

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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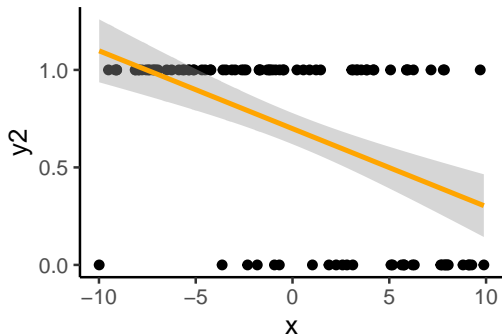
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- “Play time”

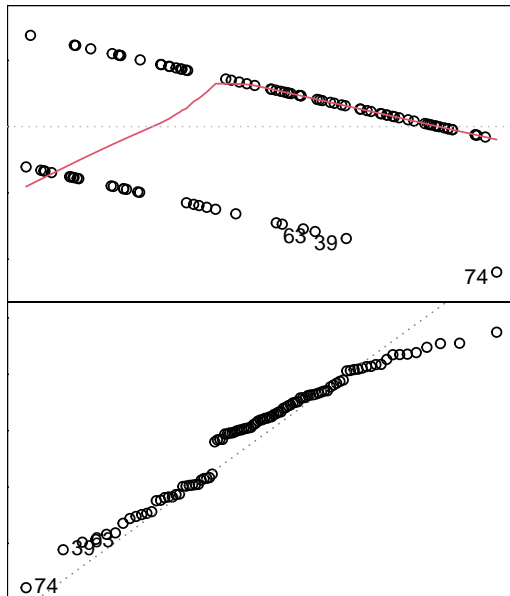


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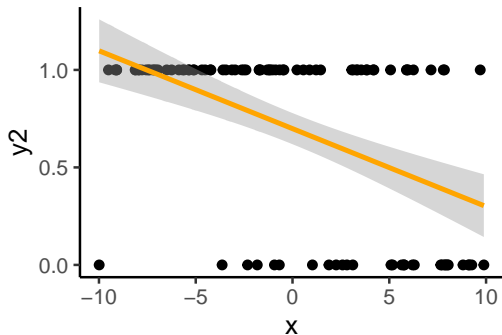
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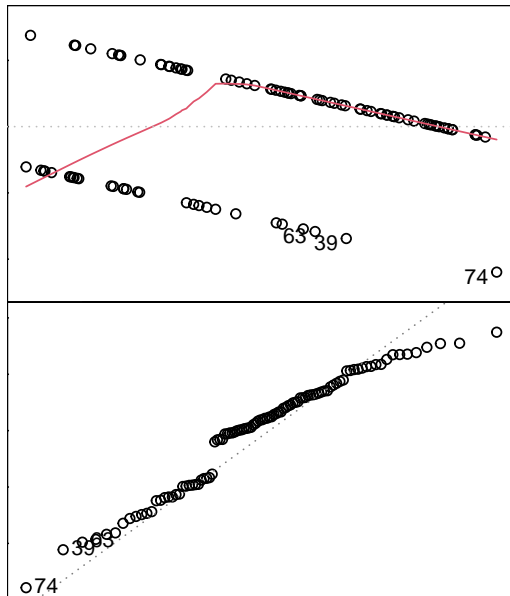
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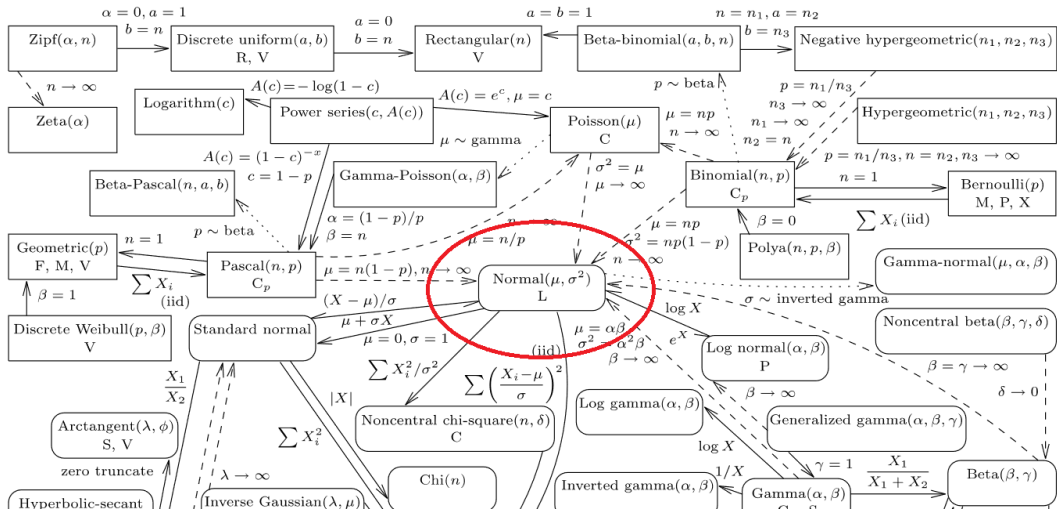
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- Some types of data can never be transformed to make the residuals normal
- Solution: **use the distribution that generates the data!**

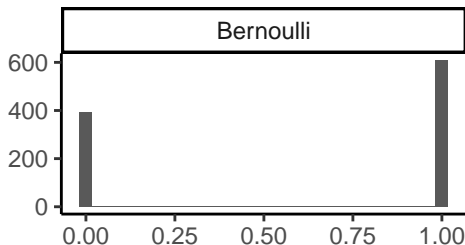
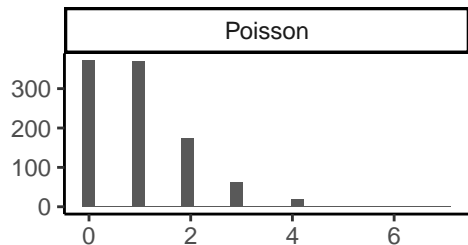
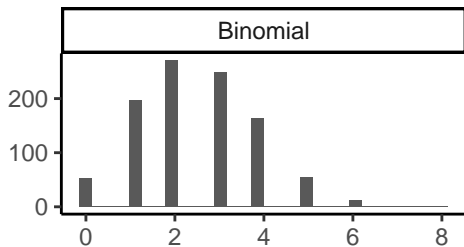
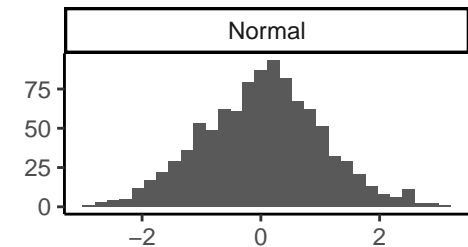


But how do I know which distribution to use?



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!

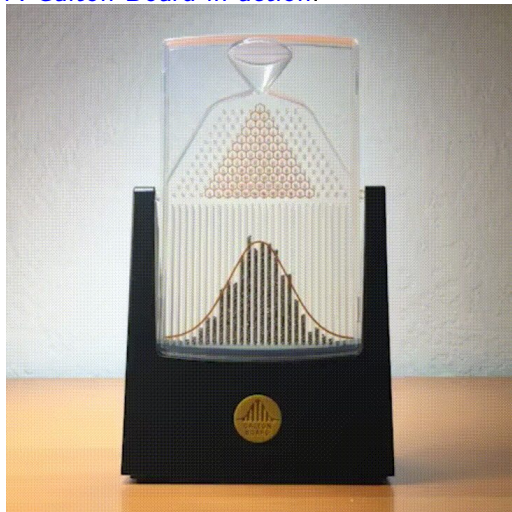


Time to meet the Exponential family!

The Normal Distribution (aka *Gaussian*)

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

A Galton Board in action:



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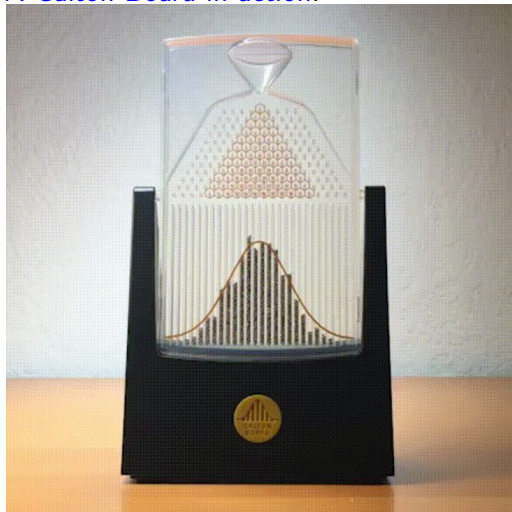
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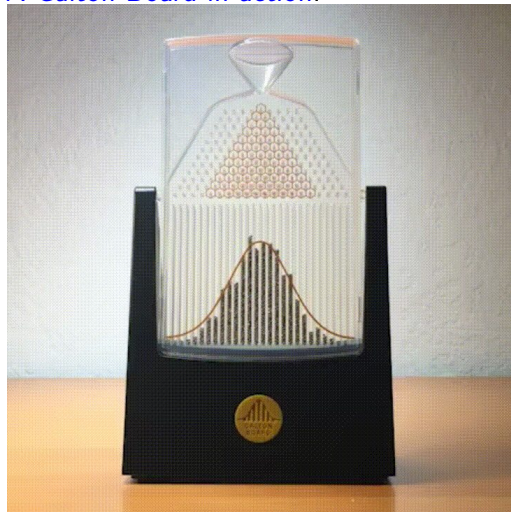
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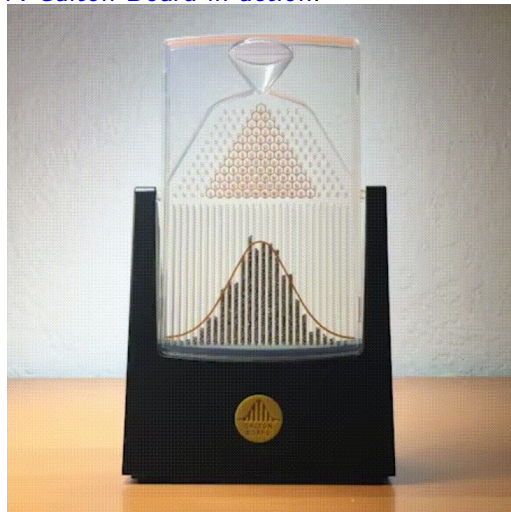
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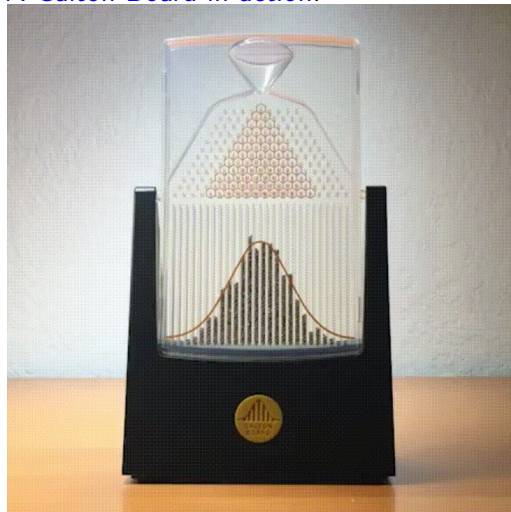
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 - e.g. Height is driven by many sets of genes

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

In R, this is easy:

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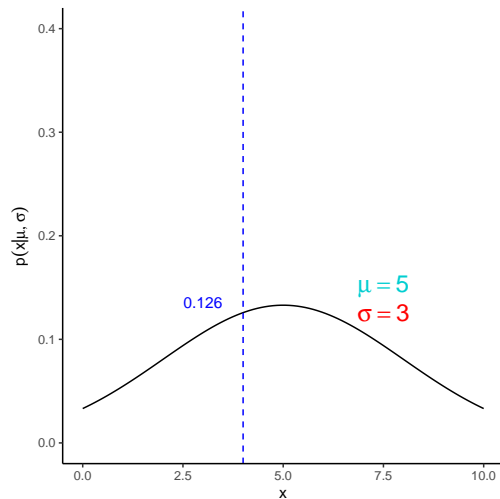
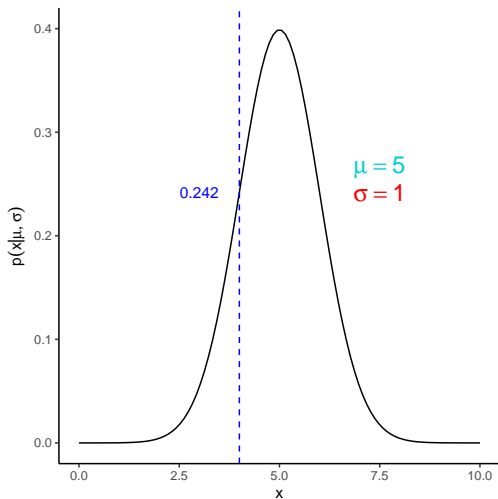
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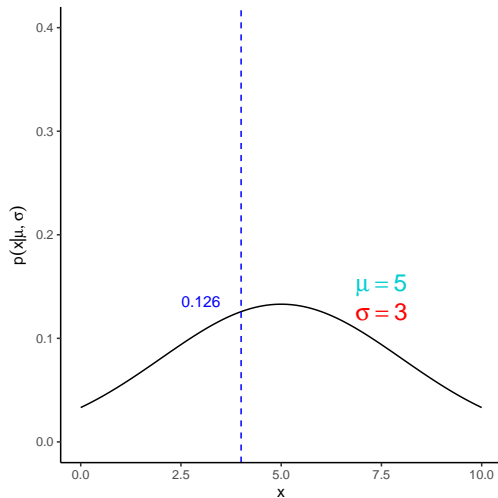
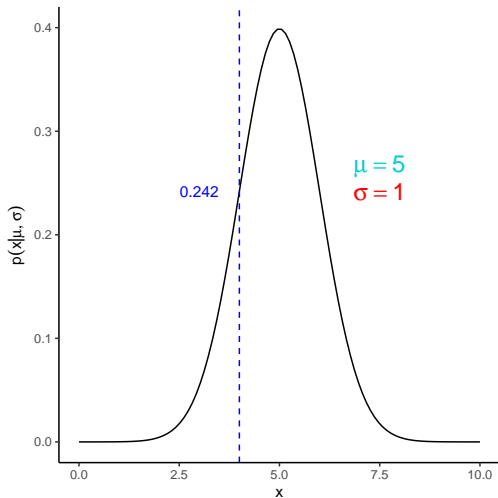
```
#d stands for "density"  
dnorm(x=4, mean=5, sd=1)  
## [1] 0.2419707
```

The Normal Distribution



- Probability of x changes with μ and σ

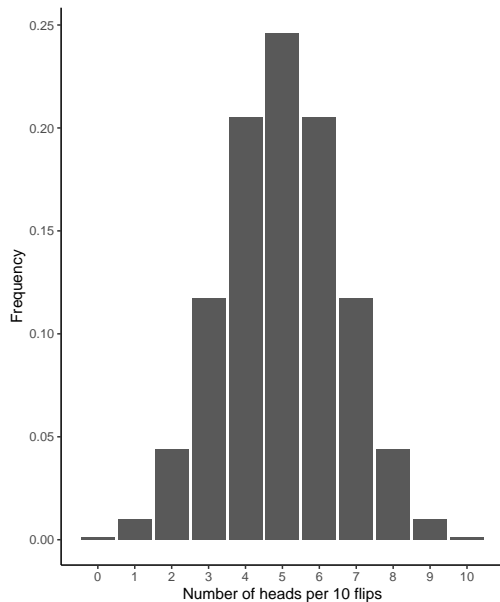
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- Left: $\sigma = 1$, Right: $\sigma = 3$

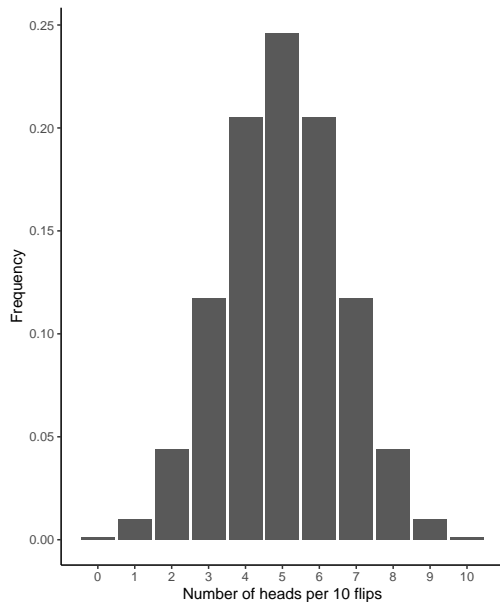
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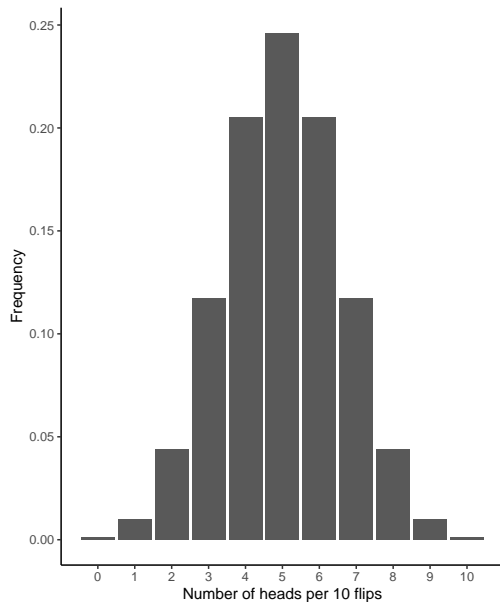
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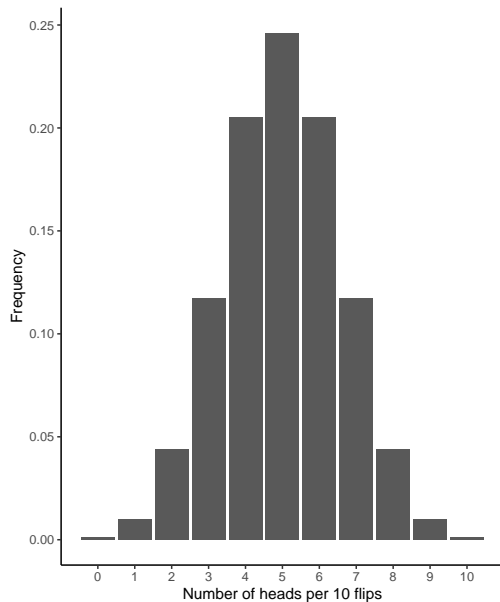
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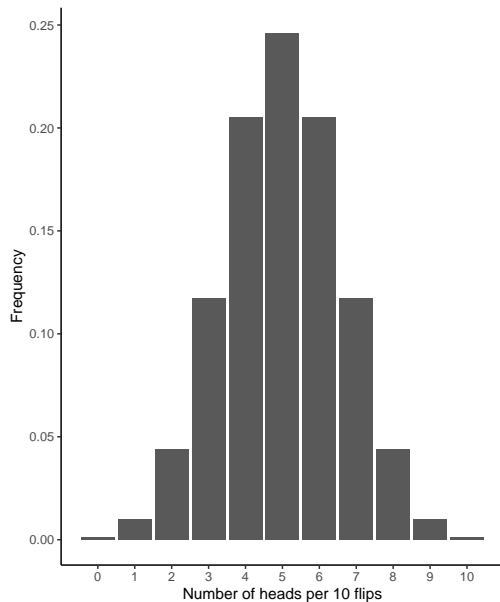
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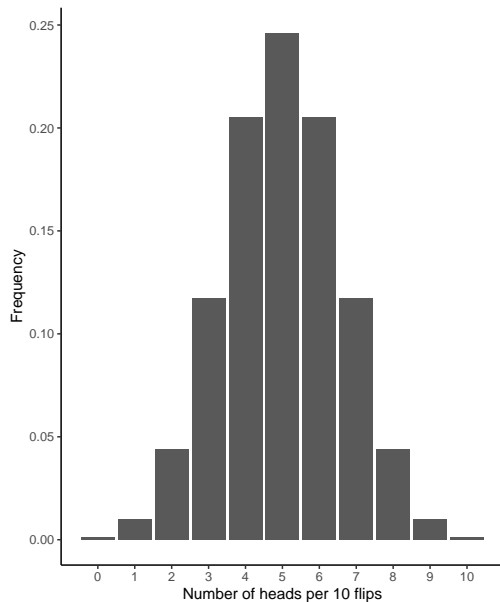
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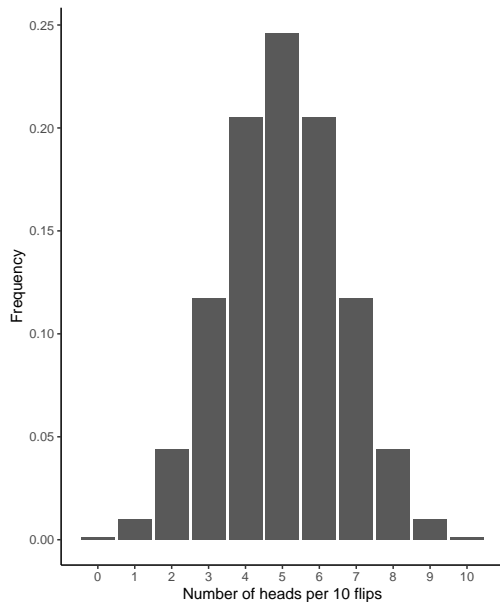
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- If $N = 1$, this is called a *Bernoulli trial*



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

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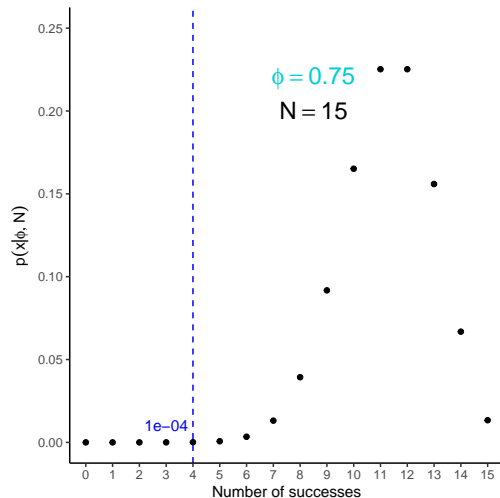
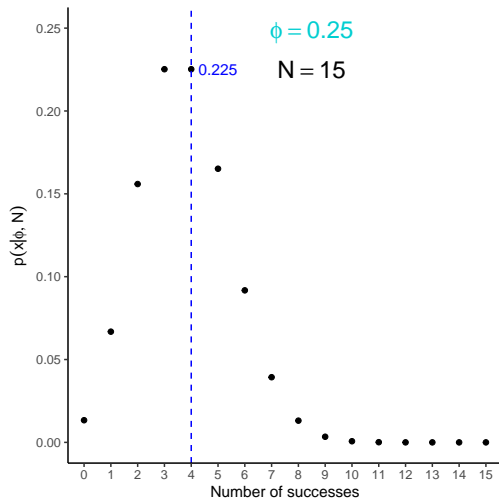
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In R, this is easy:

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

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

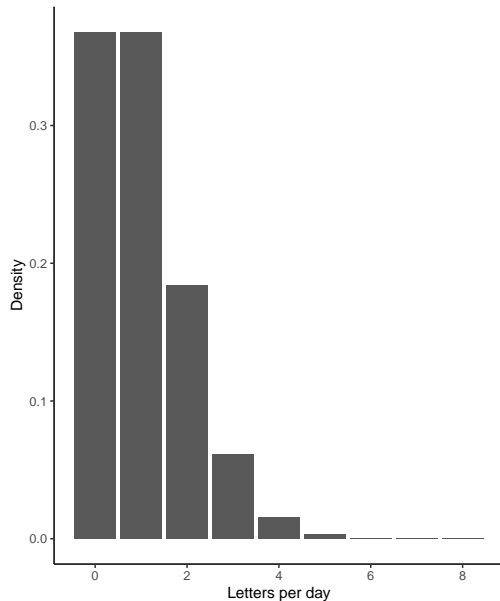
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- Probability of x “successes” changes with ϕ and N

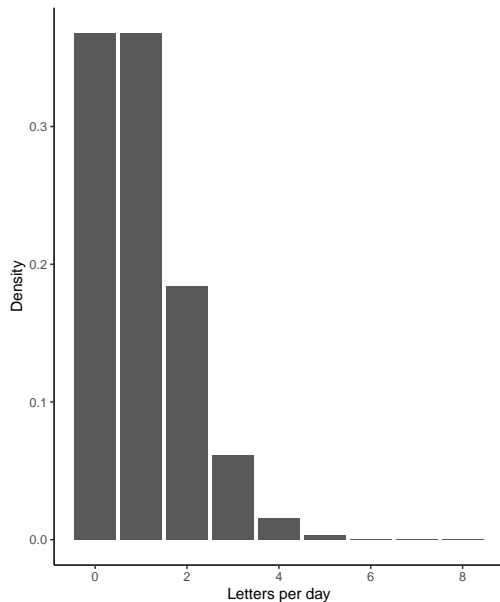
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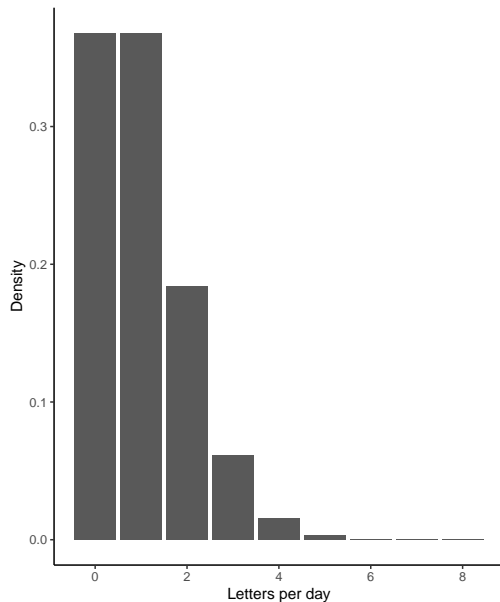
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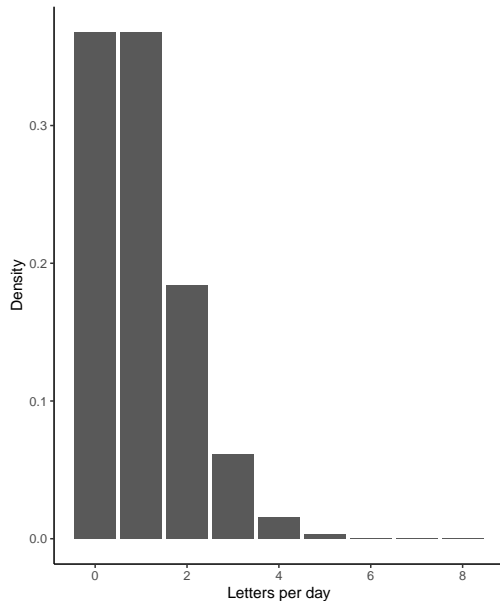
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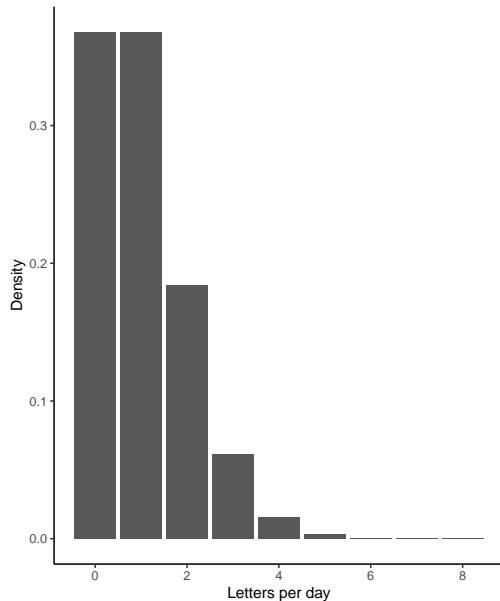
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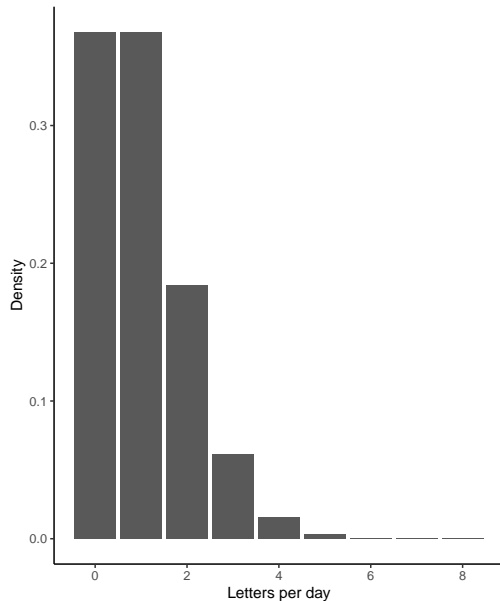
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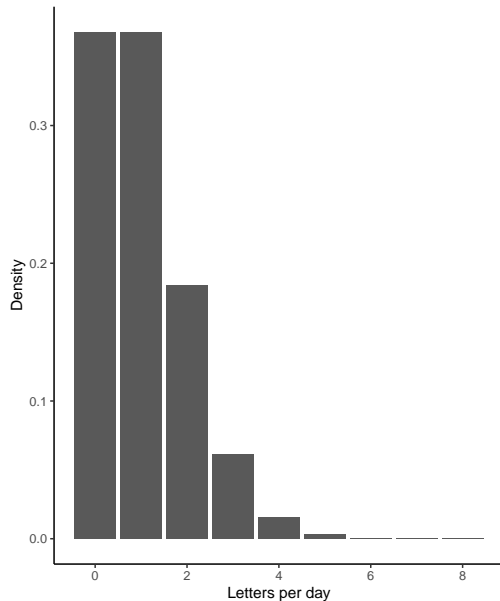
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- Equivalent to Binomial distribution, where N is unknown



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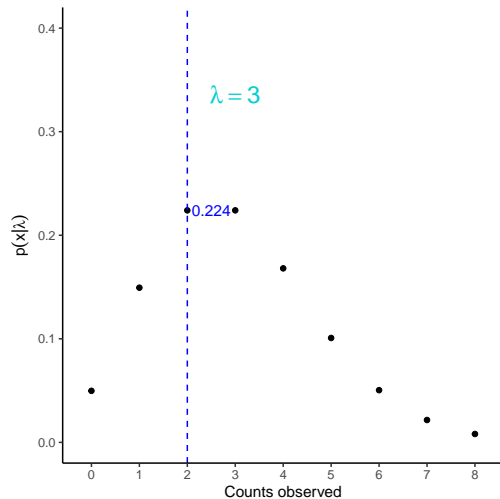
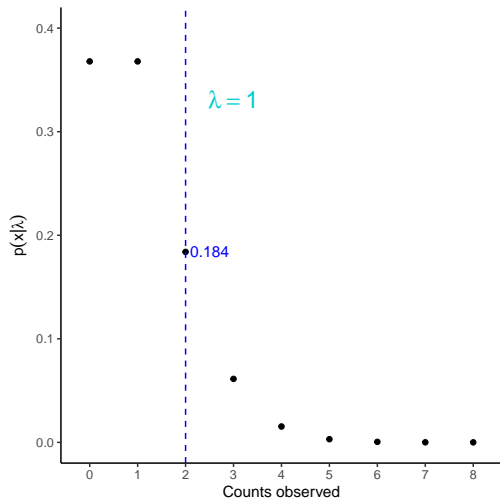
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In R, this is easy:

```
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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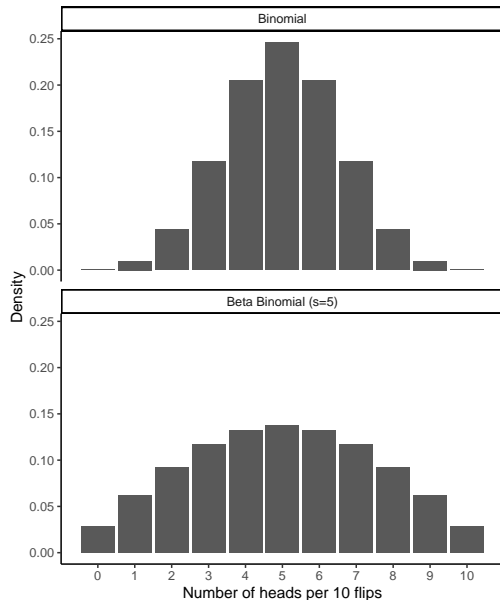
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#Extra distributions

```
library(rmutil)
```

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



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- Negative Binomial is similar to a Poisson, but can have longer tails
- Also called: *Polya* distribution (nbinom2 in many GLM commands)
- Parameters: μ and θ (if θ is large, close to Poisson)

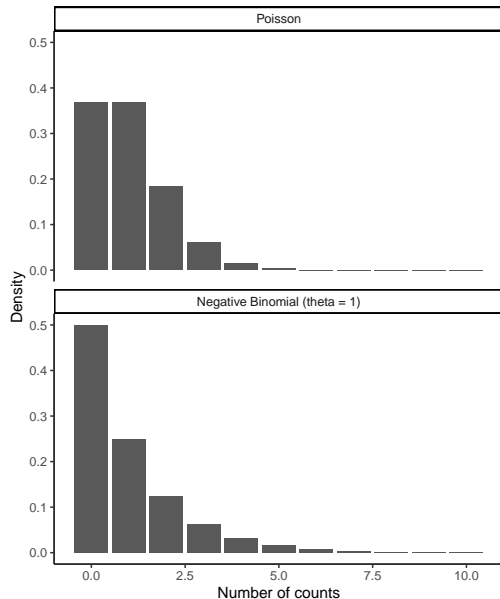
The Negative Binomial Distribution

- Unfortunately, *almost nothing* in ecology actually follows a Poisson distribution
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```
#size = theta parameter  
dnbinom(x,mu,size=1)
```



Summary of Common “Starter” Distributions

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

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Let's say that you've collected data at 2 different sites. Which distributions would you start with for the following data?

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Part 2: Maximum likelihood and GLMs

Outline

- Maximum likelihood

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 - A way to think about data

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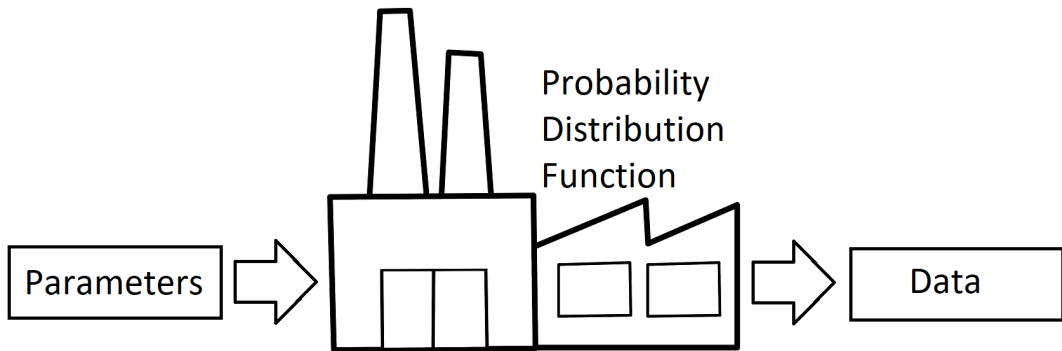
Outline

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 - Predictors \rightarrow Linear model

How is our data made?

Making data can be thought of as a *factory*

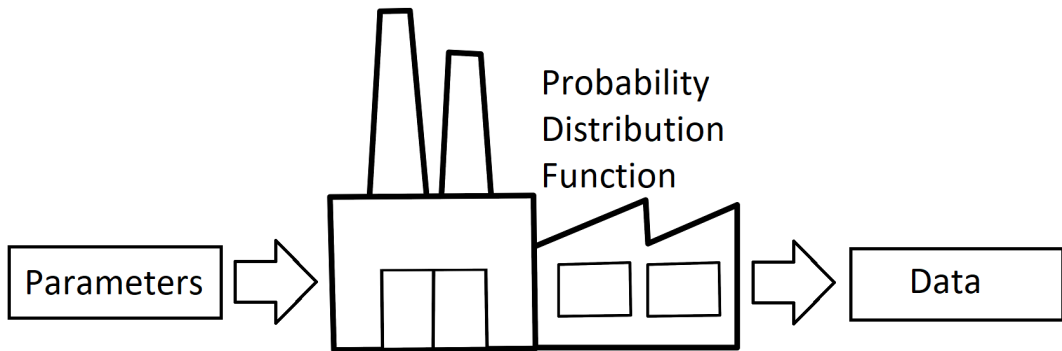
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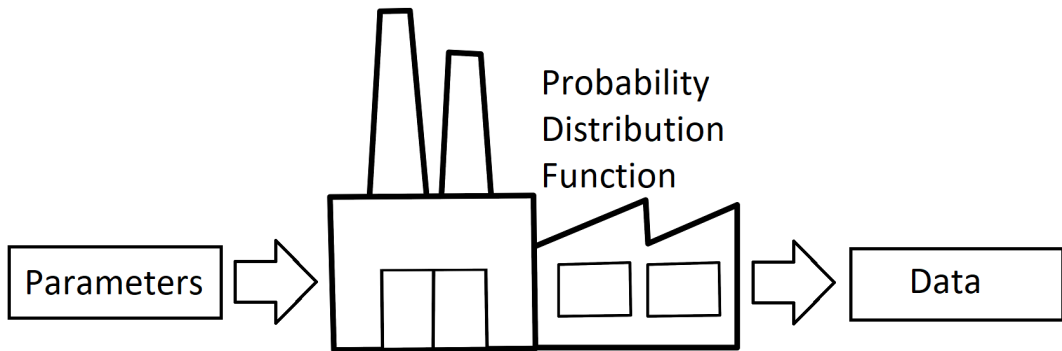
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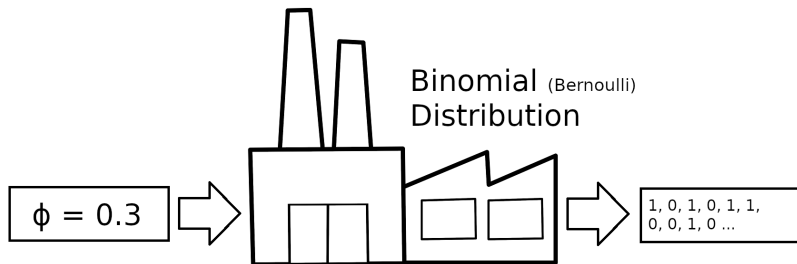
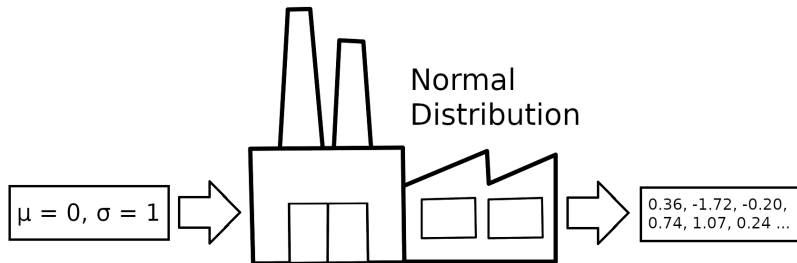
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- Process: **probability function**
- Output: **data** (things made by the process)

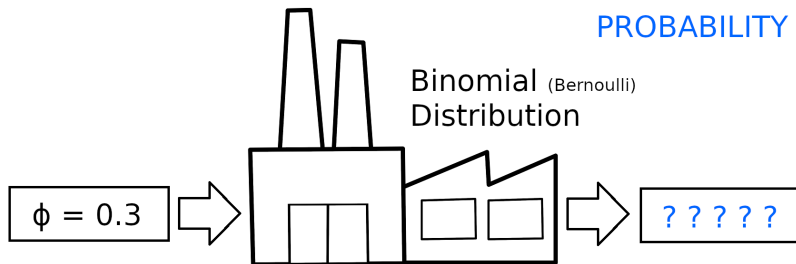


Examples

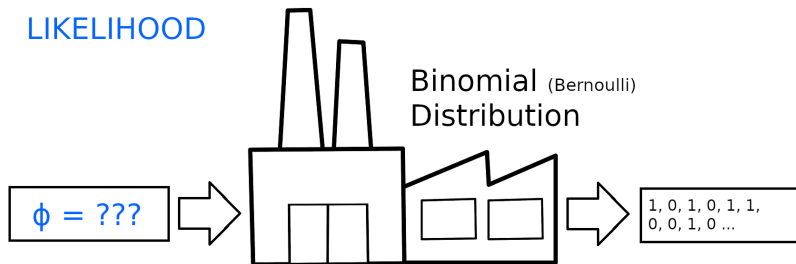


Likelihood vs Probability

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?”

```
dbinom(1,1,0.3)*dbinom(1,1,0.3)*dbinom(0,1,0.3)
```

```
## [1] 0.063
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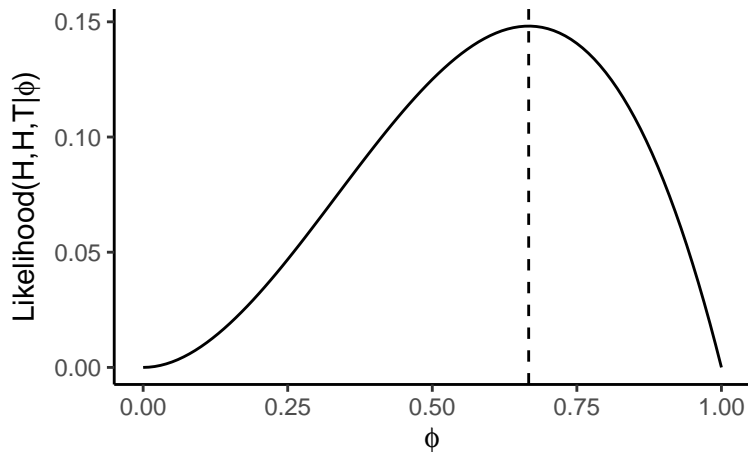
```
## [1] 0.063
```

```
#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  
## Residual deviance: 3.8191  on 2  degrees of freedom  
## 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!

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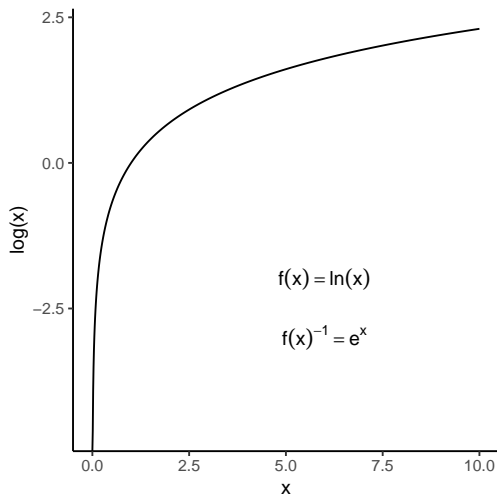
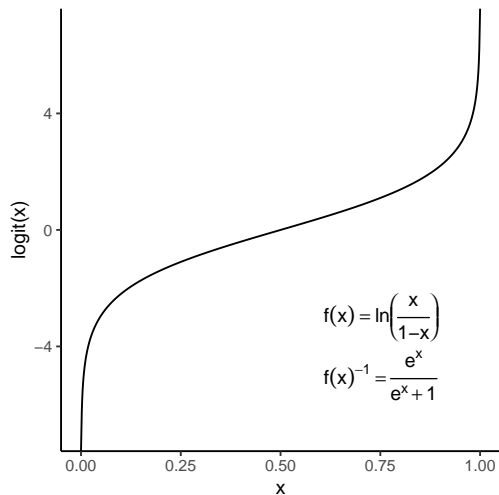
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 - Normal: Identity (i.e. $\times 1$)
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- $\text{logit}(0.693) = 0.666$, so the GLM actually got it right!

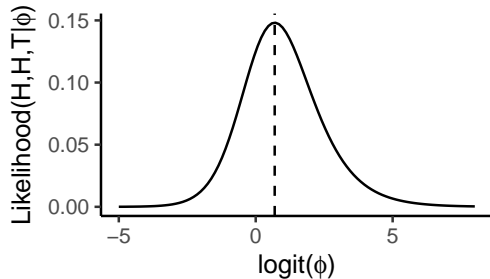
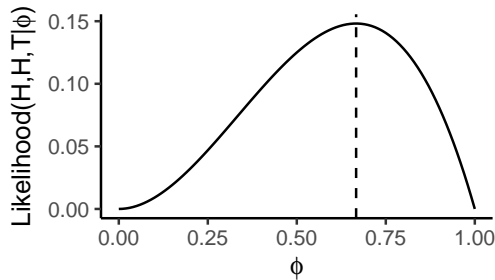
What do these functions look like?



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

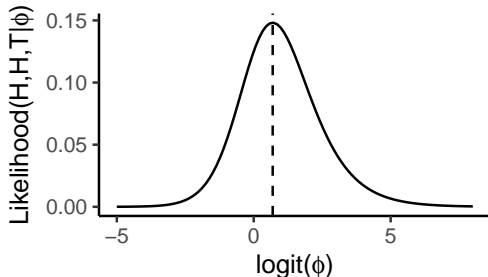
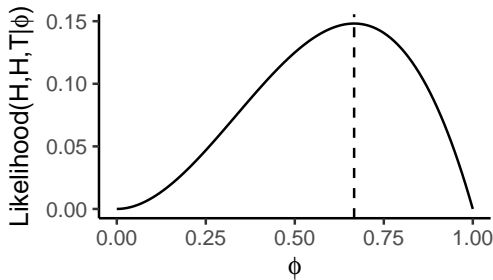
Why do we bother with these link function?

- Likelihood functions are not symmetrical on the regular scale



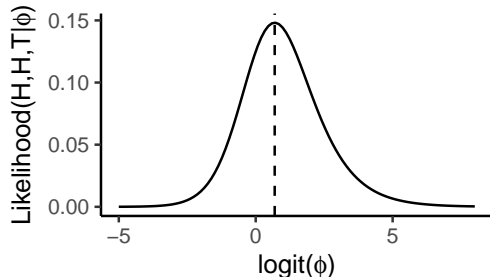
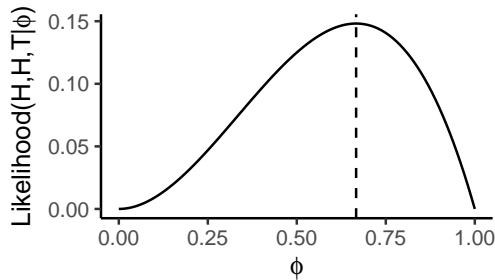
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Why do we bother with these link function?

- Likelihood functions are not symmetrical on the regular scale
- On the link-scale, they are closer to a normal distribution
- Makes it easier for R to find the ML estimate (and confidence intervals)



How do linear models fit into this?

- Usually we aren't interested in finding only a single parameter ϕ .

$$\hat{y} = b_0 + b_1 x_1 \dots + b_i x_i$$

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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`

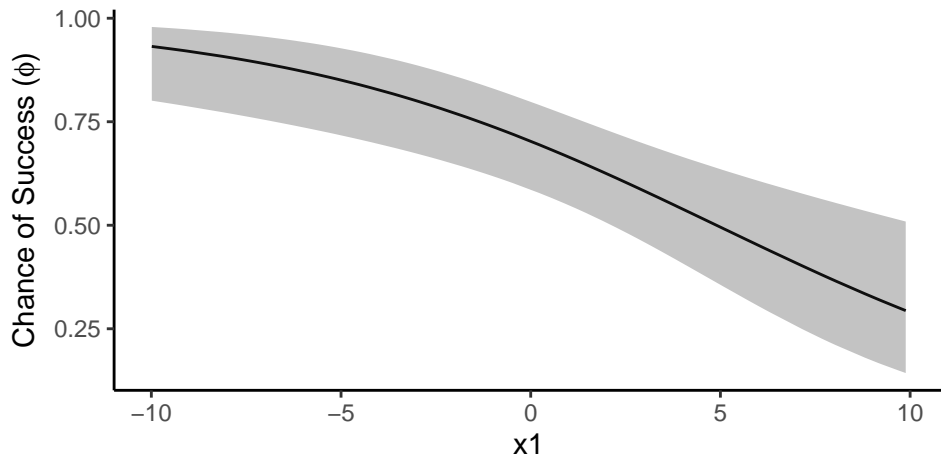
```
# y ~ x, where x is the predictor of y
mod_binomial <- glm(y2 ~ x1 + x2 , data = d1, family = 'binomial') #Fit a binomial GLM
summary(mod_binomial)
```

```
##
## 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?

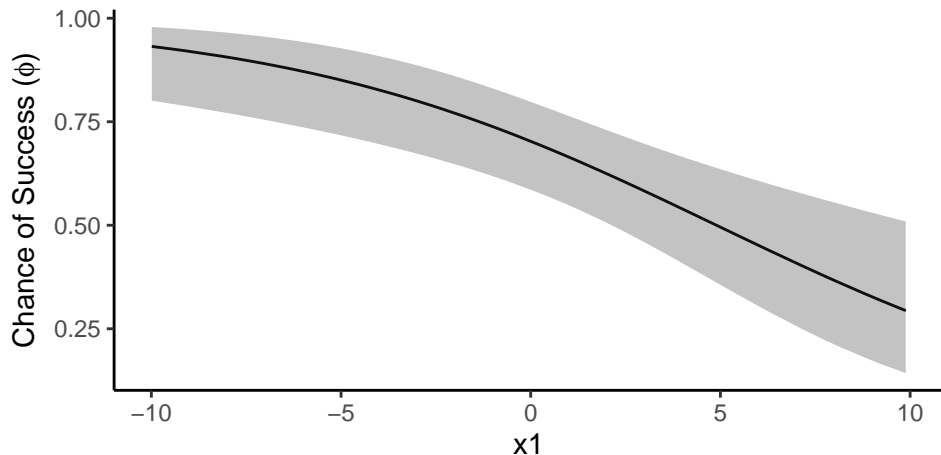
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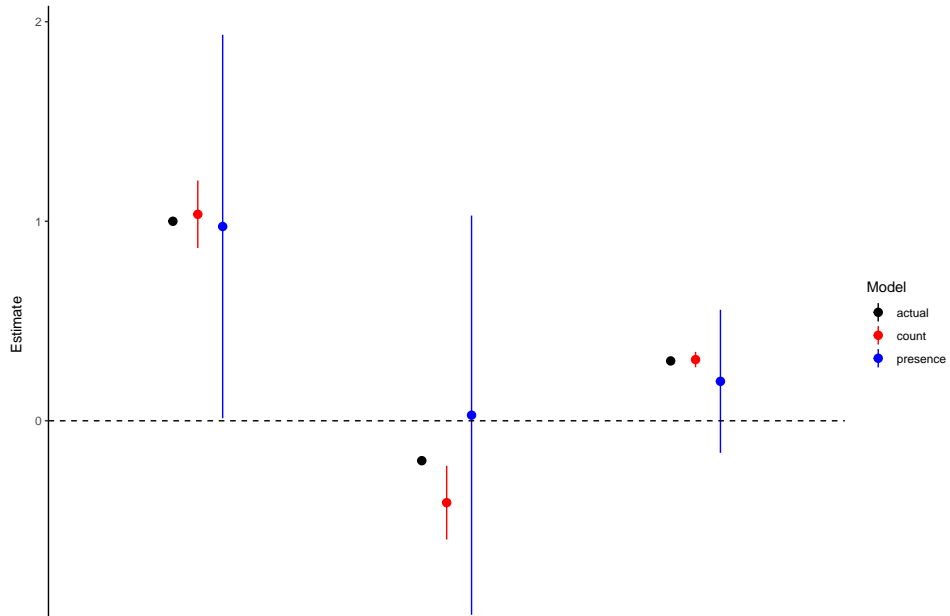
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 - Bonus: make a partial regression plot of terms in the Poisson GLM

Model results



Part 3: Models behaving badly

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- Are my model results reliable?

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- Show-and-tell!

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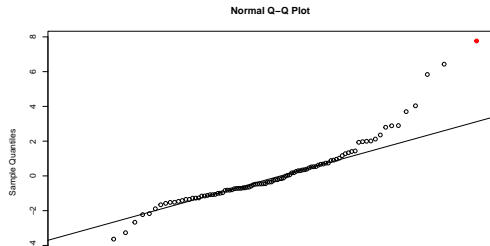
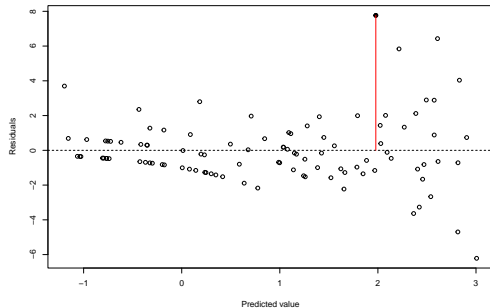
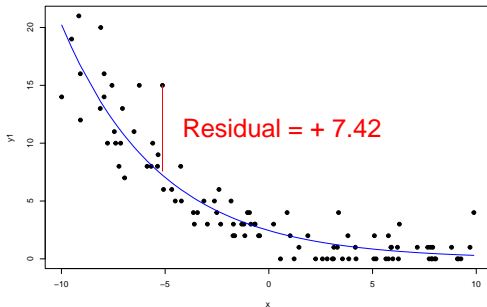
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There are *many* kinds of residuals!

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

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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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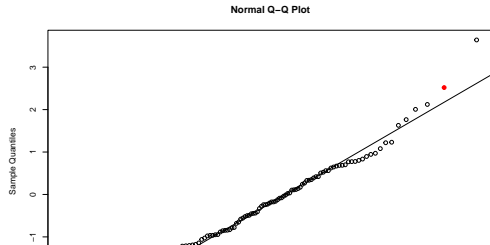
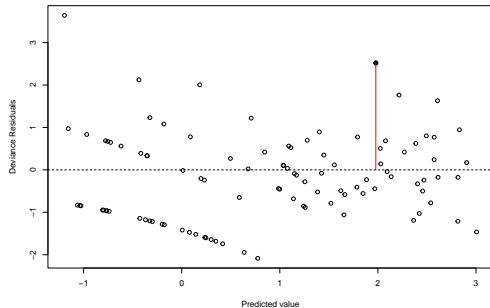
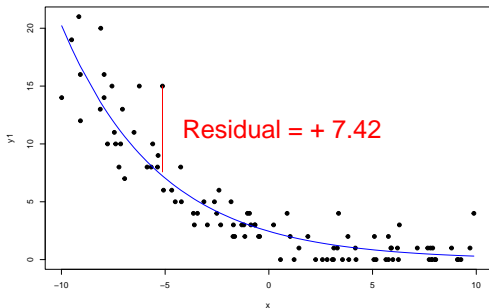
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- These are analogous to regular residuals in LMs
- For more about the different kinds of residuals, see [here](#)

Solution: use deviance residuals for GLMs

Keep in mind:

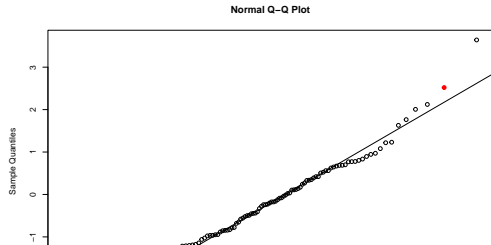
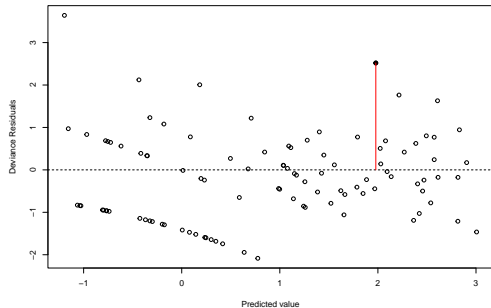
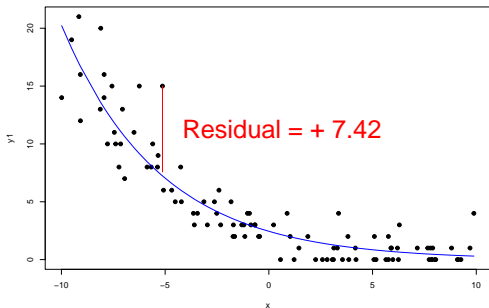
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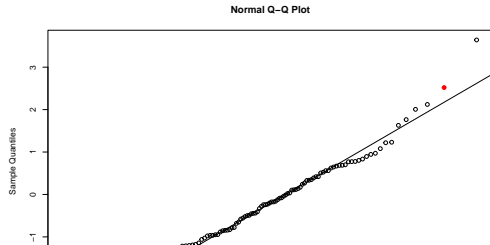
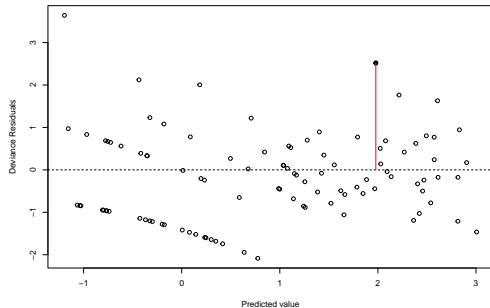
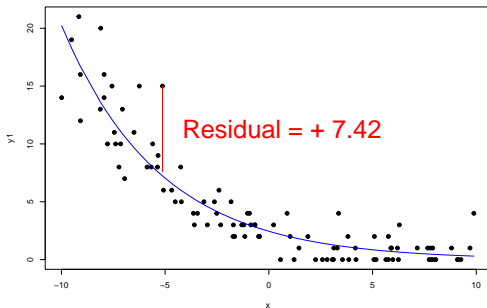
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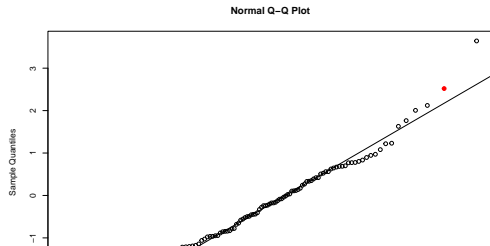
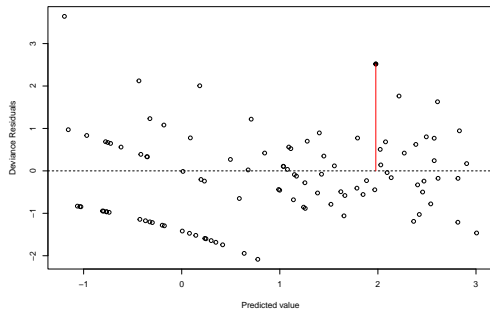
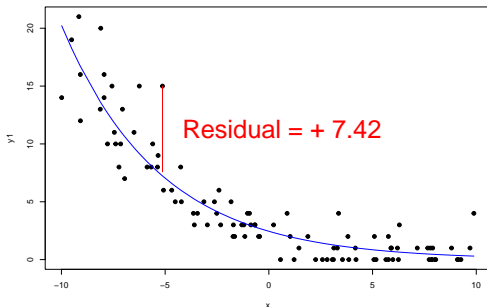
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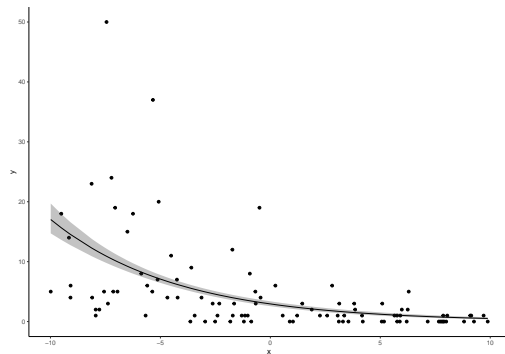
Keep in mind:

- 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

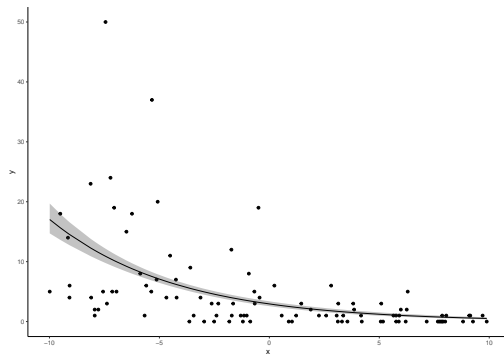
- Binomial and Poisson families have **no** variance term (e.g. SD).



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

Problem 2: Overdispersion

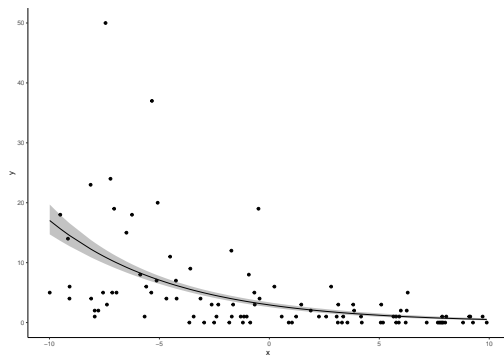
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Problem 2: Overdispersion

- 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

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```
##
## 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 ($106.2 \div 98 = 1.08$)

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```
##
## 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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- 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
 - e.g. Very short observation period
- 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

Solutions for overdispersion

Try the following (in this order):

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 - 1 Fixed effects

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Try the following (in this order):

- ① Consider terms that may have been left out
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 - ② Random effects
- ② Try distributions that account for overdispersion

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Solutions for overdispersion

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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 - 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 :(

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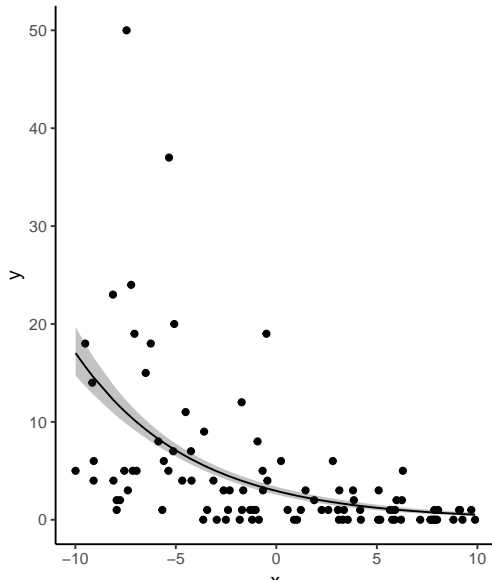
Negative Binomial Regression

```
library(MASS) #Required for NB models  
m3 <- glm.nb(y2~x,data=d1)  
summary(m3) #No longer overdispersed!
```

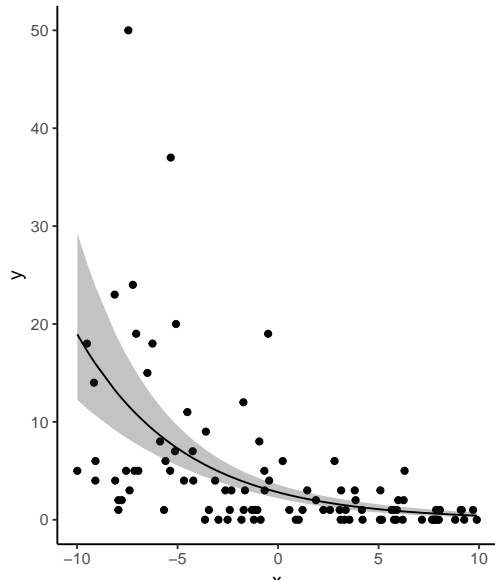
```
##  
## Call:  
## glm.nb(formula = y2 ~ x, data = d1, init.theta = 1.075023363,  
##      link = log)  
##  
## Coefficients:  
##              Estimate Std. Error z value Pr(>|z|)  
## (Intercept)  1.03037    0.12281   8.390  <2e-16 ***  
## x           -0.19131    0.02222  -8.609  <2e-16 ***  
## ---  
## 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

Poisson regression



Negative Binomial Regression

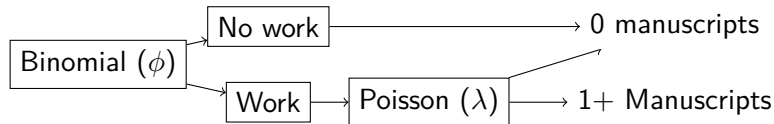


Zero-inflation: drunk monks

An analogy:

- 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)

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

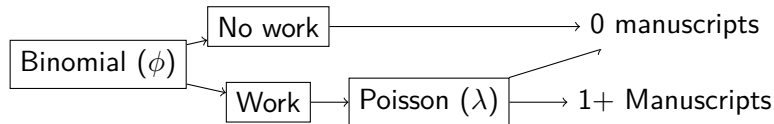


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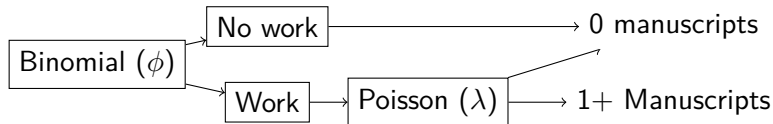


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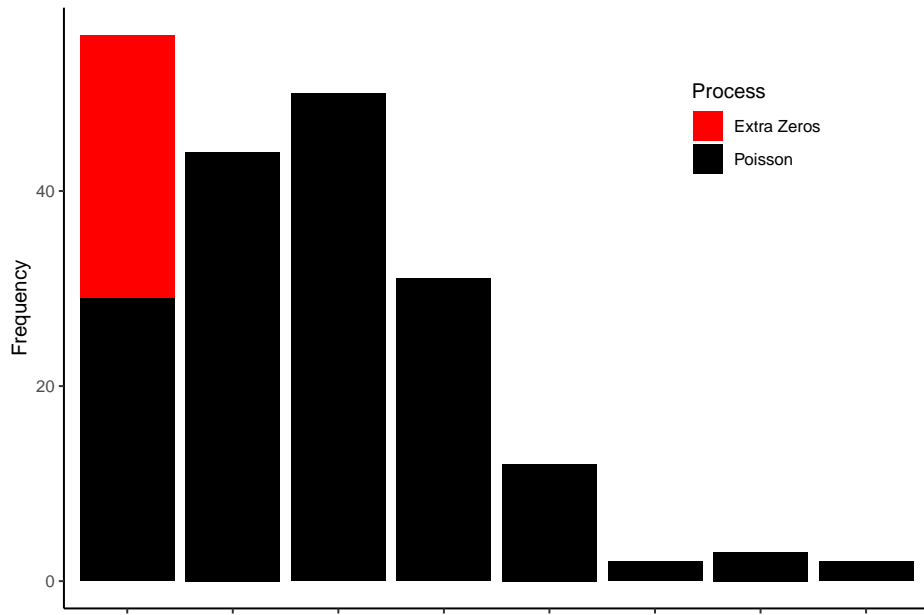
An analogy:

- 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)
- 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*

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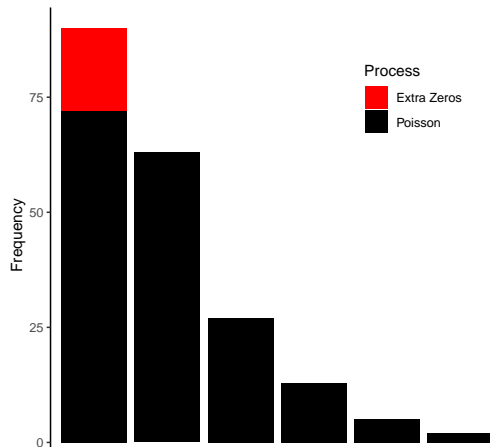
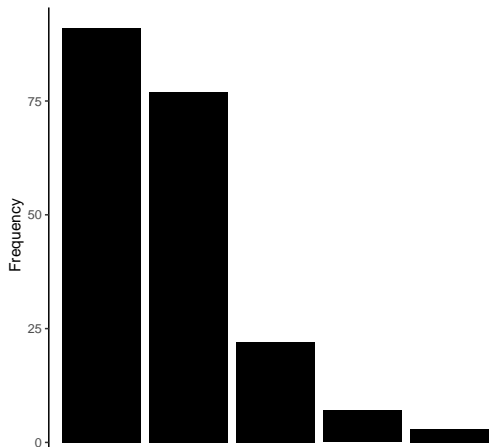


Zero-inflation: graphical model



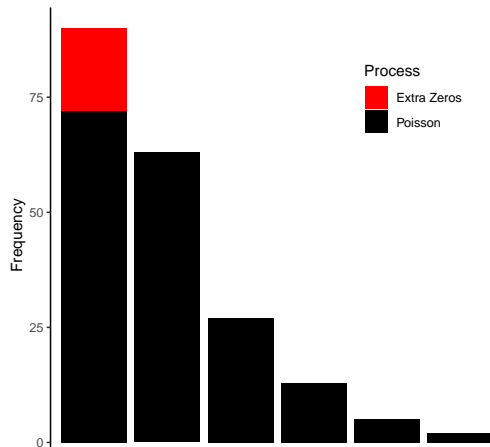
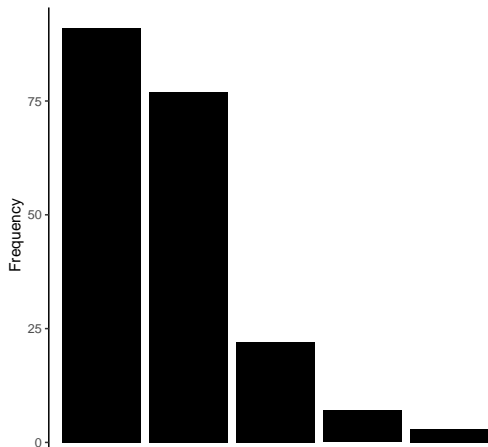
Problem: hard to fit

- 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



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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- 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!

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Binomial GLMs with >1 trial

- If you're measuring single “success/failures”, 1s and 0s are used

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#Number of females and males are in 2 separate columns in d1  
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This will correctly account for different numbers of critters (“trials”) at each site

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- Example: "I counted male and female critters at different sites. Does temperature affect sex ratios?"

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- Poisson/NB models assume that counts occur over the same period of time

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#hours = observation time at each site, and  
# must be log-transformed before being used in an offset  
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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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R-squared for GLMs

- Bad news: there isn't really any good way to get R^2 (explained variance) for non-lm models

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

⁴But 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.

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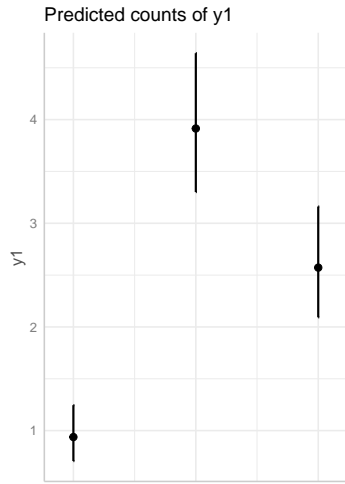
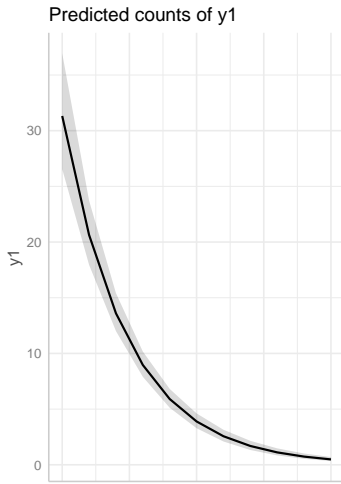
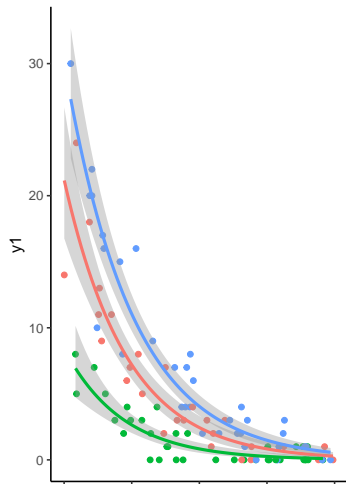
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- See [here](#), [here](#) or [here](#) for more info on R^2
- Try `rsquaredglmm()` from `piecewiseSEM` or `r.squaredGLMM()` from `MuMIn`

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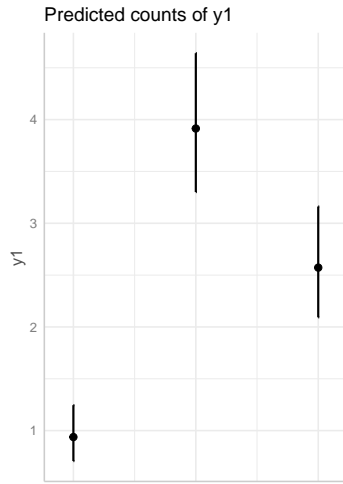
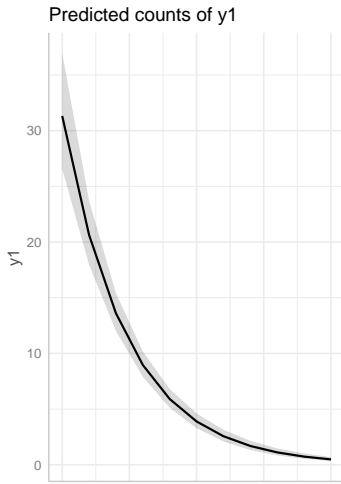
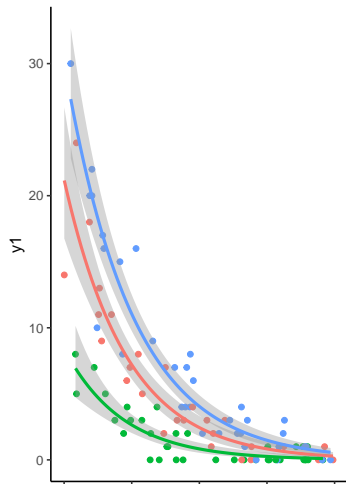
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- `library(ggeffects)` and `library(effects)` work for partial effects plots, but...
- Residuals are tricky to display, unless you plot them on the link scale

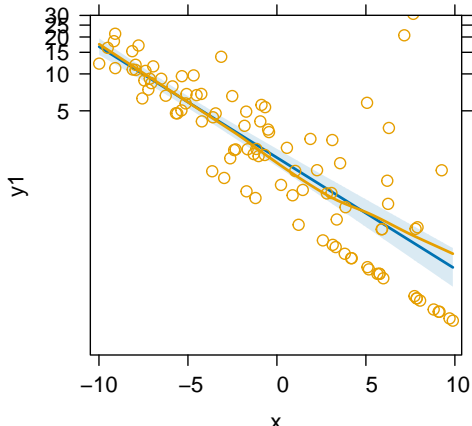


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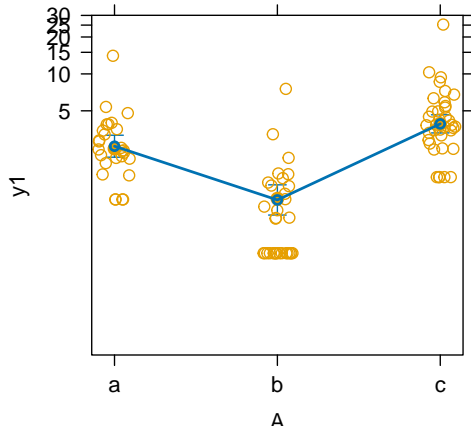
- Plots from effects use *working residuals* (not on the link scale)

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

x effect plot



A effect plot



Show-and-tell!

