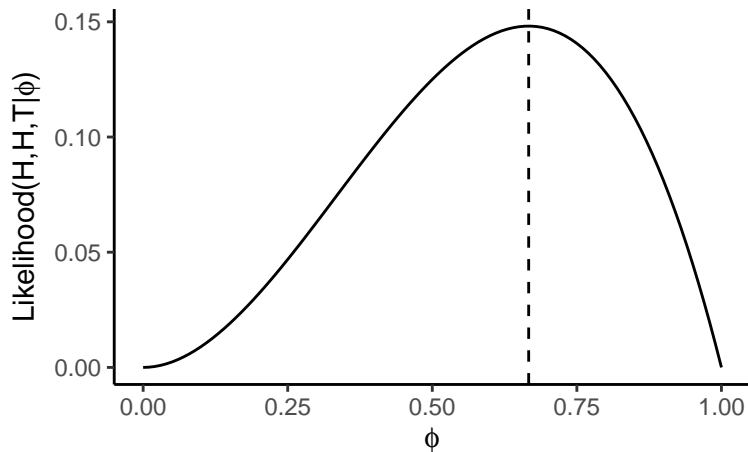
```
## [1] 0.063
```

```
#phi = 0.7  
dbinom(1,1,0.7)*dbinom(1,1,0.7)*dbinom(0,1,0.7)
```

```
## [1] 0.147
```

Likelihood of $\phi = 0.7$ is higher, i.e. $\phi = 0.7$ matches our data *better*

Likelihood



The best match (**maximum likelihood** value) is at $\phi = 0.666$ (2 heads out of 3 flips)

Generalized Linear Models

`glm()` will fit a model like this, and find the ML solution

```
dat <- data.frame(flips=c(1,1,0)) #Data (2 heads, 1 tail)  
mod1 <- glm(flips~1,data=dat,family='binomial') #Note family specification  
summary(mod1)
```

```
##  
## Call:  
## glm(formula = flips ~ 1, family = "binomial", data = dat)  
##  
## Coefficients:  
##             Estimate Std. Error z value Pr(>|z|)  
## (Intercept)   0.6931     1.2247   0.566   0.571  
##  
## (Dispersion parameter for binomial family taken to be 1)  
##  
##      Null deviance: 3.8191  on 2  degrees of freedom  
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## AIC: 5.8191  
##  
## Number of Fisher Scoring iterations: 4
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Wait... our estimate should be 0.666 (2/3), not 0.693!

Link functions

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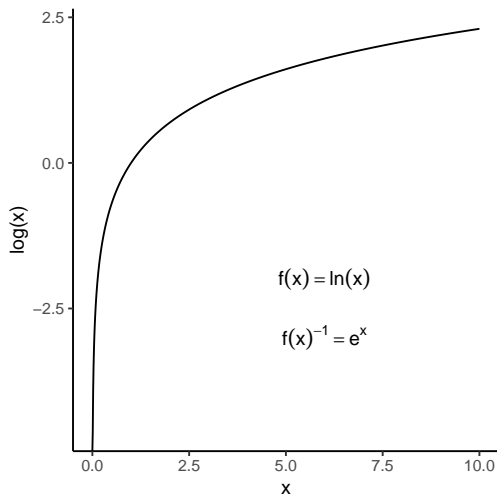
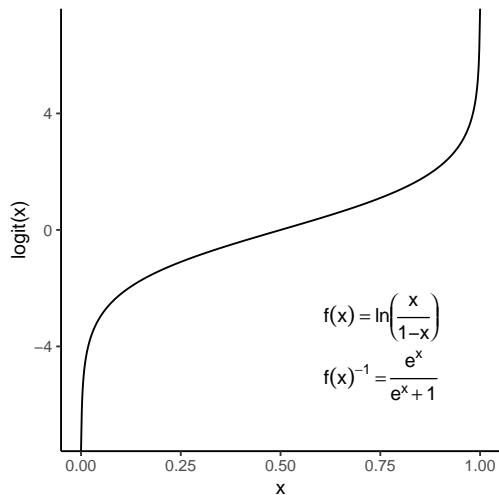
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- $\text{logit}(0.693) = 0.666$, so the GLM actually got it right!

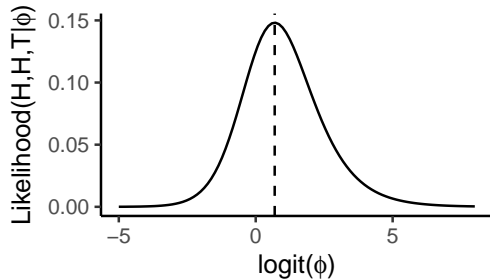
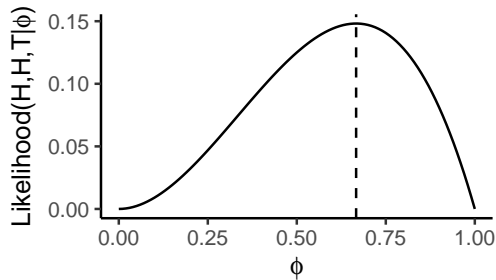
What do these functions look like?



- These functions map parameter values from the appropriate range (0-1 or 0- ∞) onto $-\infty$ to $+\infty$

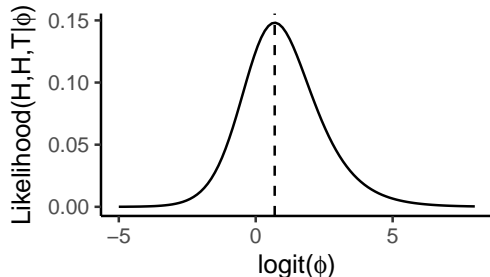
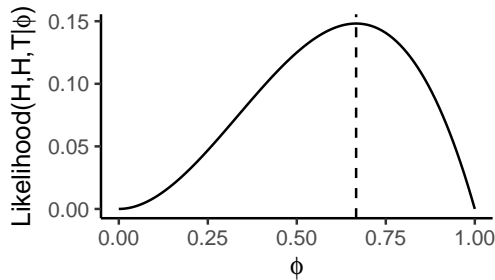
Why do we bother with these link function?

- Likelihood functions are not symmetrical on the regular scale



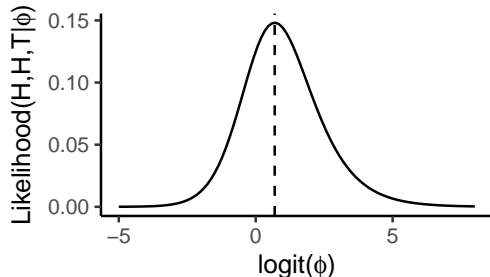
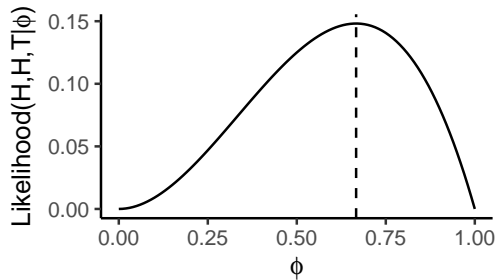
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- On the link-scale, they are closer to a normal distribution
- Makes it easier for R to find the ML estimate (and confidence intervals)



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$$\text{logit}(\hat{\phi}) = b_0 + b_1x_1 \dots + b_ix_i$$

$$\text{flips} \sim \text{Binomial}(\hat{\phi})$$

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 - Solution: ϕ becomes a *linear* function of the predictors
 - Remember: simple linear models take the form:
- Generalized linear models are similar, except that:
 - ① Expected value (ϕ) fed through a link function
 - ② Data is fit to a non-normal probability function

$$\hat{y} = b_0 + b_1x_1 \dots + b_ix_i$$

$$y \sim \text{Normal}(\hat{y}, \sigma)$$

$$\text{logit}(\hat{\phi}) = b_0 + b_1x_1 \dots + b_ix_i$$

$$\text{flips} \sim \text{Binomial}(\hat{\phi})$$

Instead of finding ϕ , R finds the coefficients ($b_0, b_1 \dots b_i$) that create ϕ

How do I fit GLMs in R?

Syntax and model output is very similar to `lm`

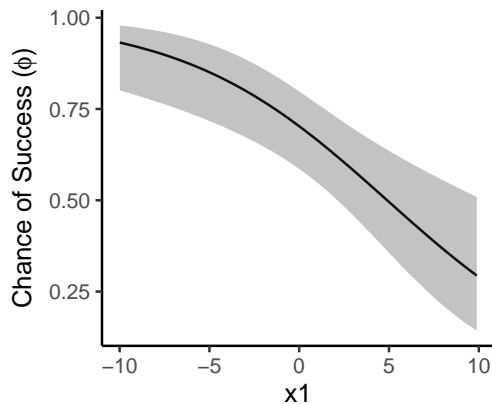
```
# y ~ x, where x is the predictor of y
mod_binomial <- glm(y2 ~ x1 + x2 , data = d1, family = 'binomial') #Fit a binomial GLM
```

```
##
## Call:
## glm(formula = y2 ~ x1 + x2, family = "binomial", data = d1)
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.81748    0.25851   3.162 0.001565 **
## x1          -0.17576    0.04871  -3.608 0.000309 ***
## x2           0.30193    0.09950   3.034 0.002410 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 129.49  on 99  degrees of freedom
## Residual deviance: 102.98  on 97  degrees of freedom
## AIC: 108.98
##
## Number of Fisher Scoring iterations: 4
```

Dispersion and deviance will be discussed later...

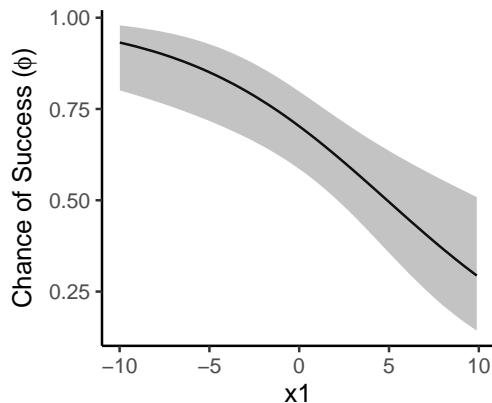
How do I get partial effects plots?

- `crPlot` (from `car`) and `ggpredict` (`ggeffects`) work with fitted `glm` models:



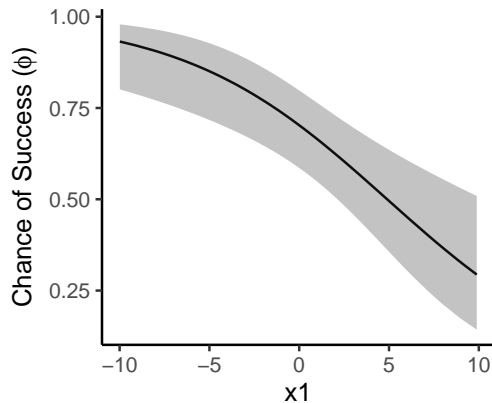
How do I get partial effects plots?

- `crPlot` (from `car`) and `ggpredict` (`ggeffects`) work with fitted `glm` models:
- Why is the line not straight? Why are the confidence intervals not symmetrical?



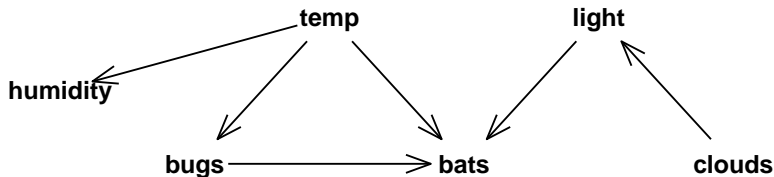
How do I get partial effects plots?

- `crPlot` (from `car`) and `ggpredict` (`ggeffects`) work with fitted `glm` models:
- Why is the line not straight? Why are the confidence intervals not symmetrical?
- Answer: the model is *linear* on the link scale, but *nonlinear* on the data scale



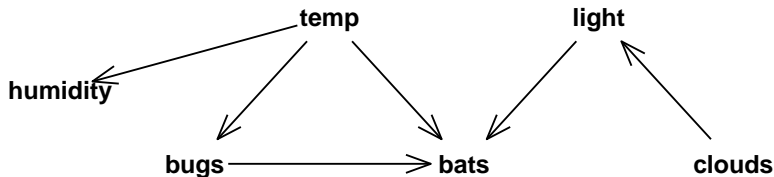
Second challenge

- Remember that bat data from last week? (Found [here](#) in `batDat.csv`). We used a `lm` last week to fit it, but it actually came from a `glm`



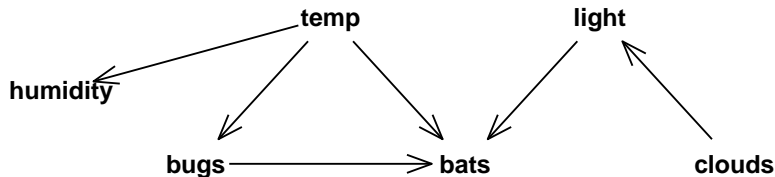
Second challenge

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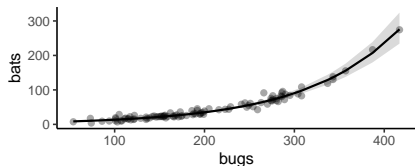
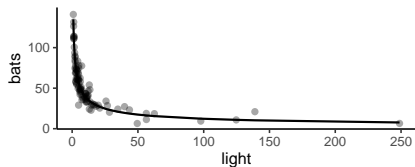
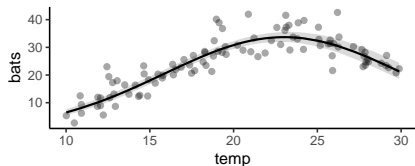


Second challenge

- Remember that bat data from last week? (Found [here](#) in `batDat.csv`). We used a `lm` last week to fit it, but it actually came from a `glm`
- Fit a `glm` to those data, check how the model fits, and make some partial effects plots
- Recall: this is the “true” causal relationship here (no interactions)



Model results



```
##
## Call:
## glm(formula = bats ~ poly(temp, 2) + log(light) + bugs, family = "poisson",
##      data = batDat)
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    2.756999   0.077780   35.45  <2e-16 ***
## poly(temp, 2)1    3.253942   0.321972   10.11  <2e-16 ***
## poly(temp, 2)2   -2.765370   0.160287  -17.25  <2e-16 ***
## log(light)      -0.508112   0.011943  -42.54  <2e-16 ***
## bugs            0.009513   0.000346   27.49  <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: 8237.284  on 99  degrees of freedom
## Residual deviance:  91.794  on 95  degrees of freedom
## AIC: 645.77
##
## Number of Fisher Scoring iterations: 4
```

Part 3: Models behaving badly

Motivation

- Are my model results reliable?

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 - Residual checks

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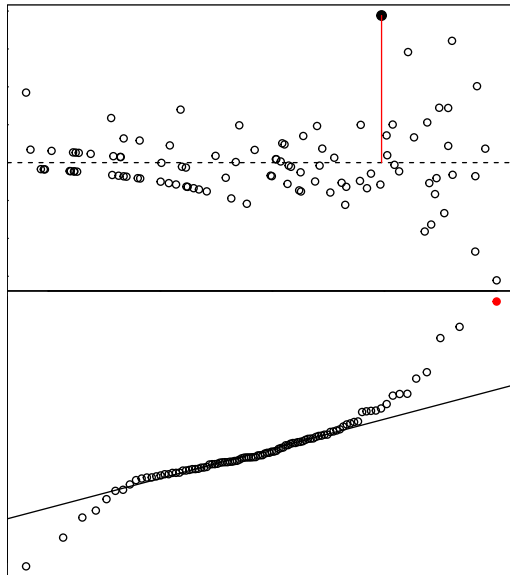
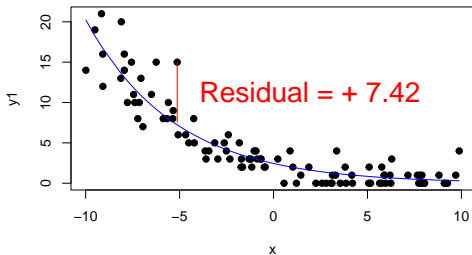
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Deviance residuals use *likelihood*:

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

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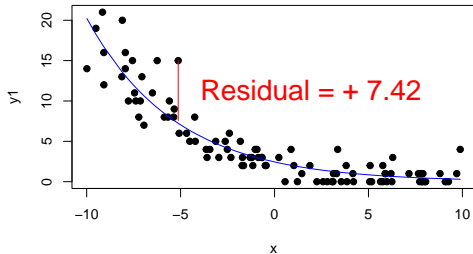
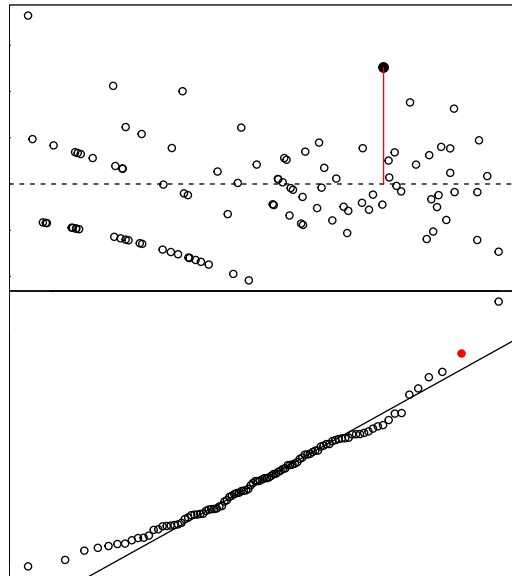
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- For more about the different kinds of residuals, see [here](#)

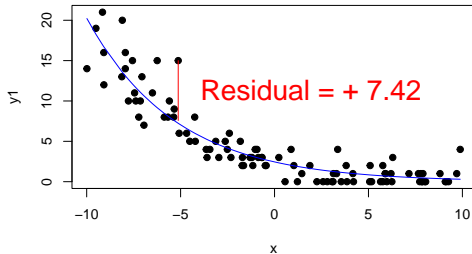
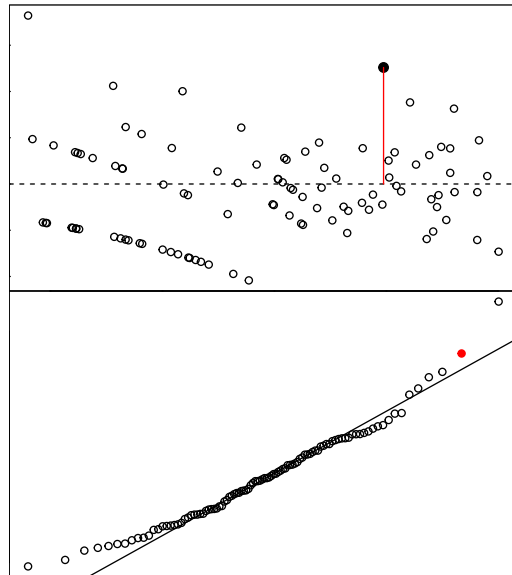
Solution: use deviance residuals for GLMs

- Residuals from GLMs will never be as “pretty” as those from LMs



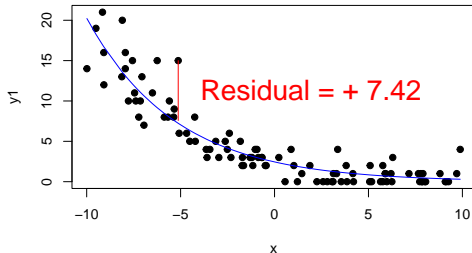
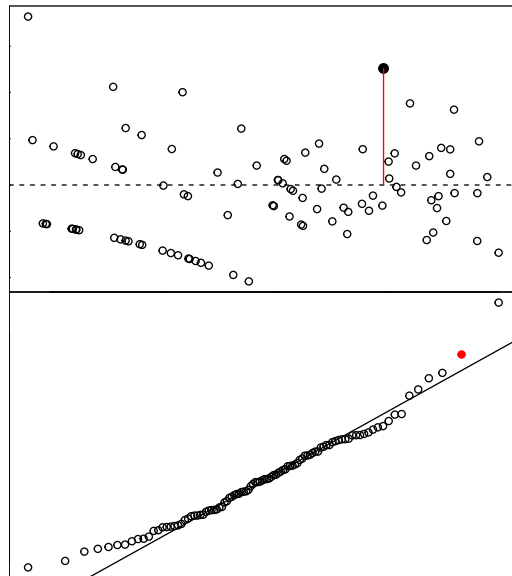
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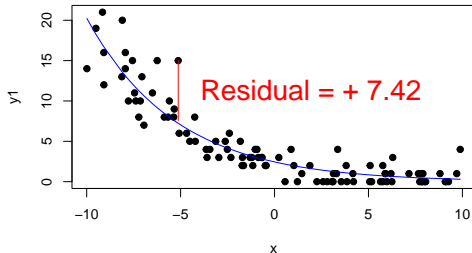
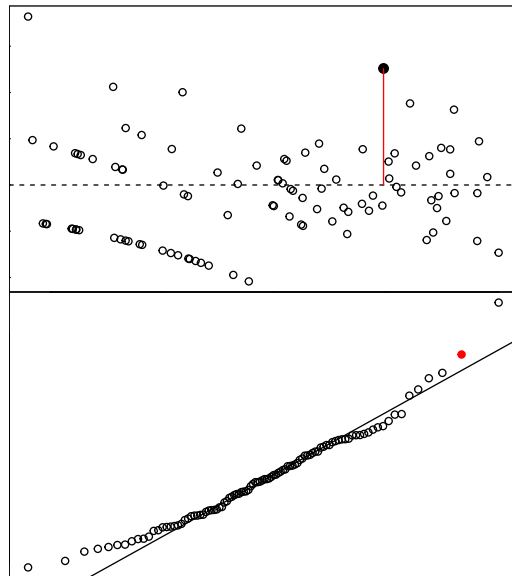
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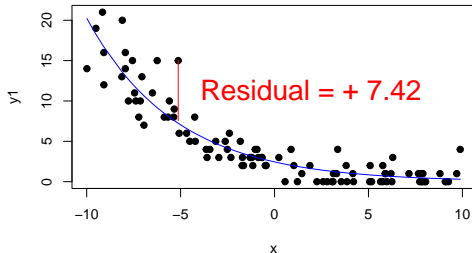
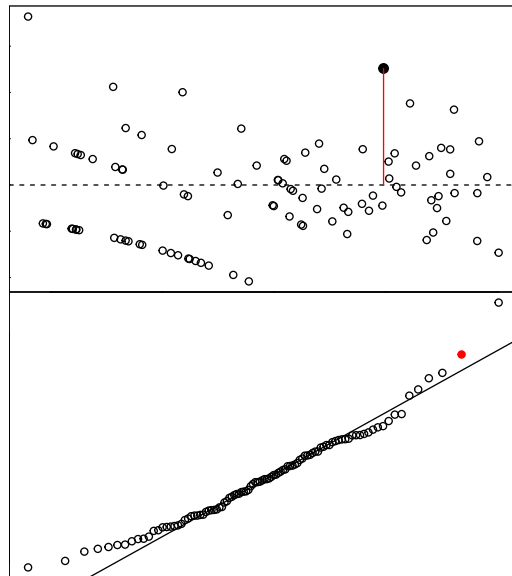
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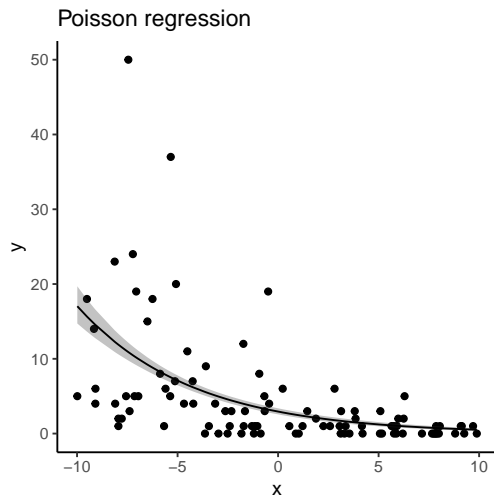
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- Residuals from GLMs will never be as “pretty” as those from LMs
- *Especially* true for:
 - Binomial GLMs
 - Poisson/Negative Binomial GLMs with many zeros
- Next week we will deal with *simulation testing* residuals



Problem 2: Overdispersion

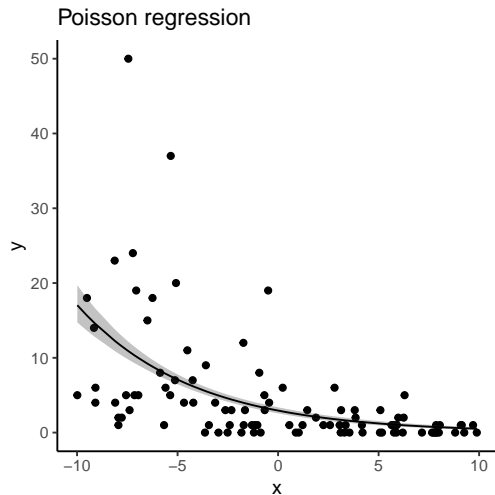
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Example: data are much more variable than the predictions from the model

Problem 2: Overdispersion

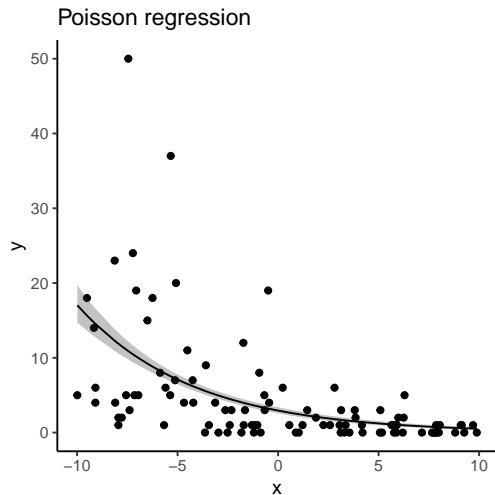
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Example: data are much more variable than the predictions from the model

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 2: Overdispersion

```
##
## Call:
## glm(formula = y1 ~ x, family = "poisson", data = d1)
##
## 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

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- 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 2: Overdispersion

```
##
## Call:
## glm(formula = y2 ~ x, family = "poisson", data = d1)
##
## 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 ($501.98 \div 98 = 5.12$)

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- 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

¹Random effects discussed later

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- Lots of zeros in count data
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- Leaving out an important term
 - e.g. An important *interaction* term was omitted
- Random effects¹not accounted for
 - e.g. Data collected at different sites, but ignored

¹Random effects discussed later

Solutions for overdispersion

Try the following (in this order):

- ① Consider terms that may have been left out

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

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- ③ Lower your expectations, and use a lower critical p-value (e.g. 0.01 instead of 0.05)
- ④ Design a better study :(

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

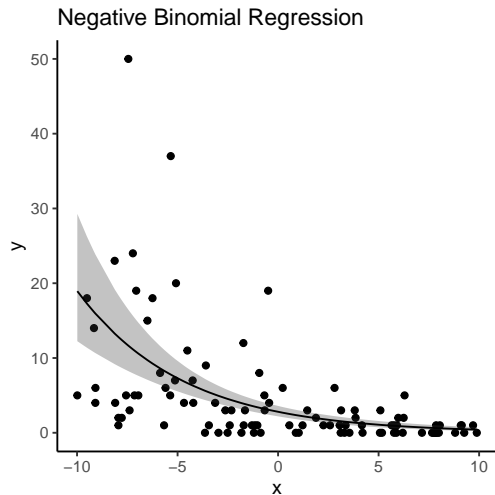
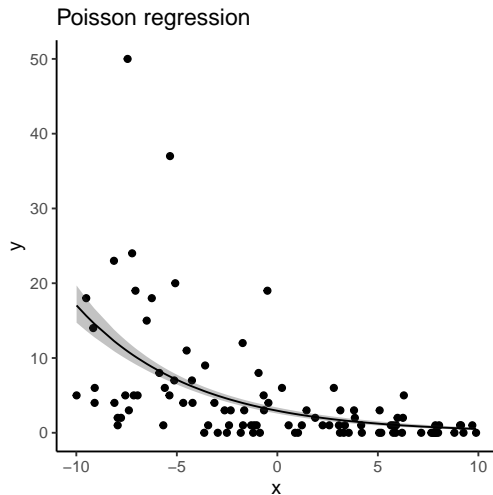
Negative Binomial Regression

```
library(MASS) #Required for NB models  
m3 <- glm.nb(y2~x,data=d1)  
summary(m3)
```

- Model no longer indicates overdispersion!

```
##  
## Call:  
## glm.nb(formula = y2 ~ x, data = d1, init.theta = 1.075023363,  
##       link = log)  
##  
## Coefficients:  
##             Estimate Std. Error z value Pr(>|z|)  
## (Intercept)  1.03037    0.12281   8.390  <2e-16 ***  
## x            -0.19131    0.02222  -8.609  <2e-16 ***  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## (Dispersion parameter for Negative Binomial(1.075) family taken to be 1)  
##  
##      Null deviance: 182.31  on 99  degrees of freedom  
## Residual deviance: 103.87  on 98  degrees of freedom  
## AIC: 458.65  
##  
## Number of Fisher Scoring iterations: 1  
##  
##  
##              Theta:  1.075  
##             Std. Err.:  0.216  
##  
## 2 x log-likelihood: -452.653
```

Negative Binomial Regression (cont.)



Zero-inflation: drunk monks

A way to think about this model:

- ① Monks at a monastery make copies of manuscripts. Most days they make very few (0 or 1), but occasionally they make many (2-5)

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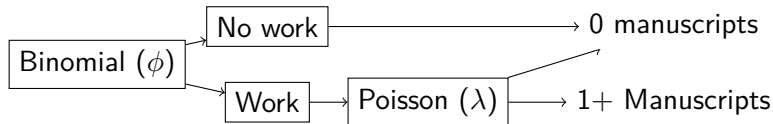
This is *mixture* of a Poisson and a Binomial:

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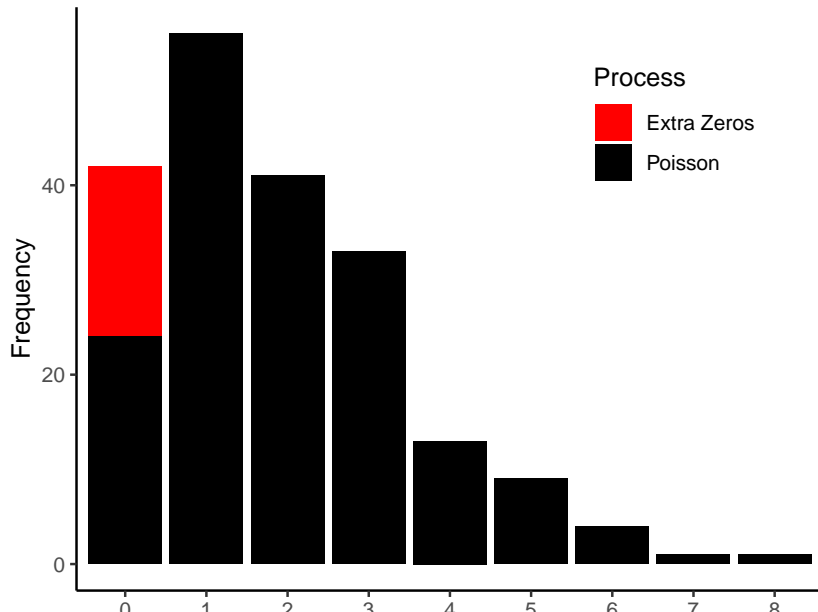
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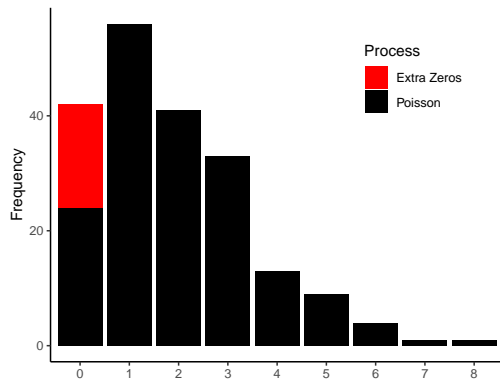
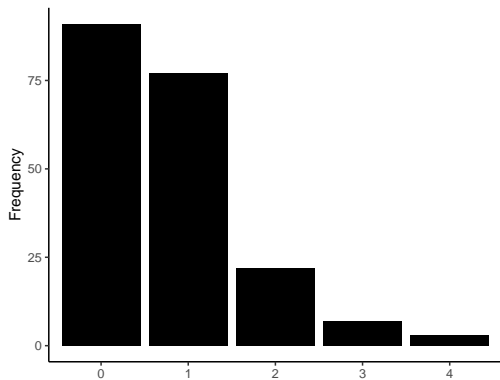


Zero-inflation: graphical model



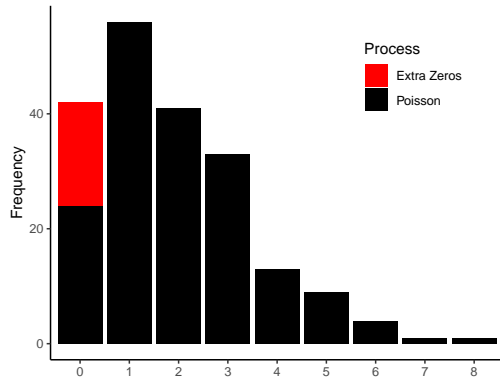
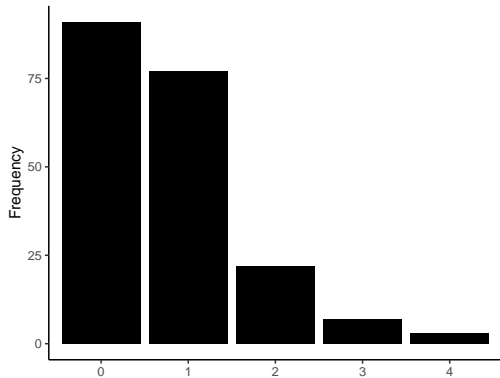
Problem: hard to fit

- Hard for R to tell the difference between ZIP/ZINB, and a Poisson/NB with a low mean (λ).



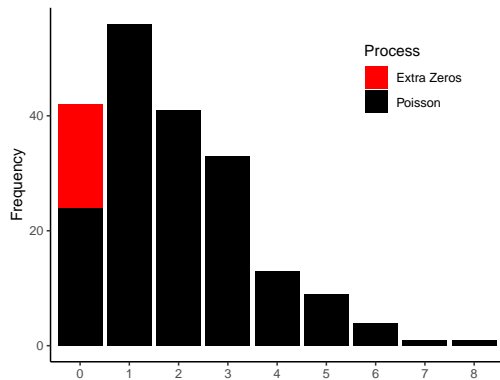
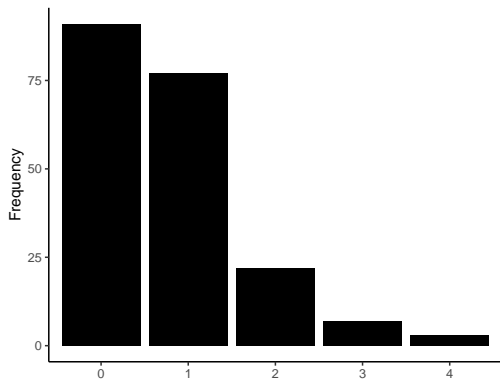
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- The modeling approaches for this are somewhat bespoke, so if you need to use this, come talk to me!



Model selection

How many terms should be in my model?

- Same principle as in regular linear models: **what do you think the process is?**

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 - AIC tests usually say the same thing as LR tests

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```
#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

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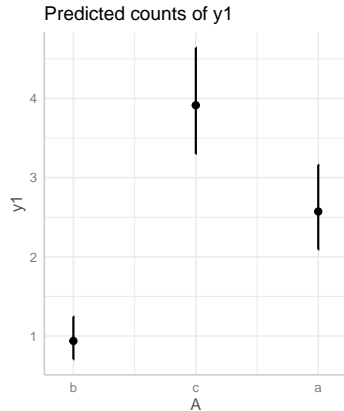
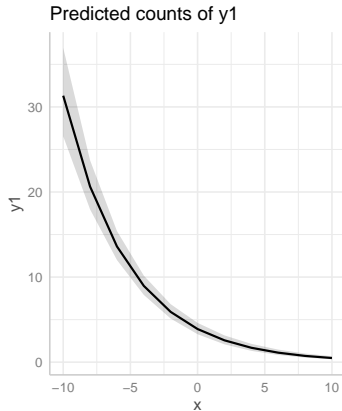
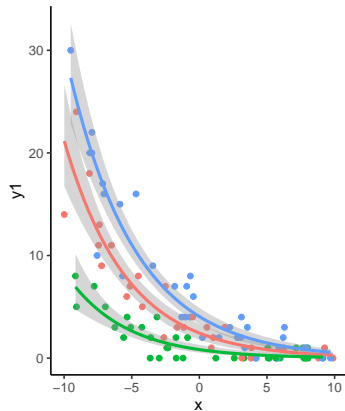
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```
#hours = observation time at each site (must be log-transformed)
glm(counts ~ offset(log(hours)) + temp, family='poisson', data = d1)
```

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

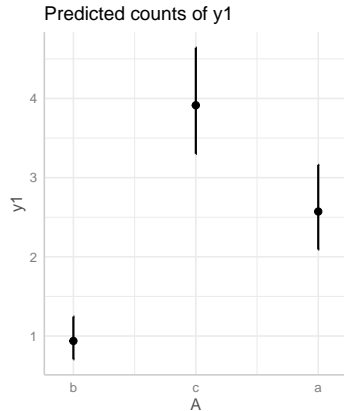
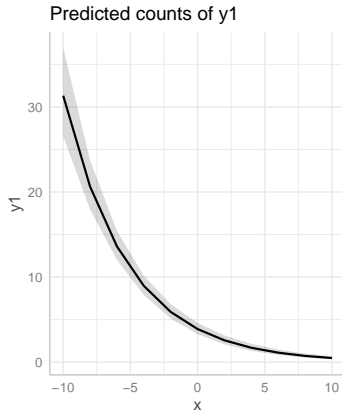
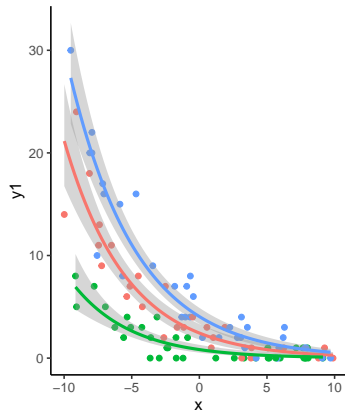
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- `library(ggeffects)` and `library(effects)` work for partial effects plots, but...
- Residuals are tricky to display, unless you plot them on the link scale

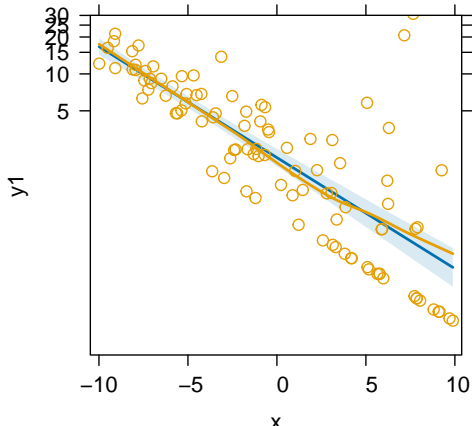


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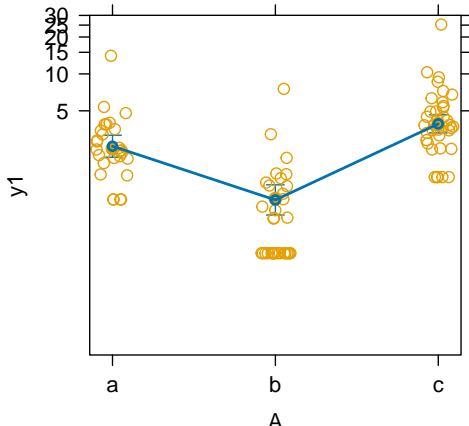
- Plots from effects use *working residuals* (not on the link scale)

```
library(effects)  
plot(allEffects(m4,residuals=TRUE))
```

x effect plot



A effect plot



Third challenge

- Dr. *Paulo Malpern* (Paul Galpern's evil nemesis) sent 2 people out to check out some bee habitats in Edmonton and Calgary. Counted bees at each site, but the other one was really lazy, and just recorded “bees or no bees” (1 or 0).

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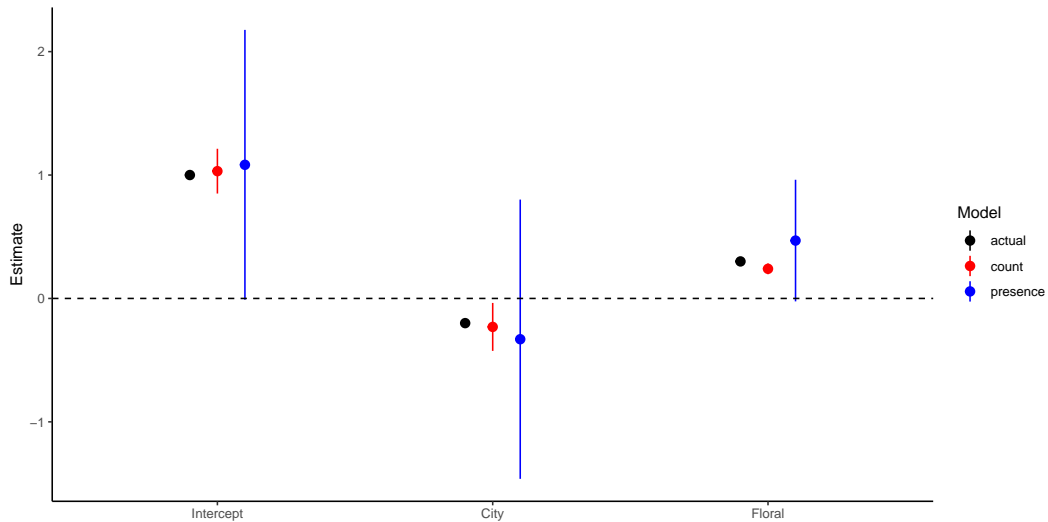
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 - Bonus: make partial regression plots of the terms each GLM

Model results



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 - Clean up this dataset (there are a couple NAs and unrealistic numbers), fit a GLM that answers my question, and make some plots of your results. Were there any important *interactions* between the `VegMass` and `Distance`?