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

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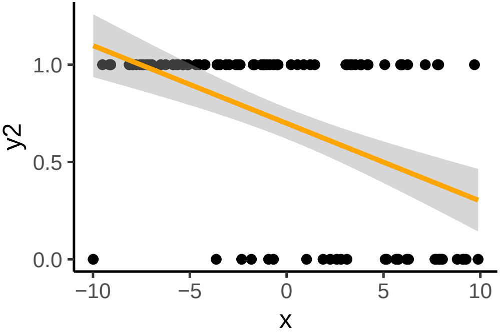
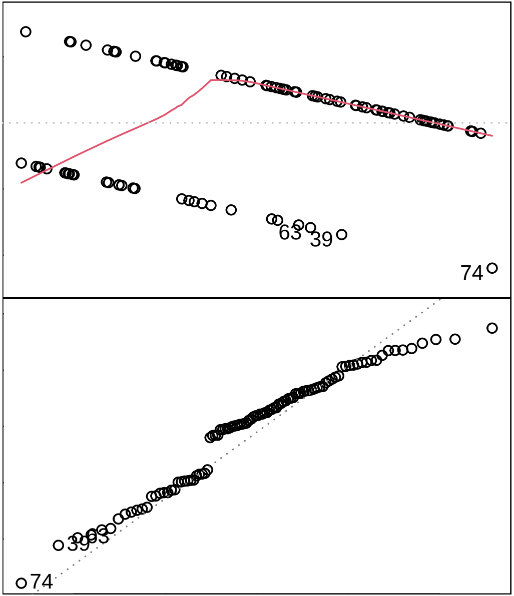
- "Play time"

Christmas gifts for the nerds in your life

Problem: not everything is normal





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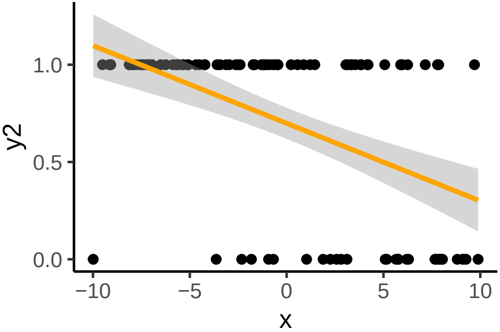
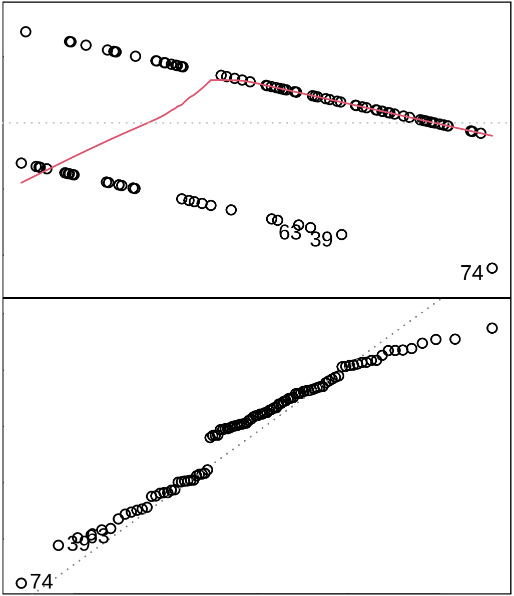
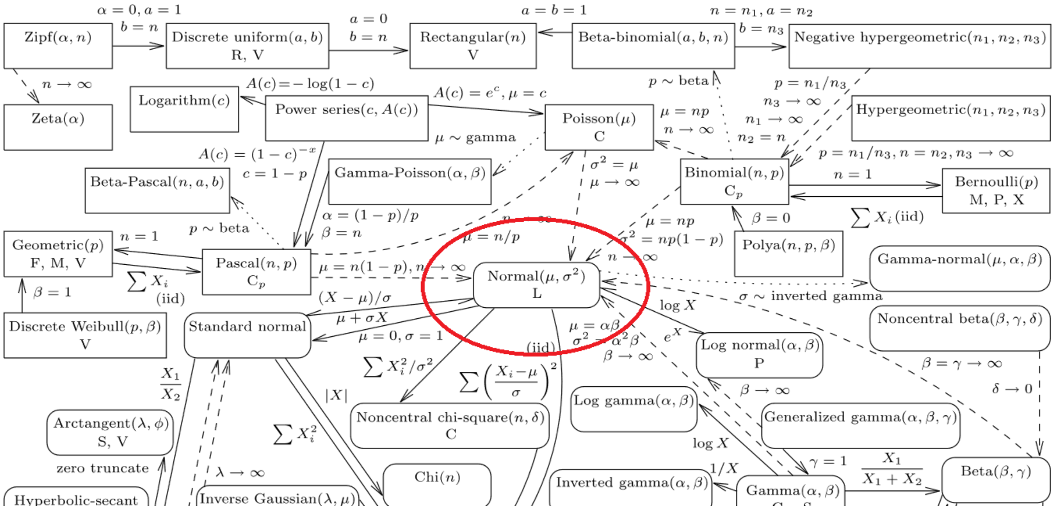




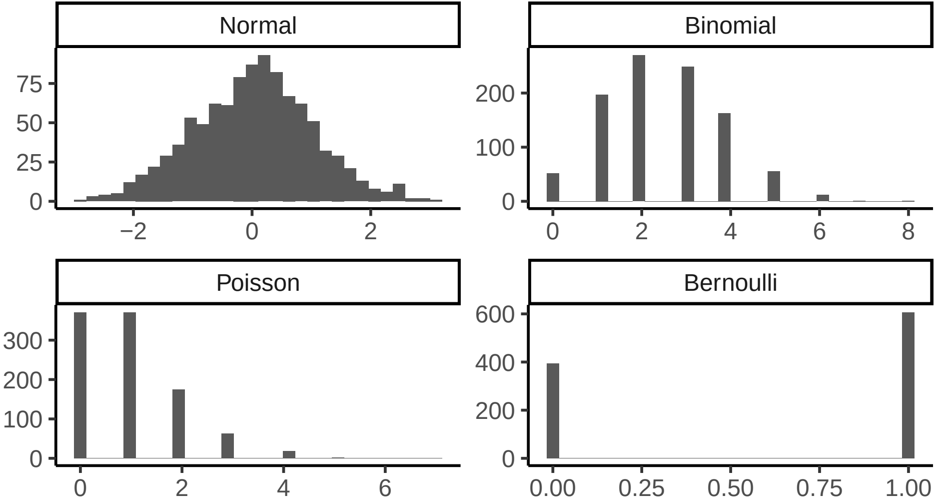
- Some types of data can never be transformed to make the residuals normal
- Solution: **use the distribution that generates the data!**

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

A Galton Board in action:

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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?

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

In R, this is easy:

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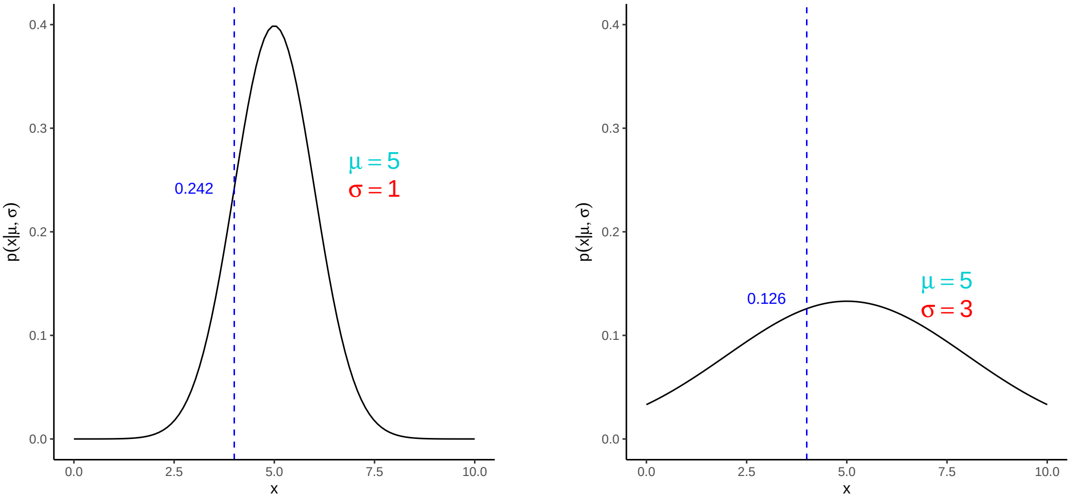
```
#d stands for "density"
dnorm(x=4,mean=5,sd=1)
```

```
## [1] 0.2419707
```

The Normal Distribution



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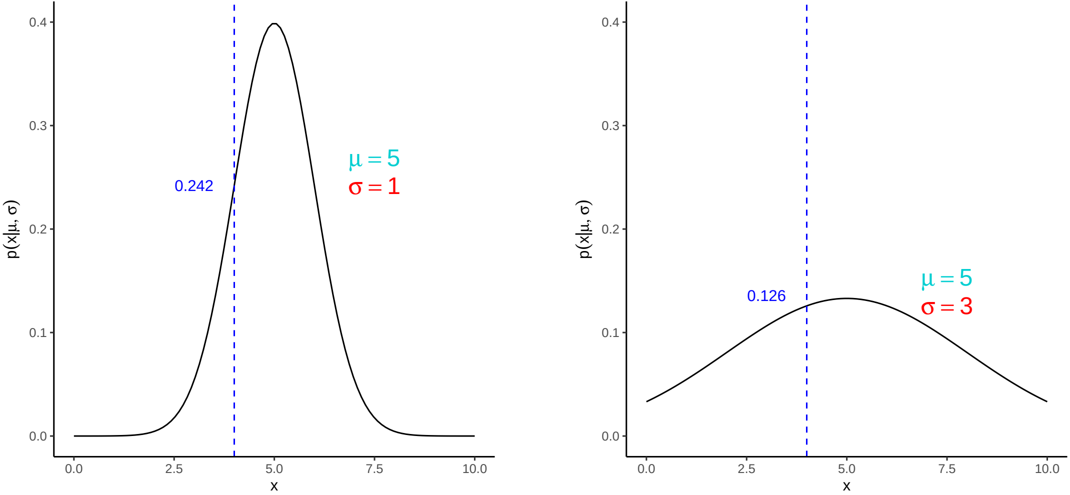
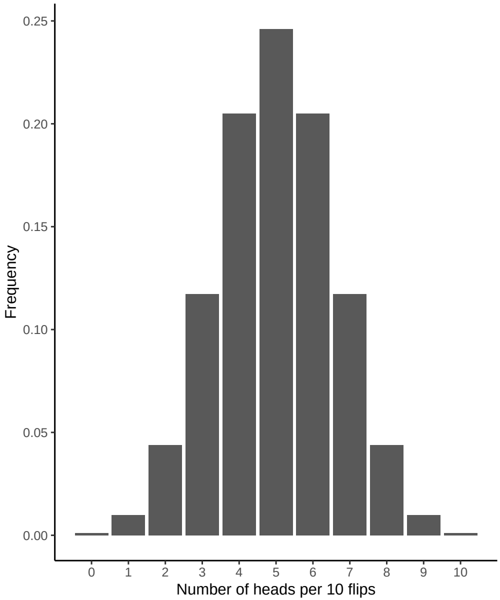


- Probability of x changes with μ and σ
- Left: $\sigma = 1$, Right: $\sigma = 3$

The Binomial Distribution

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



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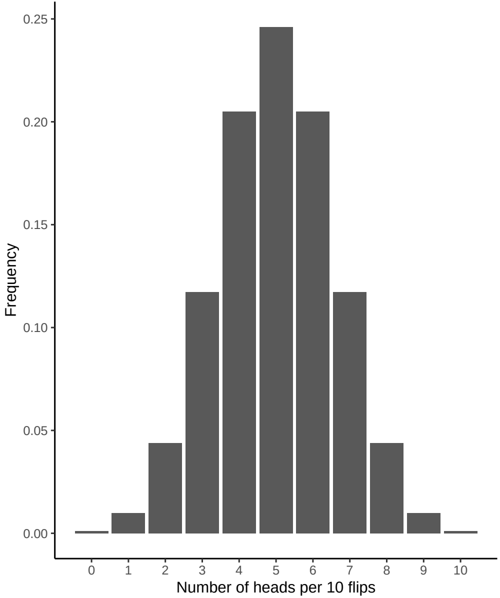

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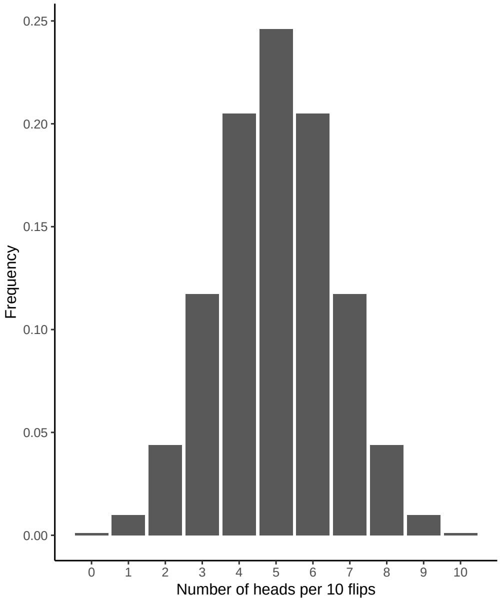

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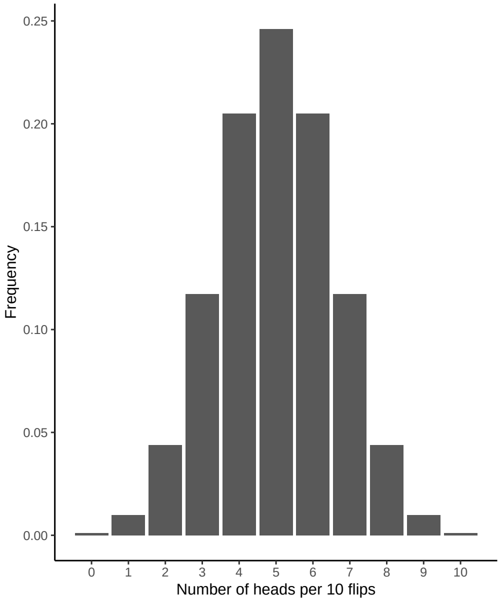

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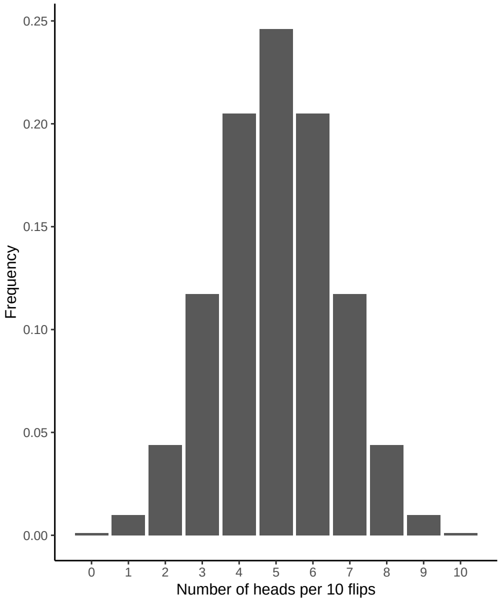

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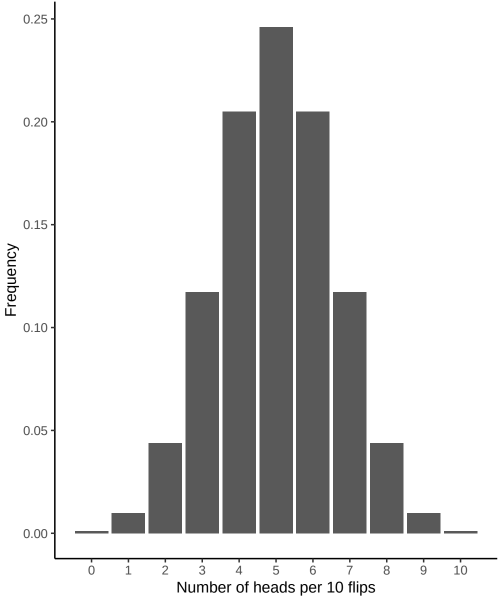

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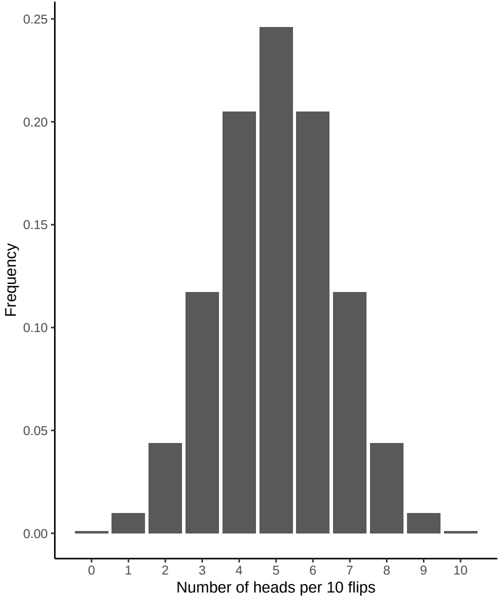
- If N $=$ 1, this is called a *Bernoulli trial*



The Binomial Distribution - scary math!

- 1 parameter: probability of success (ϕ), plus...

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

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

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

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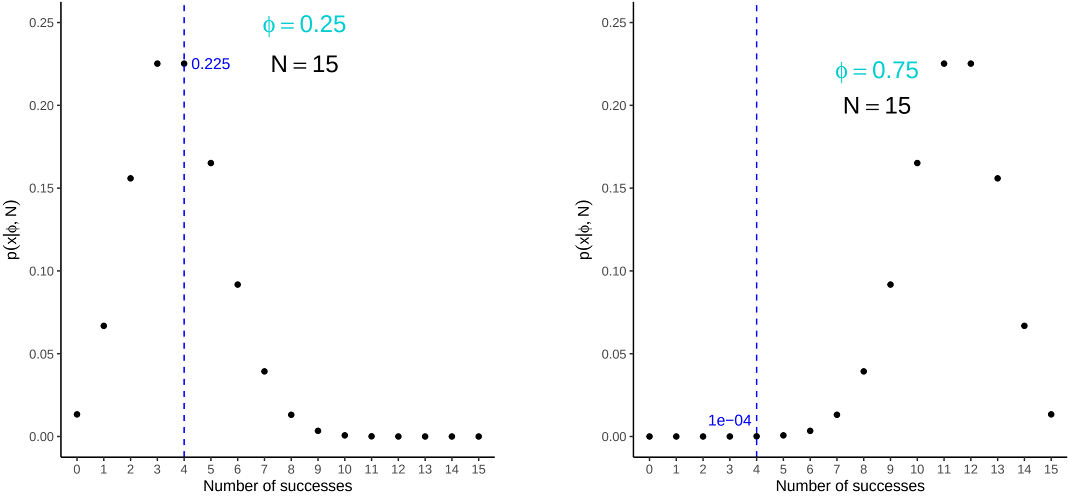

- Probability of x “successes” changes with ϕ and N

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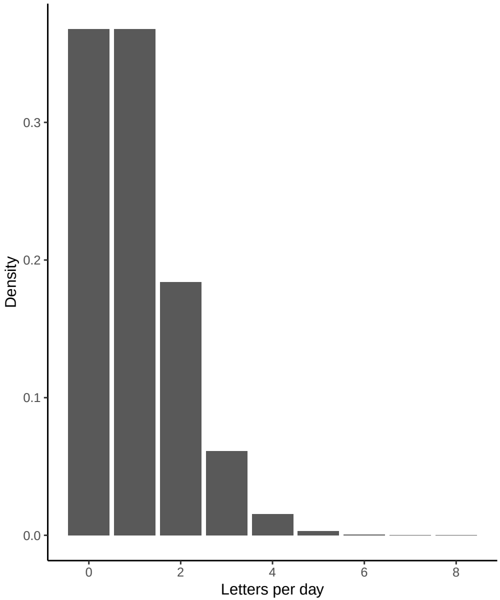
- Imagine a rare event (e.g. getting a non-junk mail letter)



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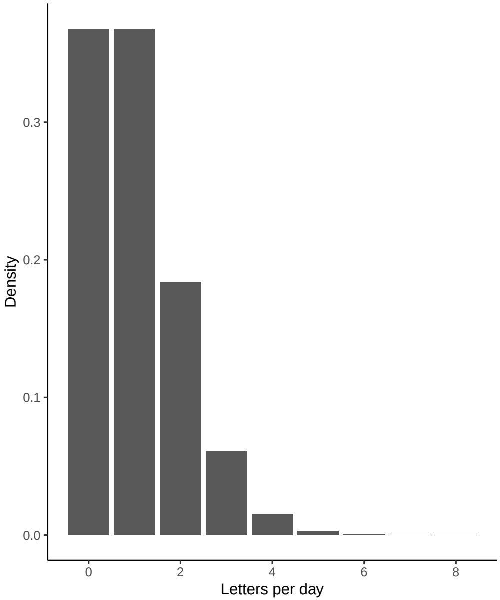

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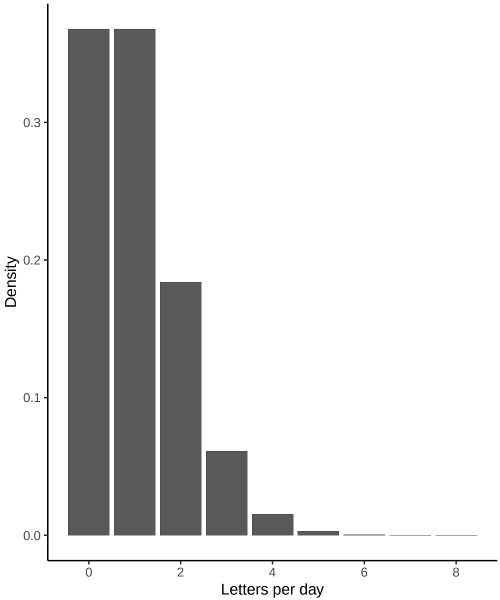

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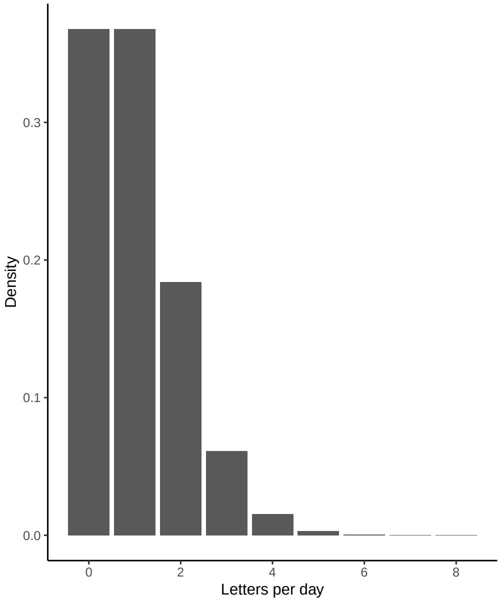

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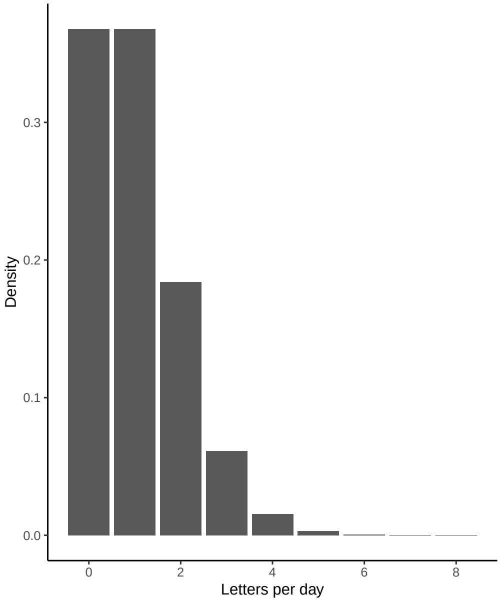

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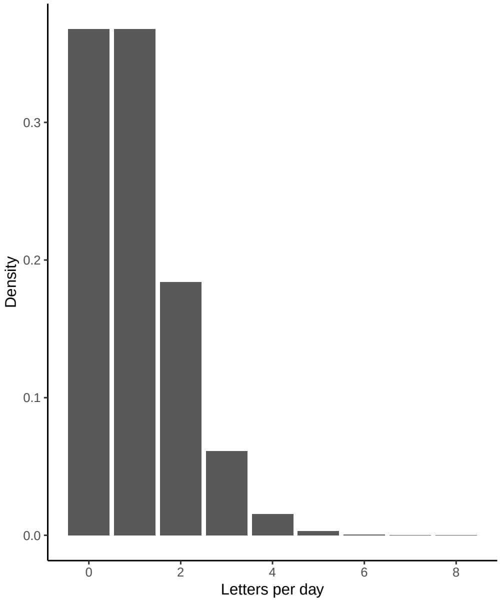

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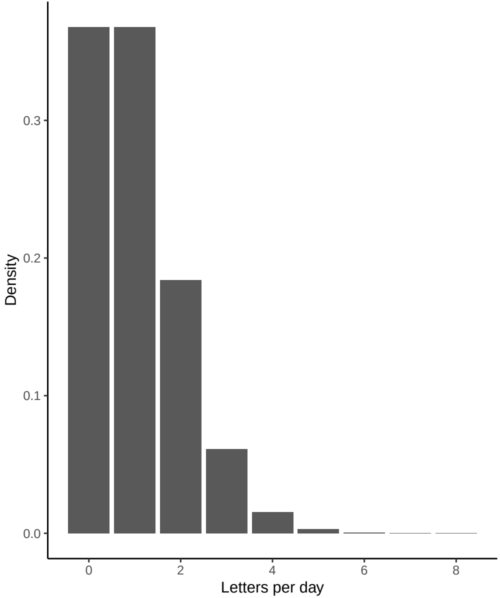
- Equivalent to Binomial distribution, where N is unknown



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$$\begin{aligned} p(2|1) &= \frac{1^{2} e^{-1}}{2!} \\ &= \sim 0.18 \end{aligned}$$

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In R, this is easy:

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

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

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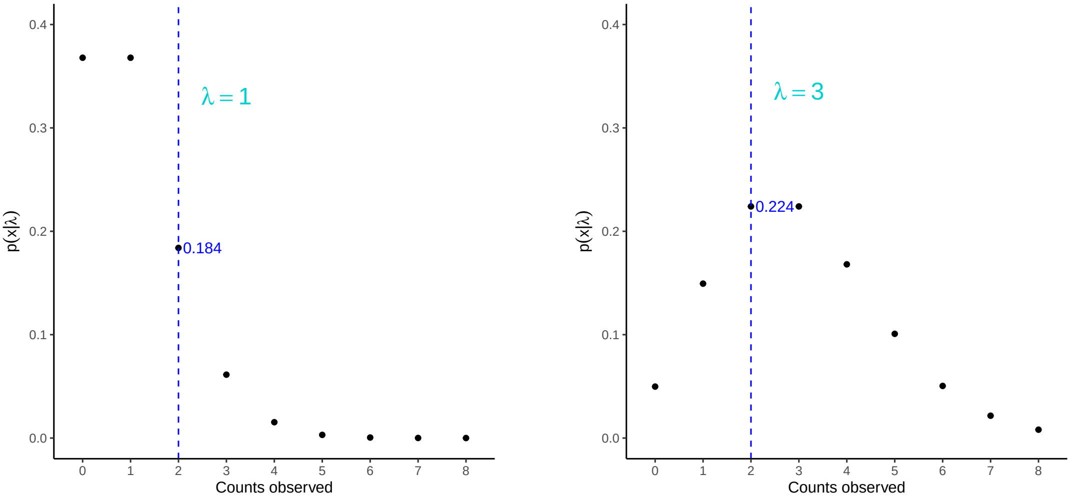

- Probability of x counts changes with λ

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  - *Beta Binomial* and *Negative Binomial* distributions

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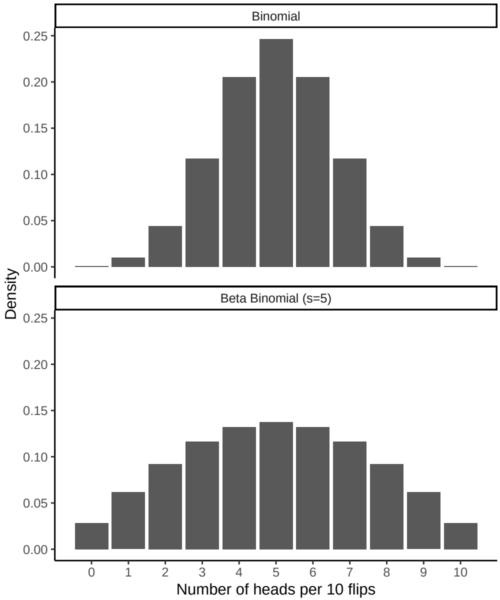
```
#Extra distributions
library(rmutil)
dbetabinom(x,m=phi,size=N,s=5)
```



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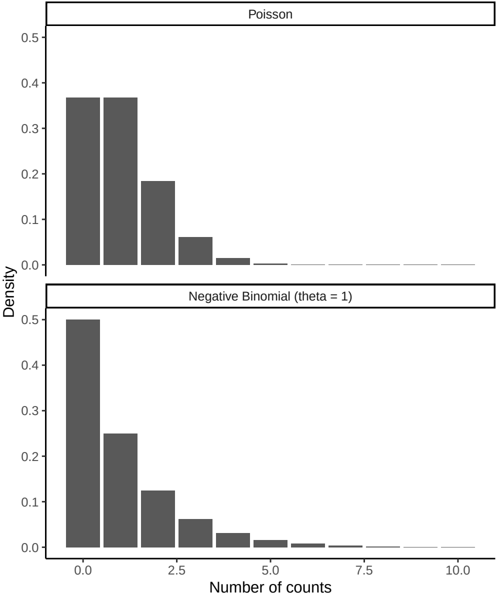
```
#size = theta parameter
dnbinom(x,mu,size=1)
```



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

First challenge (Part 1)

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Now that you've figured out which distribution, try simulating some data from each "site", and plot it!

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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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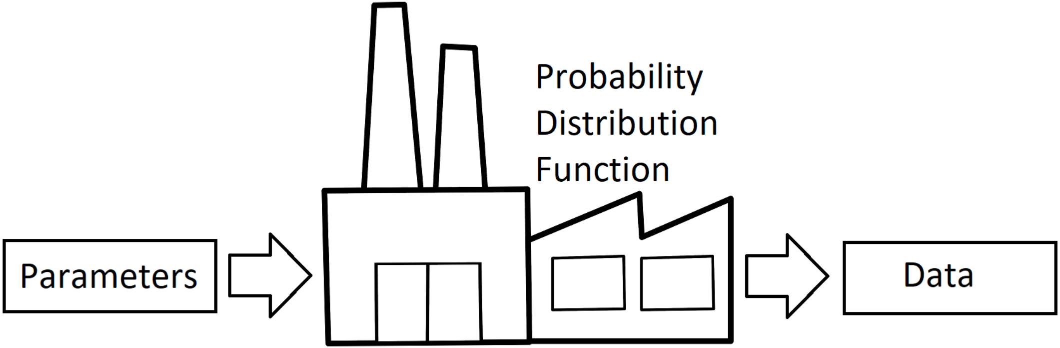
  - Predictors -> Linear model

How is our data made?

Making data can be thought of as a *factory*

- Input: **parameters** (things that guide the process)



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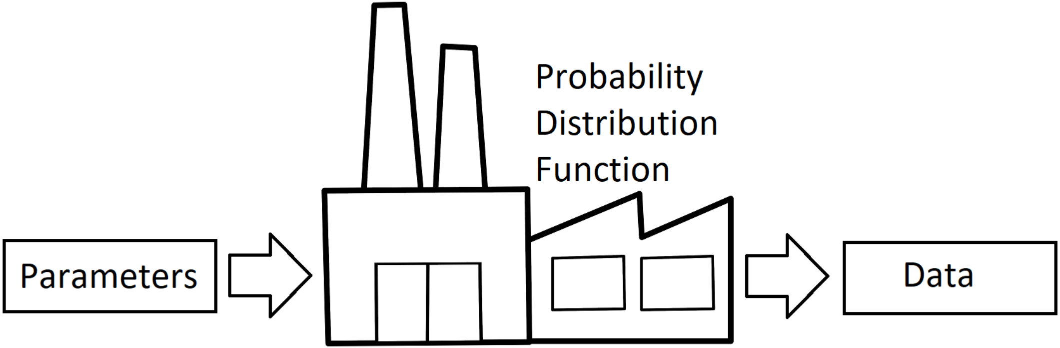

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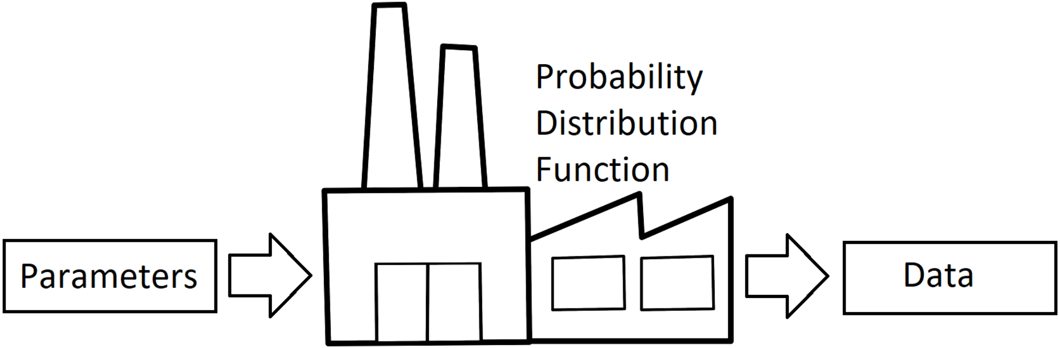
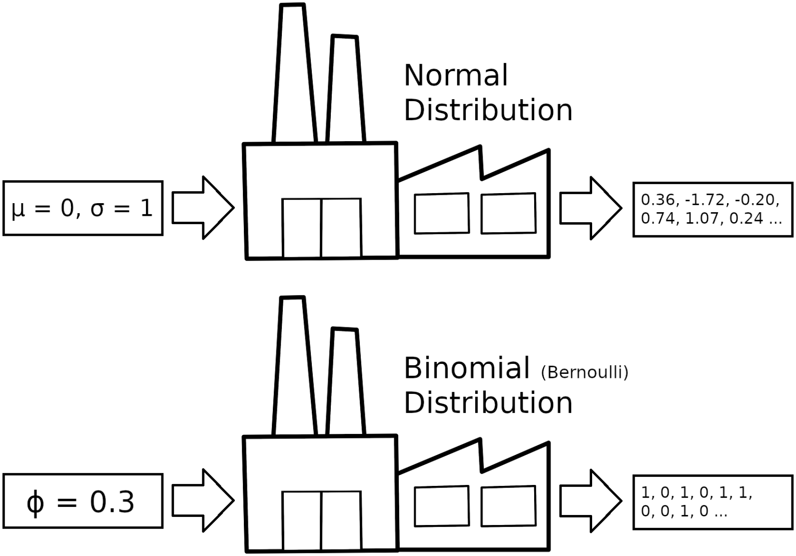
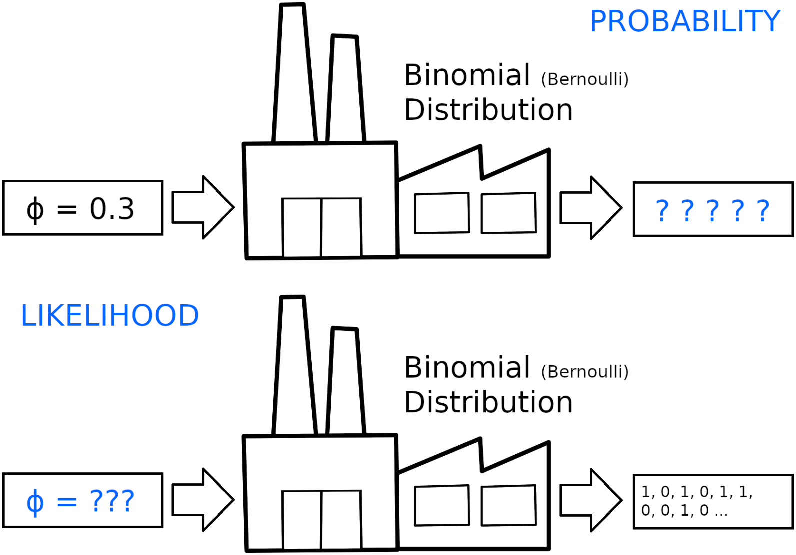
- Output: **data** (things made by the process)



Examples


μ = 0, σ = 1
Normal
Distribution
0.36, -1.72, -0.20,
0.74, 1.07, 0.24 ...
ϕ = 0.3
Binomial (Bernoulli)
Distribution
1, 0, 1, 0, 1, 1,
0, 0, 1, 0 ...

Likelihood vs Probability



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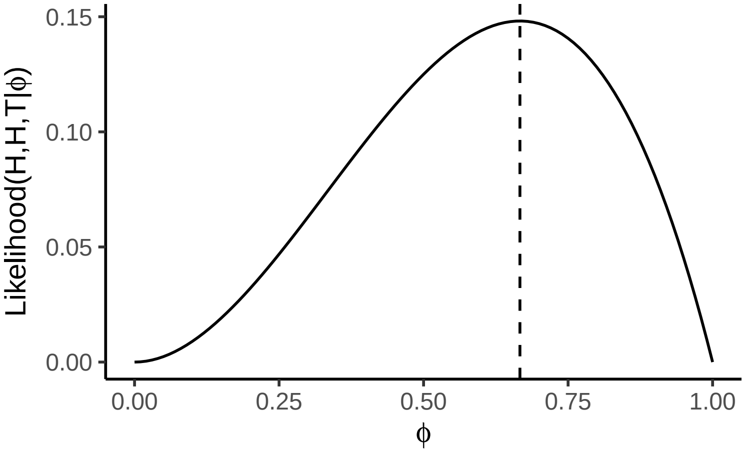
```r
#phi = 0.7
dbinom(1,1,0.7)*dbinom(1,1,0.7)*dbinom(0,1,0.7)
```

```
## [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)
##
## Deviance Residuals:
##       1        2        3
##  0.9005   0.9005  -1.4823
##
## 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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Wait... our estimate should be 0.666 (2/3), not 0.693!

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  - Normal: Identity (i.e. $\times 1$)
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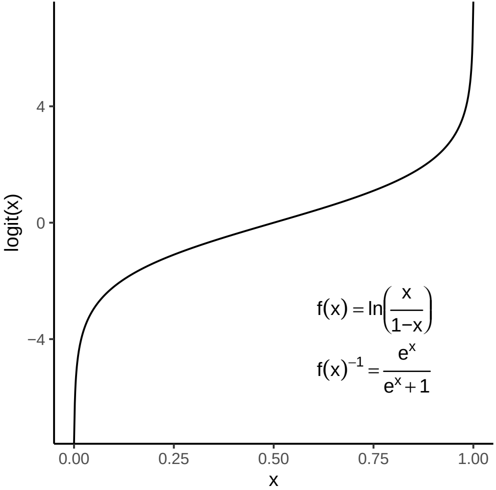
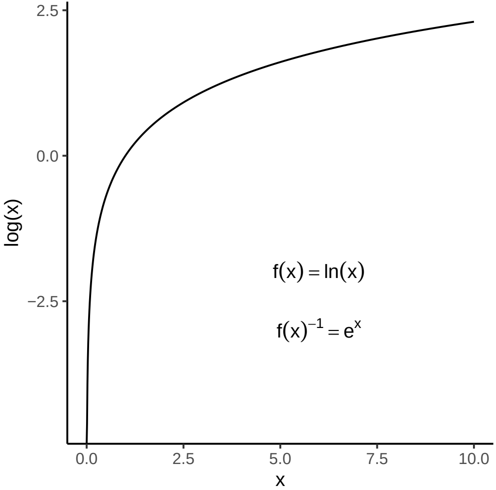
- *logit*$(0.693) = 0.666$, so the GLM actually got it right!

What do these functions look like?

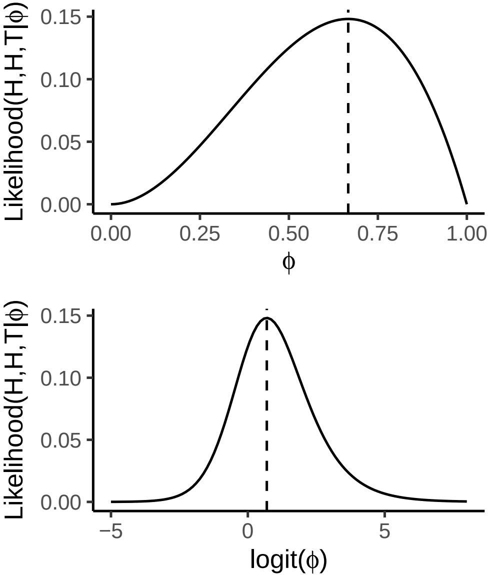




- These functions map parameter values from the appropriate range (0-1 or 0-∞) onto $-\infty$ to $+\infty$

Why do we bother with these link function?

- Likelihood functions are not symmetrical on the regular scale



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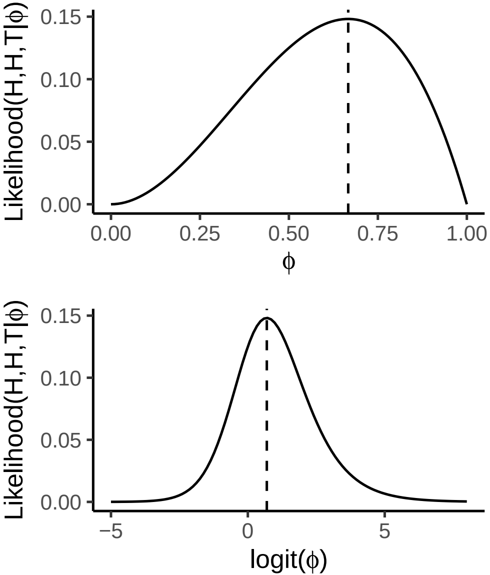

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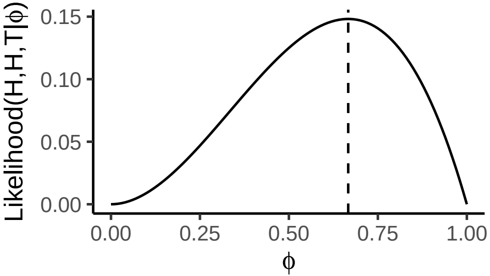
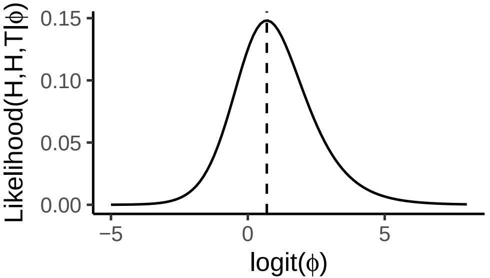
- Makes it easier for R to find the ML estimate (and confidence intervals)





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

How do I fit GLMs in R?

Syntax and model output is very similar to `lm`

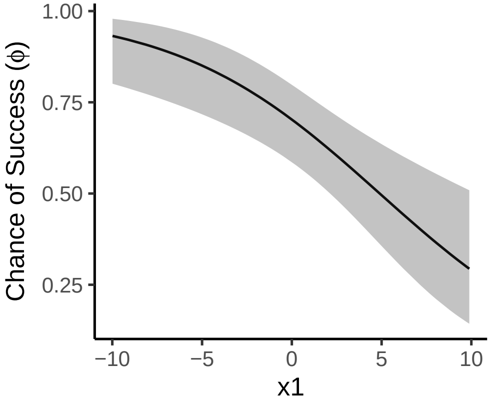
```r
# y ~ x, where x is the predictor of y
mod_binomial <- glm(y2 ~ x1 + x2 , data = d1, family = 'binomial') #Fit a binomial GLM
```

```
##
## Call:
## glm(formula = y2 ~ x1 + x2, family = "binomial", data = d1)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.0050  -0.9493   0.3924   0.8336   1.6806
##
## 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:



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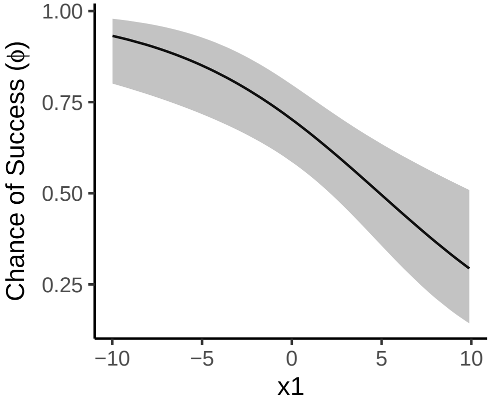

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- `crPlot` (from `car`) and `ggpredict` (`ggeffects`) work with fitted `glm` models:
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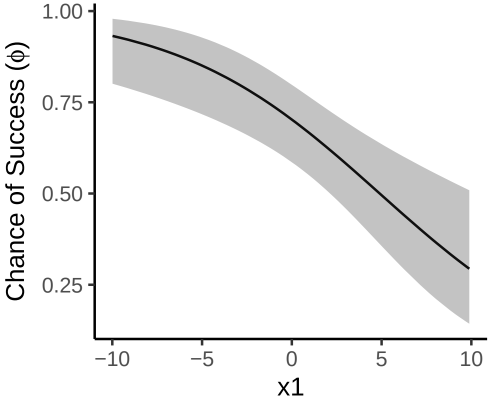
- Answer: the model is *linear* on the link scale, but *nonlinear* on the data scale



Second 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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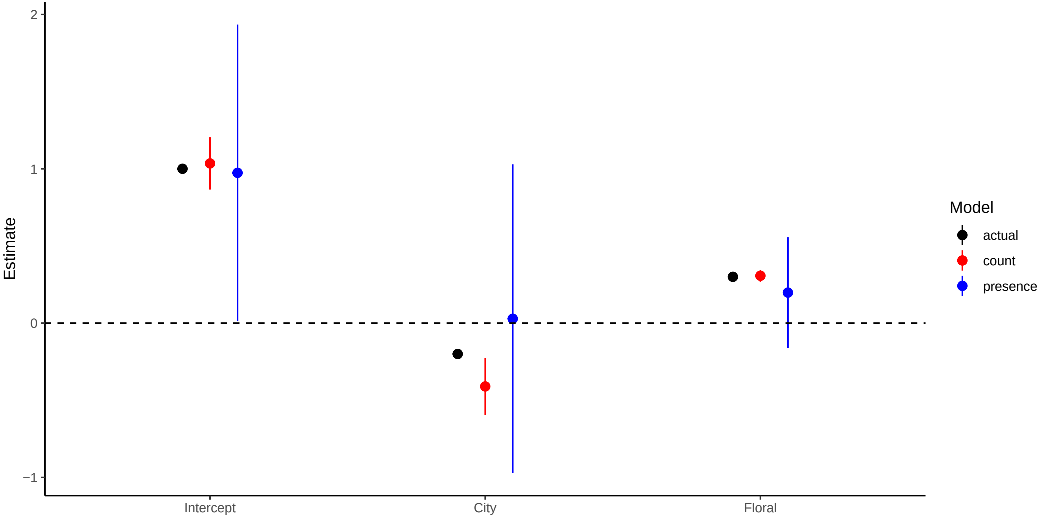
  - Bonus: make a partial regression plot of terms in the Poisson GLM

Model results



Part 3: Models behaving badly

Motivation

- Are my model results reliable?

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  - Residual checks

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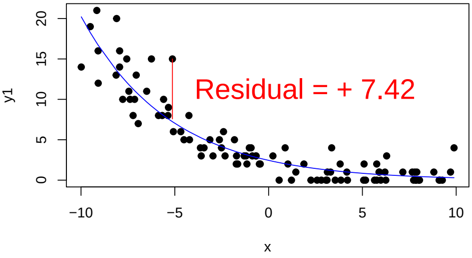

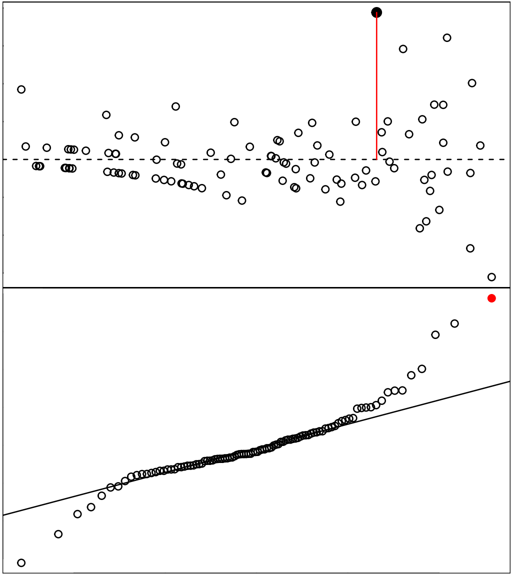

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Deviance residuals use *likelihood*:

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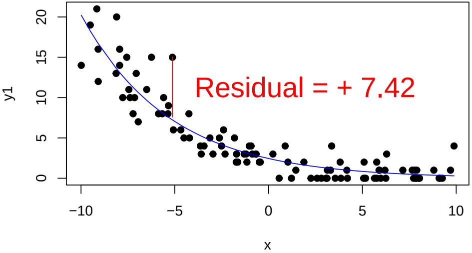
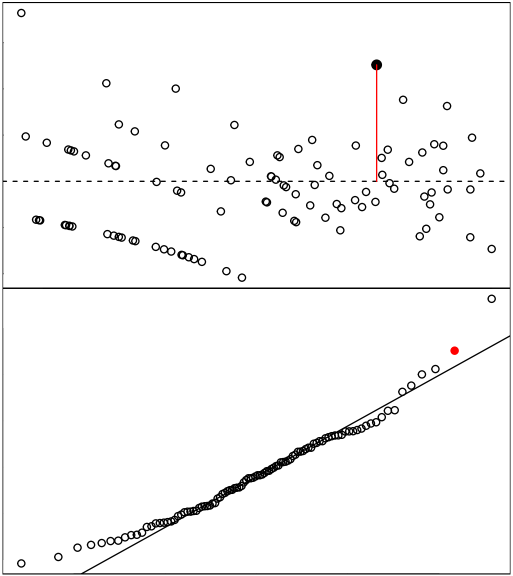
- For more about the different kinds of residuals, see here

Solution: use deviance residuals for GLMs

- Residuals from GLMs will never be as "pretty" as those from LMs





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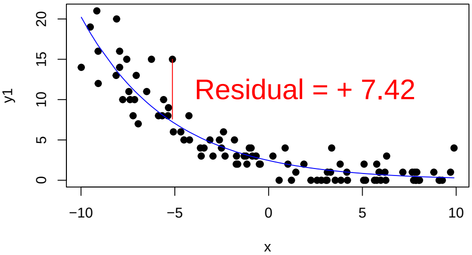

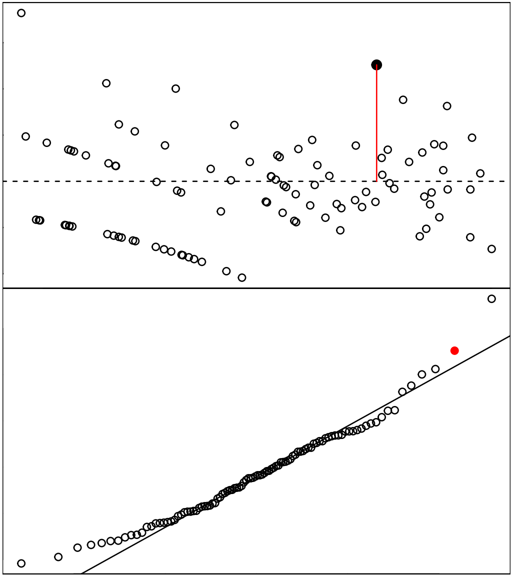

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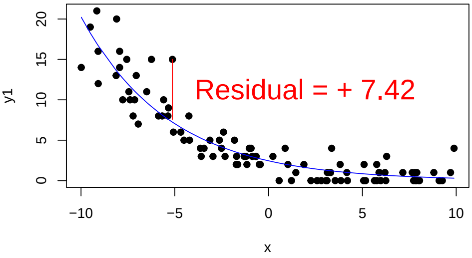

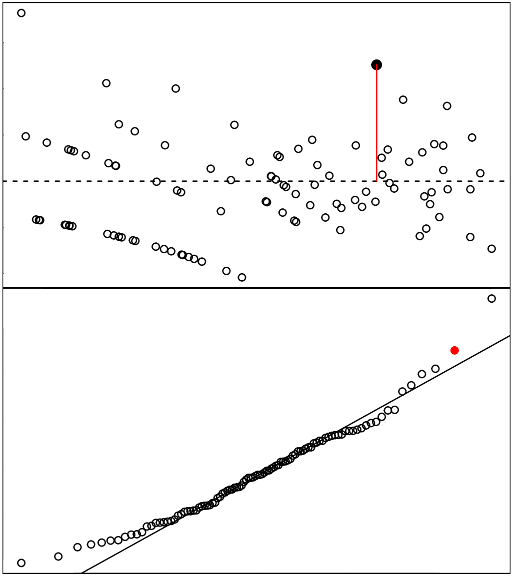

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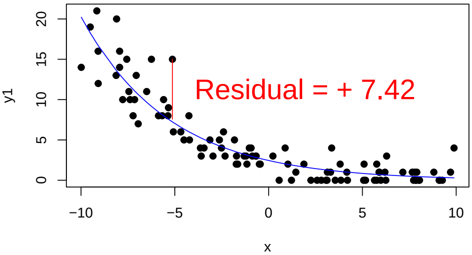

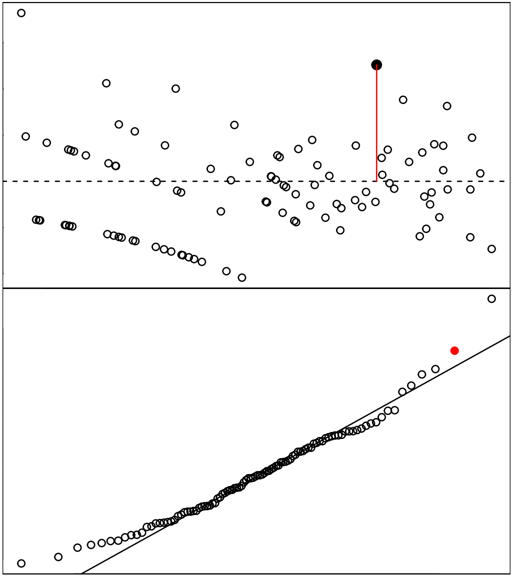

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- Residuals from GLMs will never be as "pretty" as those from LMs
- *Especially* true for:
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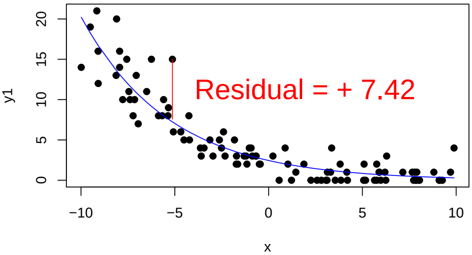
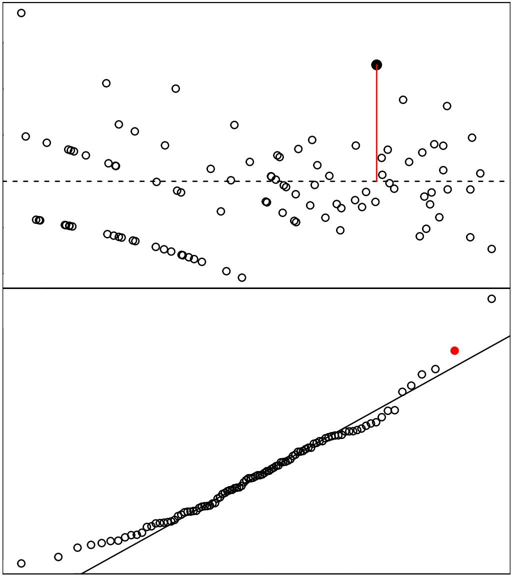
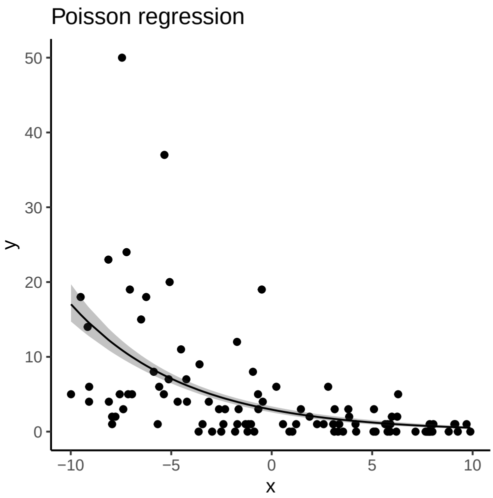
- Next week we will deal with *simulation testing* residuals





Problem 2: Overdispersion

- Binomial and Poisson families have **no** variance term (e.g. *SD*).



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

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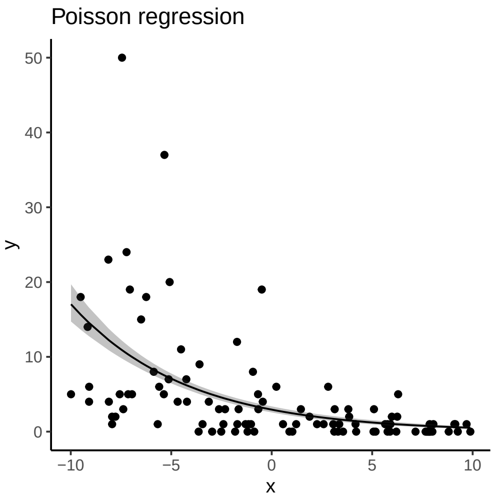

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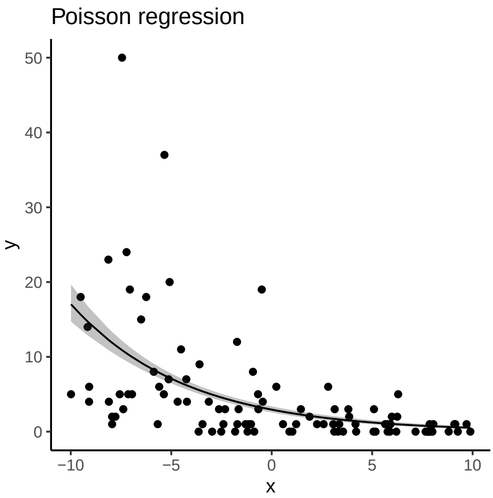

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##
## Call:
## glm(formula = y1 ~ x, family = "poisson", data = d1)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.0843  -0.9460  -0.1897   0.5333   3.6416
##
## Coefficients:
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## (Intercept)  0.89455    0.07818   11.44   <2e-16 ***
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## ---
## 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
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- In Poisson or Binomial models, Residual deviance $\div$ Degrees of Freedom should be ~ 1
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- This model looks OK ($106.2 \div 98 = 1.08$)

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## Deviance Residuals:
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## -4.1009  -1.7543  -0.8805   0.4796   8.6102
##
## Coefficients:
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## (Intercept)  1.07897    0.06871   15.70   <2e-16 ***
## x           -0.17581    0.01069  -16.44   <2e-16 ***
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##
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##     Null deviance: 851.96  on 99  degrees of freedom
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- 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

[1] Random effects discussed later

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- Random effects[1]not accounted for
  - e.g. Data collected at different sites, but ignored

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Solutions for overdispersion

Try the following (in this order):

1. Consider terms that may have been left out

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

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Try the following (in this order):

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

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   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

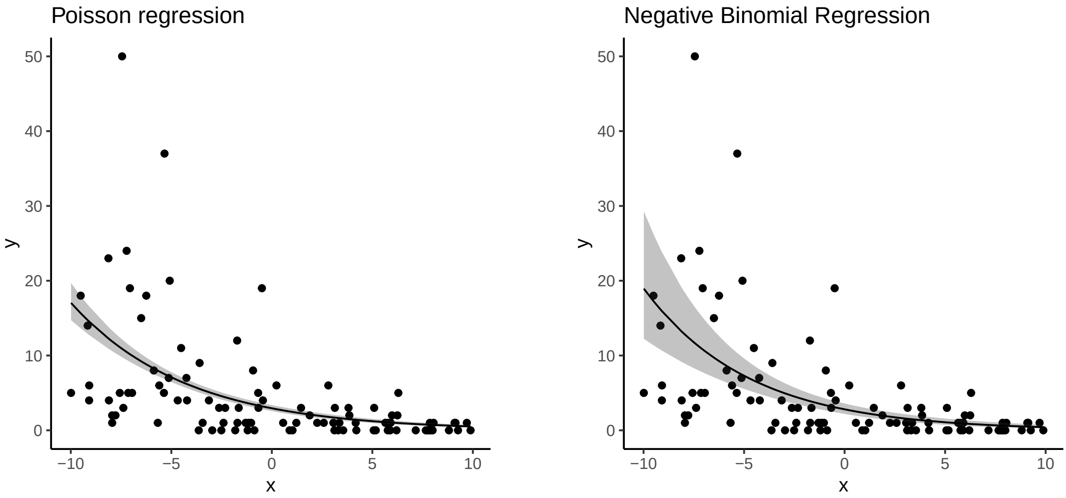
Negative Binomial Regression

```r
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)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.9829  -1.0492  -0.3989   0.3831   2.4289
##
## 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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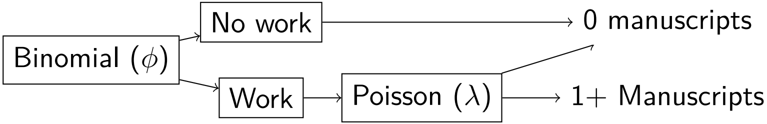
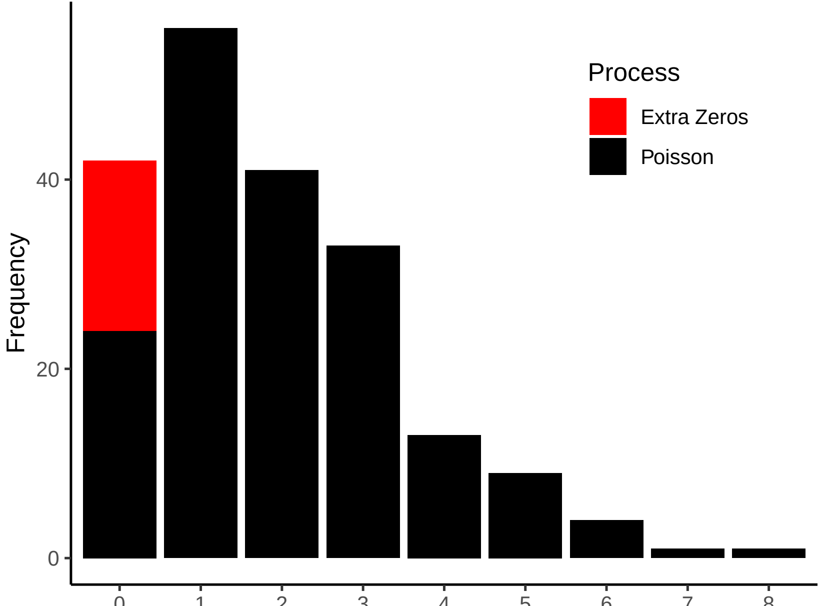
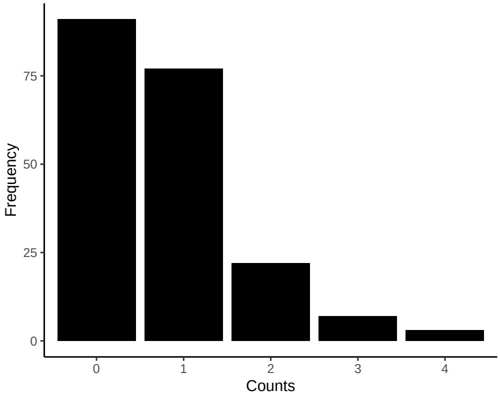


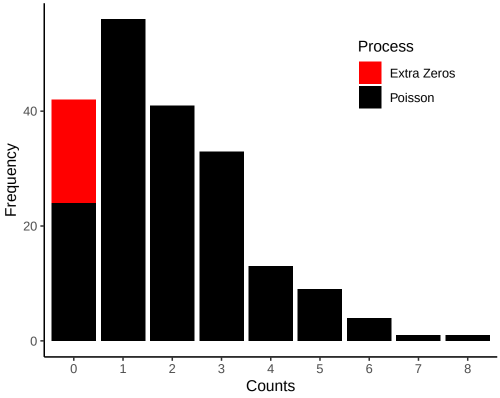
Zero-inflation: graphical model



Problem: hard to fit

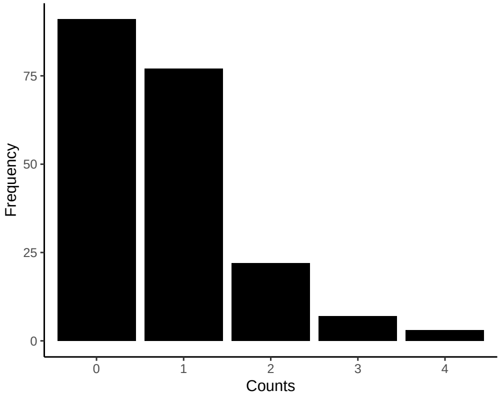
- Hard for R to tell the difference between ZIP/ZINB, and a Poisson/NB with a low mean (λ).

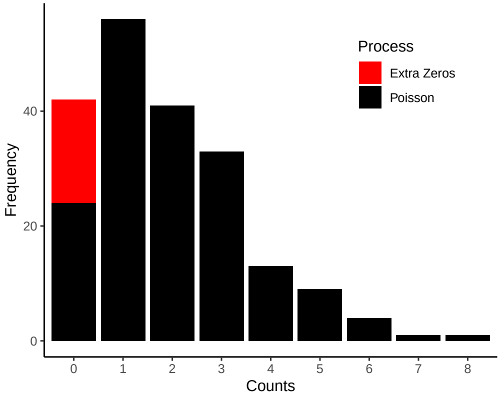




Problem: hard to fit

- 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





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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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- 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

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- 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

"I counted critters for different lengths of time at each site. Does temperature affect counts?"

- Count models use integers only, so you can't just do: $counts \div hours$

```
#hours = observation time at each site (must be log-transformed)
glm(counts ~ offset(log(hours)) + temp, family='poisson',data = d1)
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This will return estimates that have been scaled to a 1-hour observation time

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- Solution: use *offsets* to deal with different observation times
    - Predictor with a slope fixed at 1

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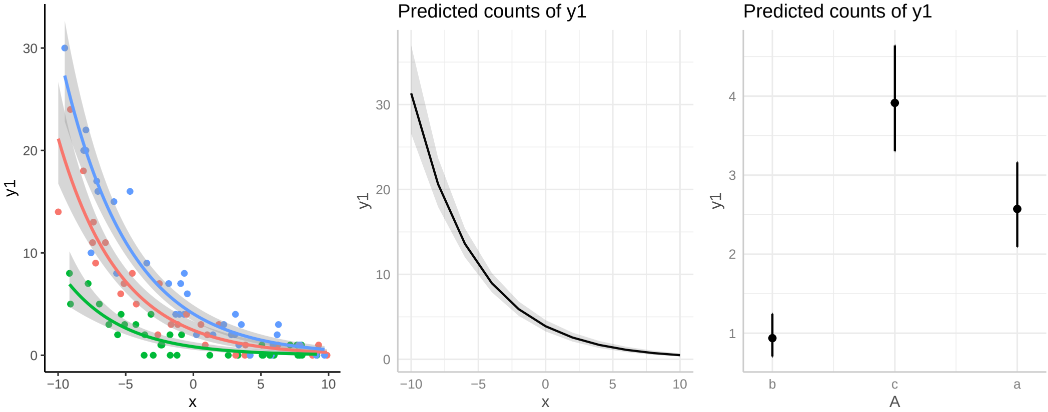
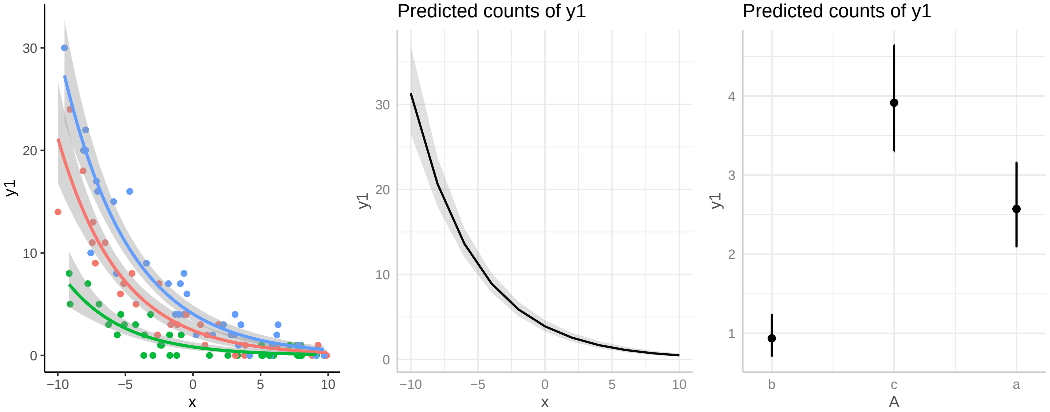
Partial effects plots

- `library(ggeffects)` and `library(effects)` work for partial effects plots, but. . .



Partial effects plots

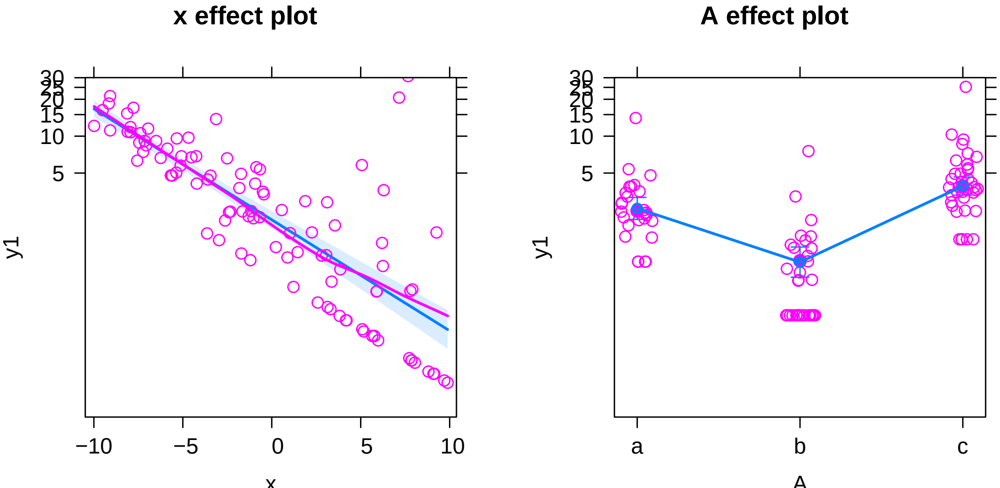
- `library(ggeffects)` and `library(effects)` work for partial effects plots, but. . .
- Residuals are tricky to display, unless you plot them on the link scale



Partial effects plots

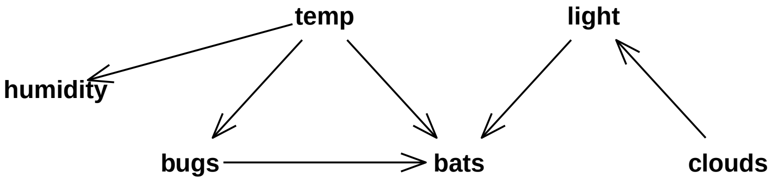
- Plots from `effects` use *working residuals* (not on the link scale)

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



Third 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`



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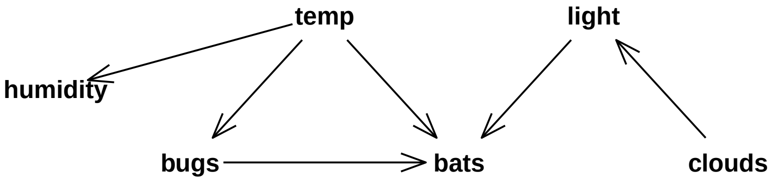

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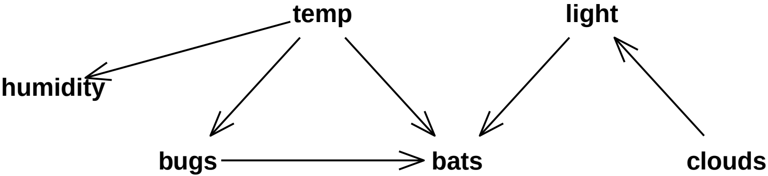
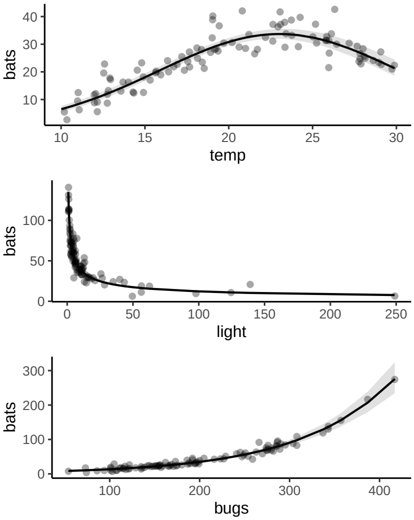
- Fit a `glm` to those data, check how the model fits, and make some partial effects plots
- Recall: this is the "true" causal relationship here (no interactions)



Solution:




```
##
## Call:
## glm(formula = bats ~ poly(temp, 2) + log(light) + bugs, family = "poisson",
##     data = batDat)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -3.1595  -0.6406  -0.0559   0.6176   2.0356
##
## 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
```

To do this week: update your models

- Some of you have non-normal data... time to update those models!

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- Some of you have non-normal data. . . time to update those models!
- For those who don't need to run GLMS, it's your lucky week!