

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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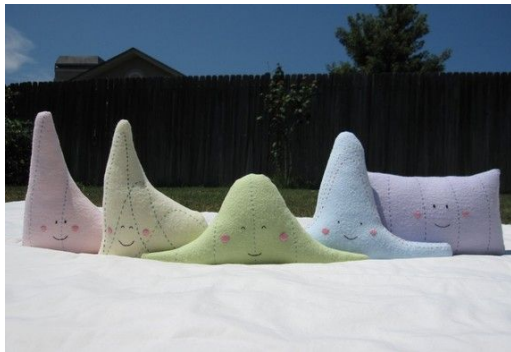
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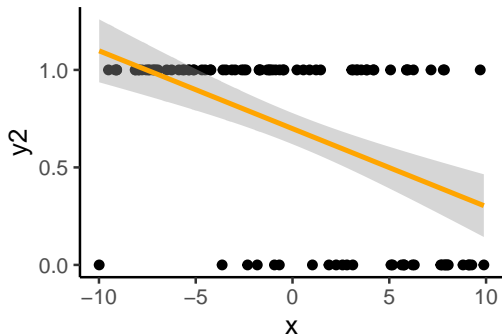
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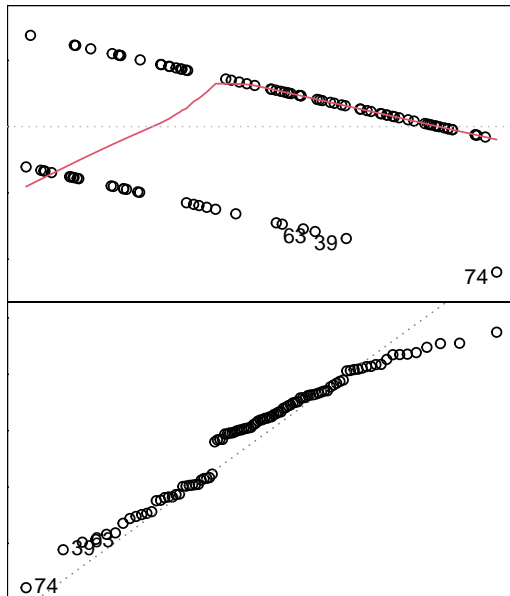


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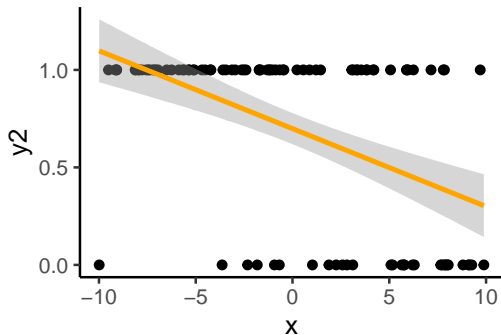
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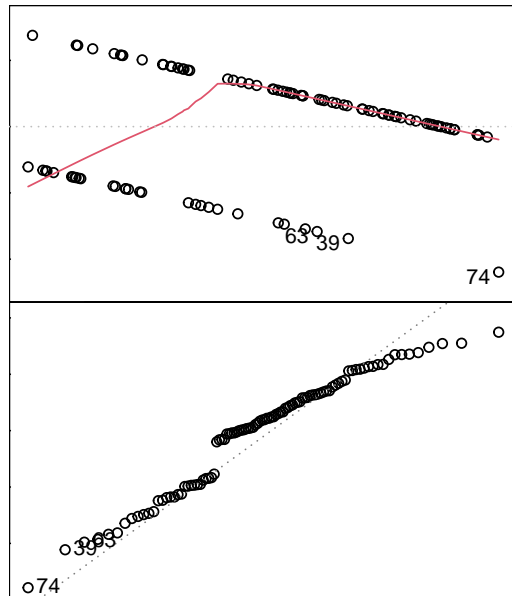
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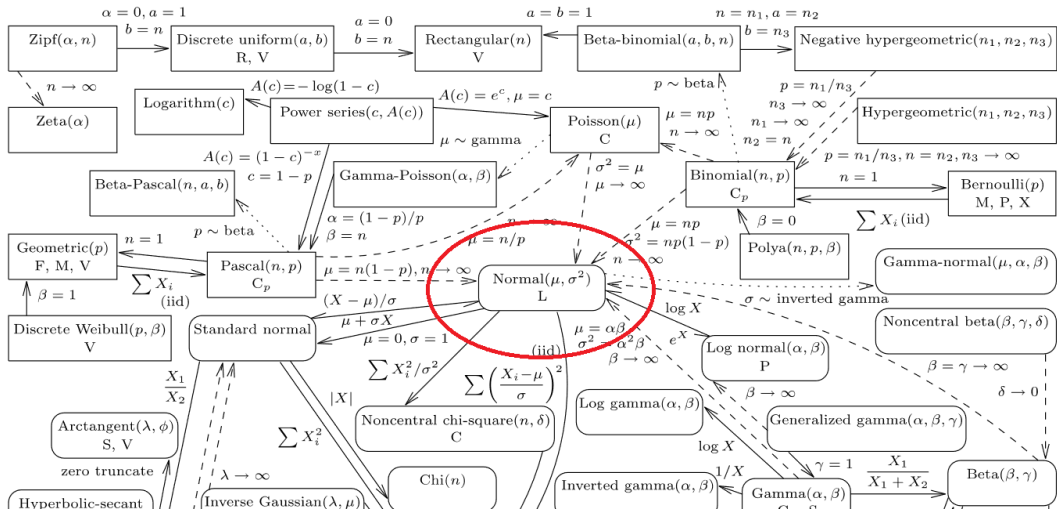
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- Some types of data can never be transformed to make the residuals normal
- Solution: **use the distribution that generates the data!**

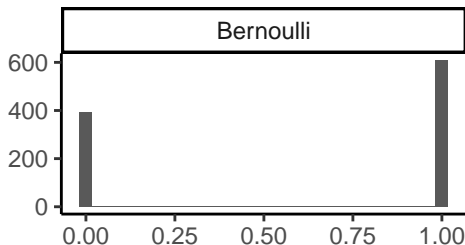
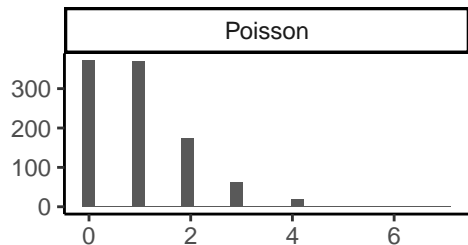
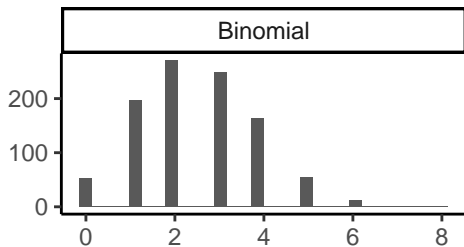
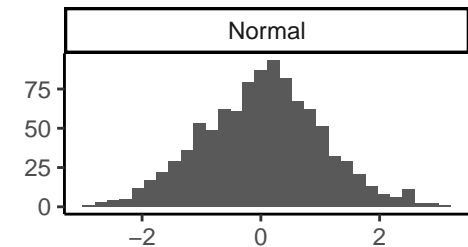


But how do I know which distribution to use?



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!

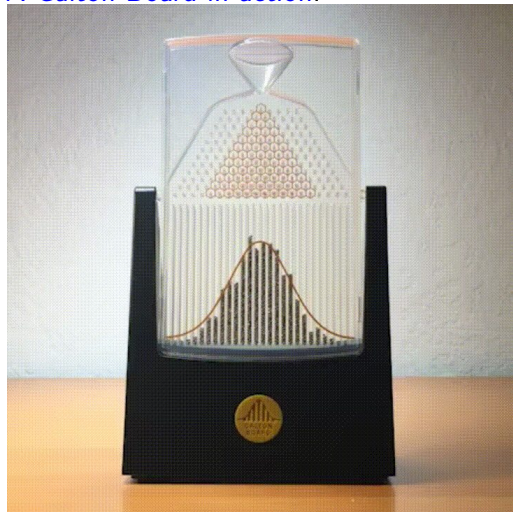


Time to meet the Exponential family!

The Normal Distribution (aka *Gaussian*)

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

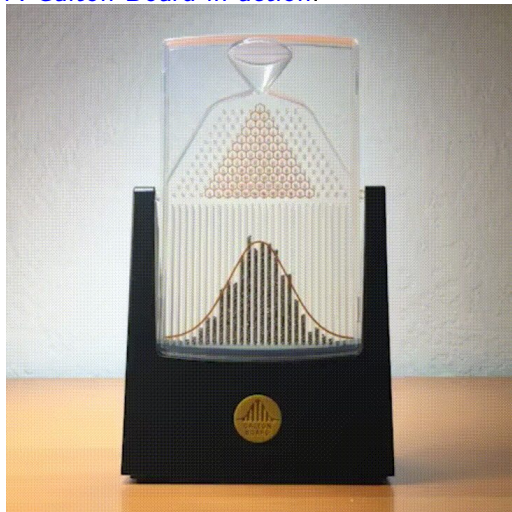
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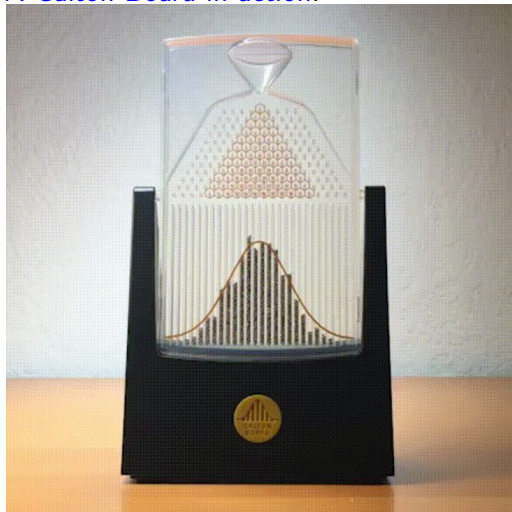
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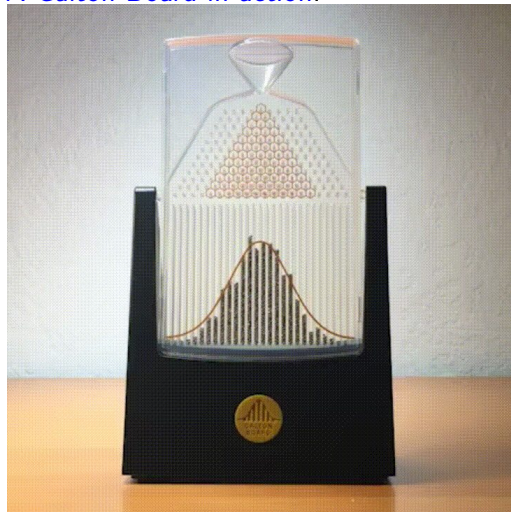
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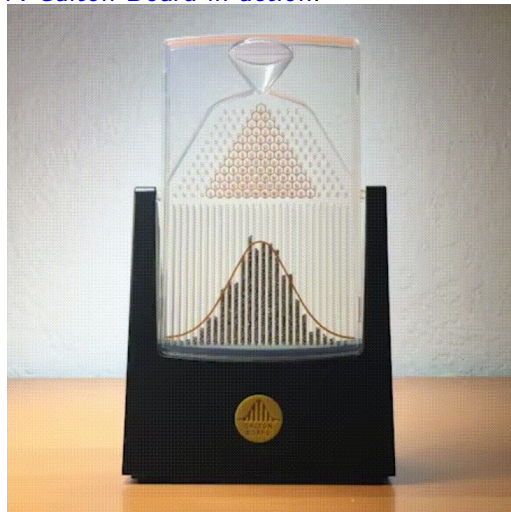
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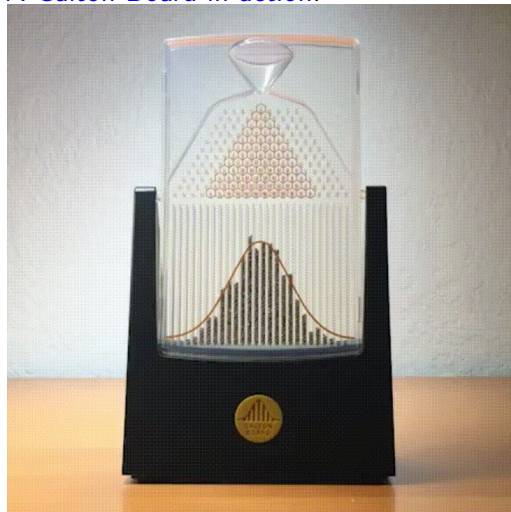
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 - e.g. Height is driven by many sets of genes

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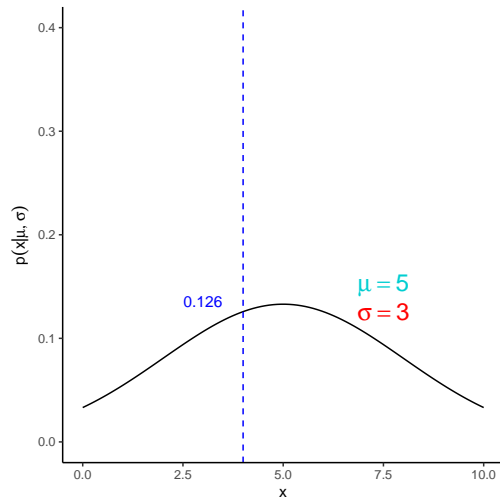
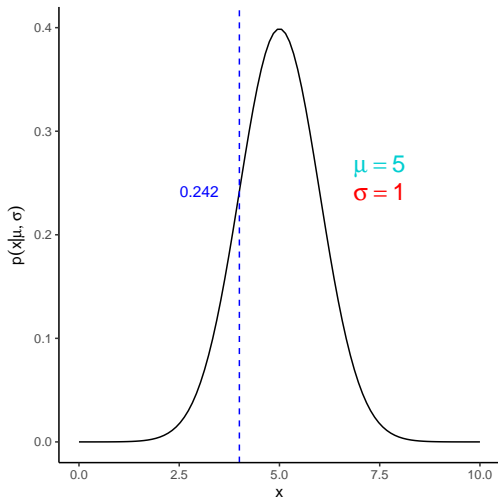
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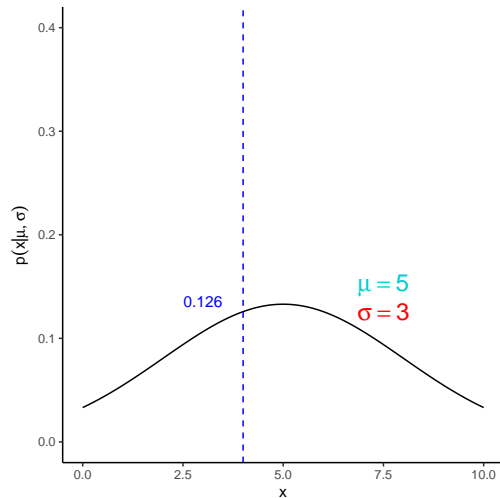
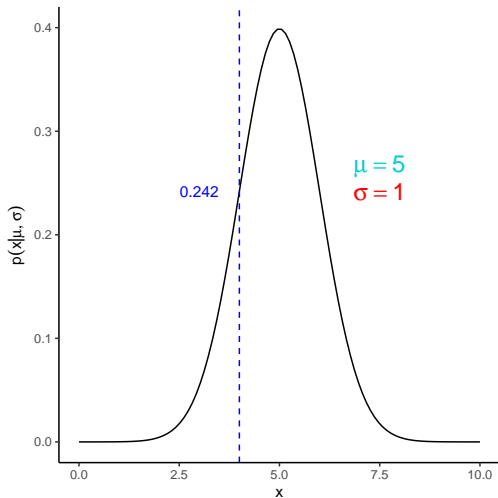
```
#d stands for "density"  
dnorm(x=4, mean=5, sd=1)  
## [1] 0.2419707
```

The Normal Distribution



- Probability of x changes with μ and σ

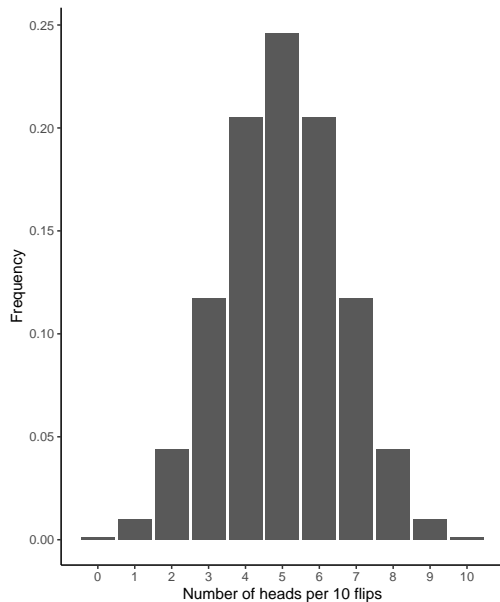
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- Left: $\sigma = 1$, Right: $\sigma = 3$

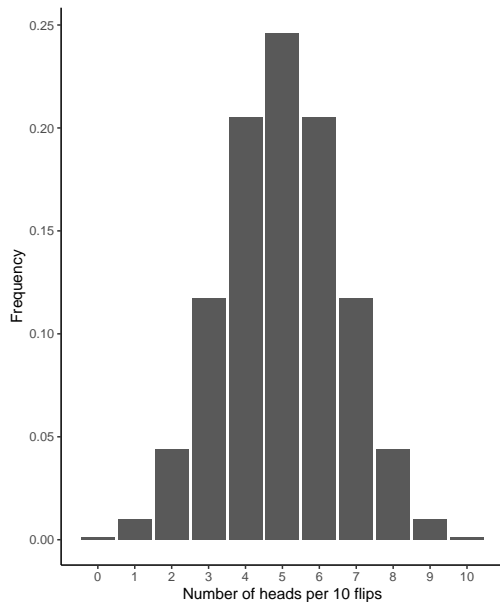
The Binomial Distribution

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



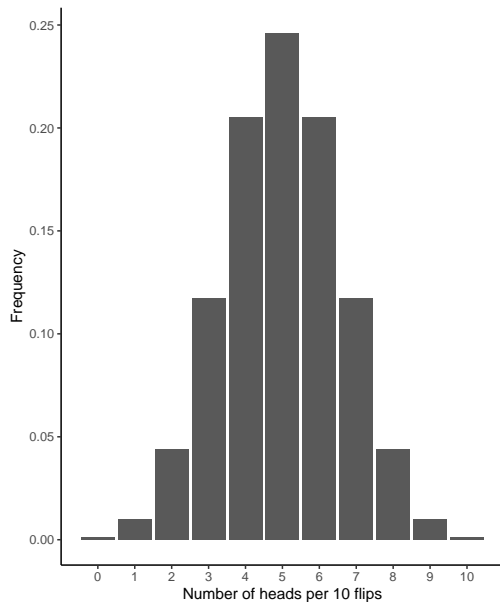
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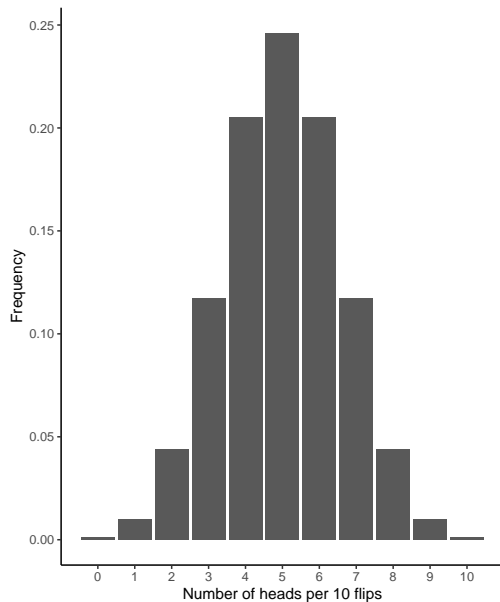
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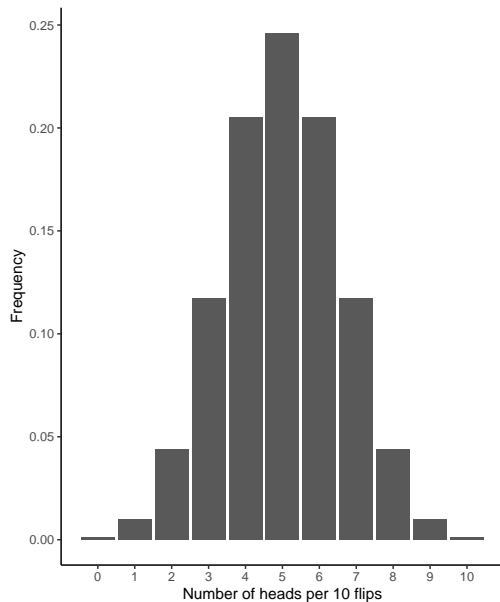
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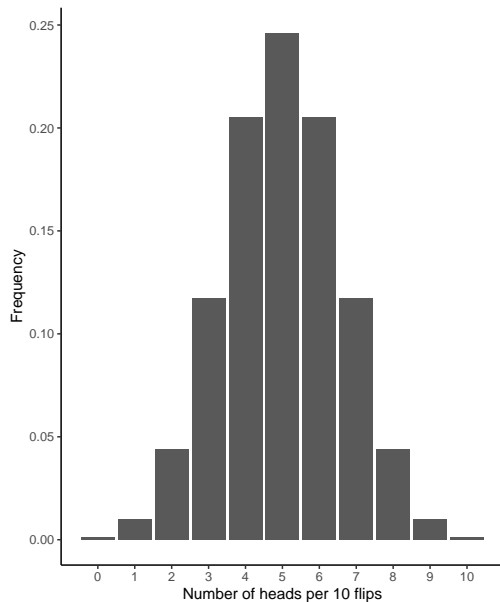
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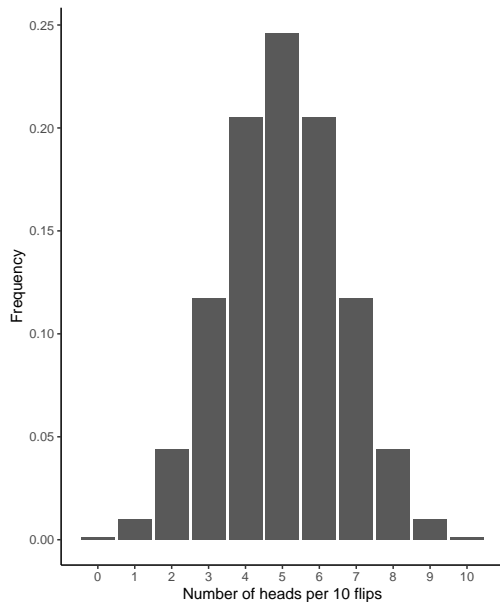
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- If $N = 1$, this is called a *Bernoulli trial*



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- 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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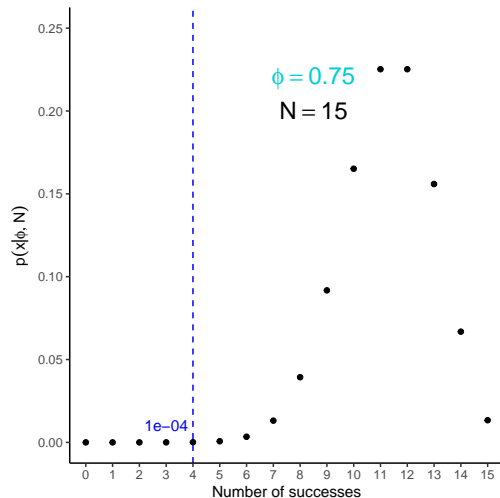
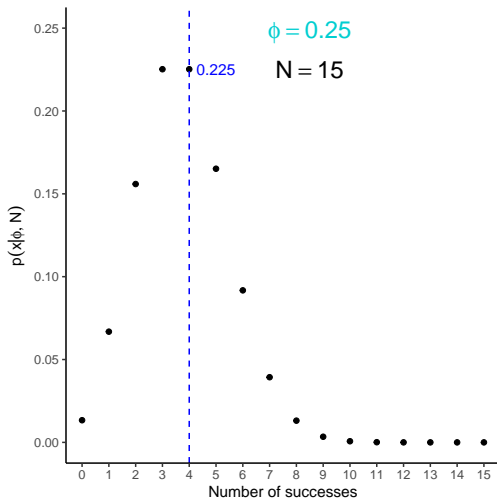
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In R, this is easy:

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

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

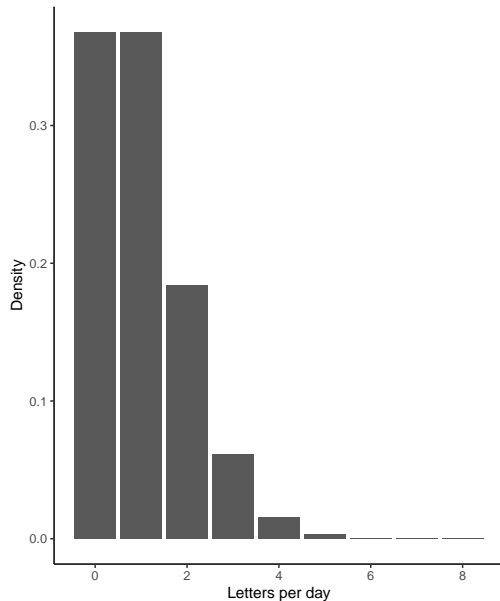
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- Probability of x “successes” changes with ϕ and N

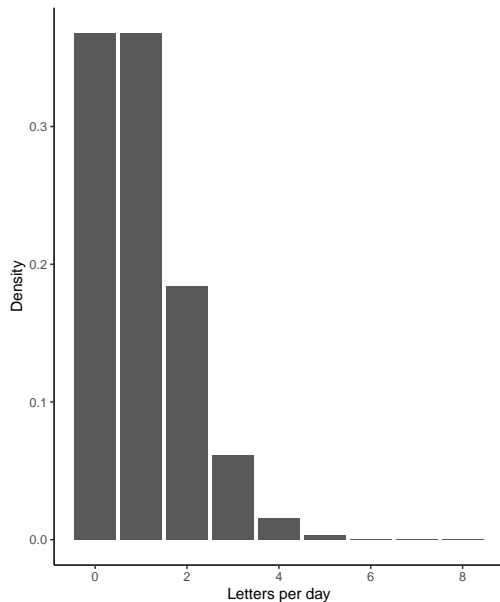
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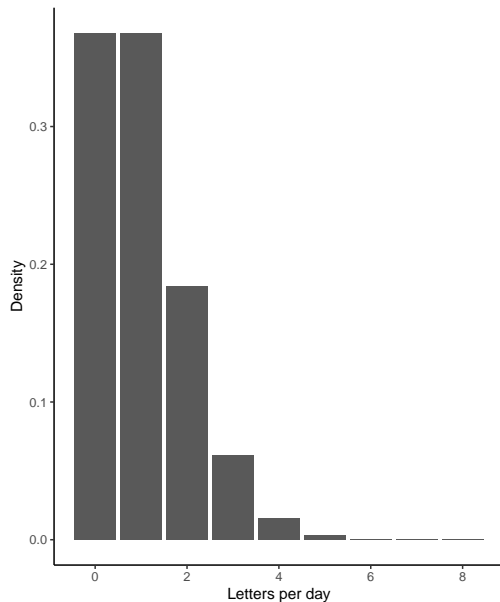
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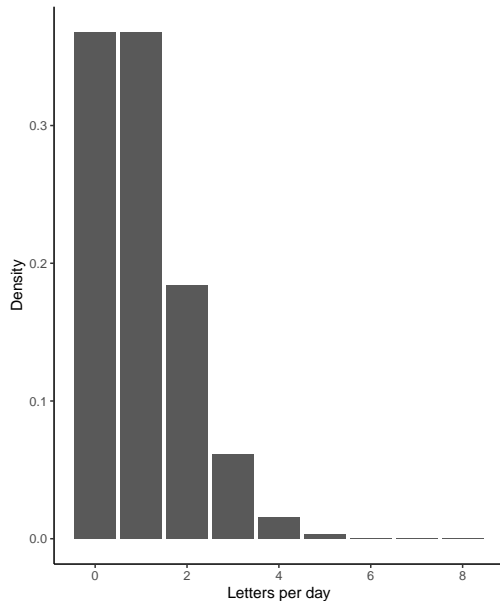
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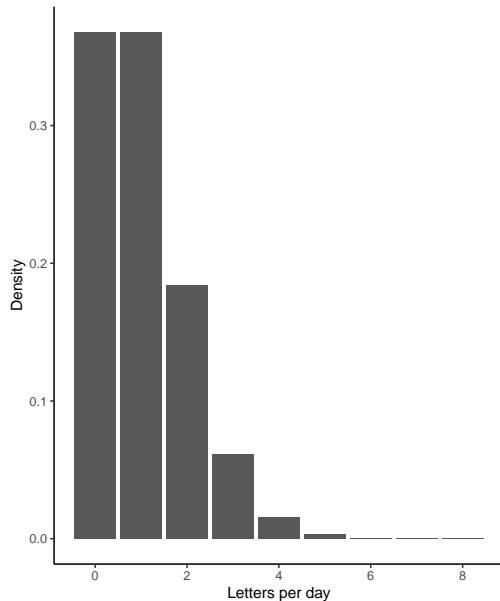
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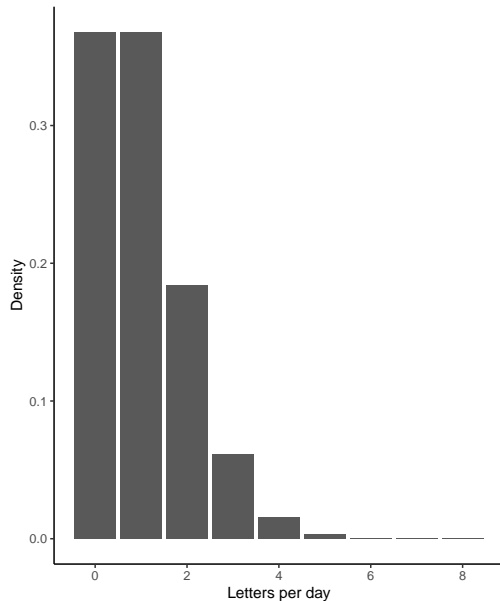
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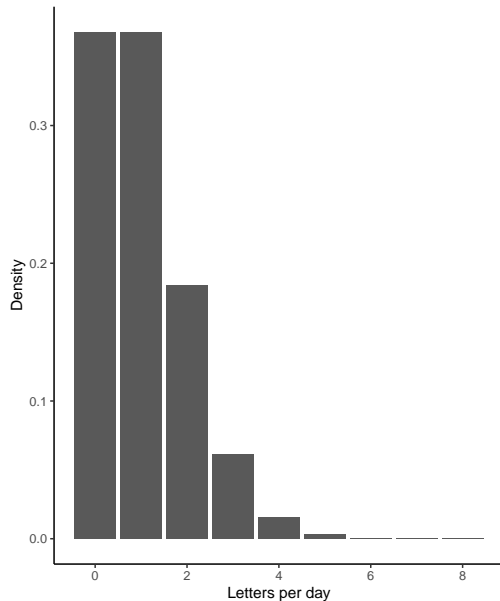
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- Equivalent to Binomial distribution, where N is unknown



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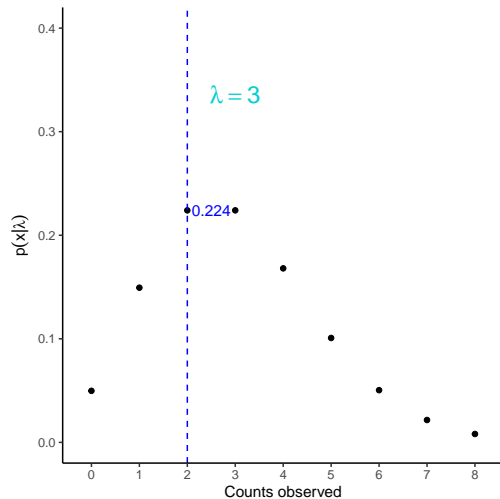
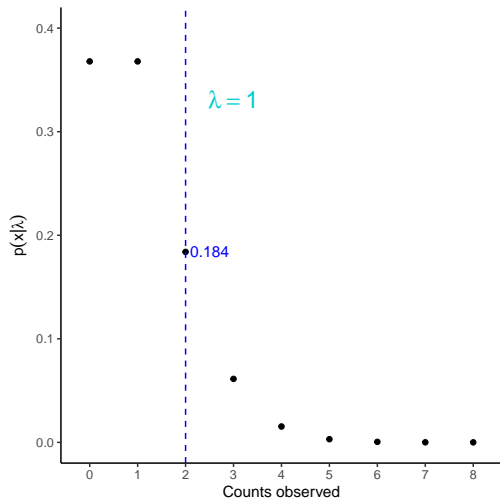
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In R, this is easy:

```
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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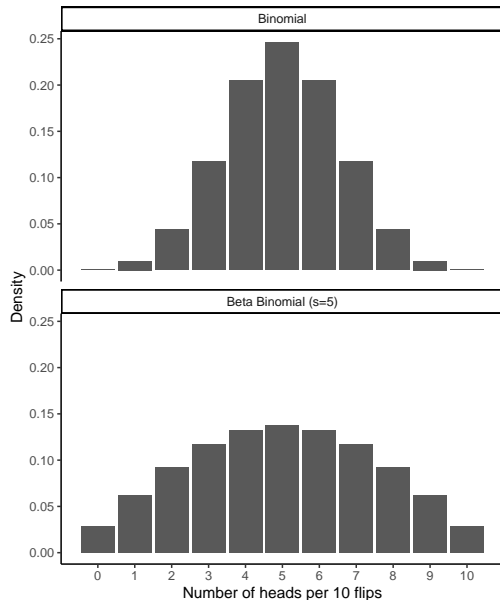
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#Extra distributions

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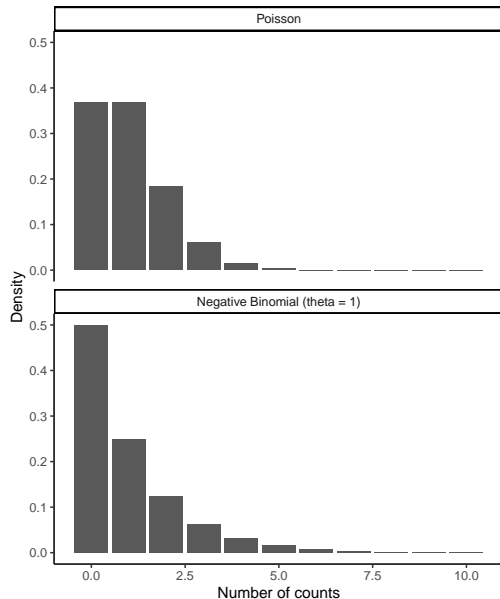
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```
#size = theta parameter  
dnbinom(x,mu,size=1)
```



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

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Part 2: Maximum likelihood and GLMs

Outline

- Maximum likelihood

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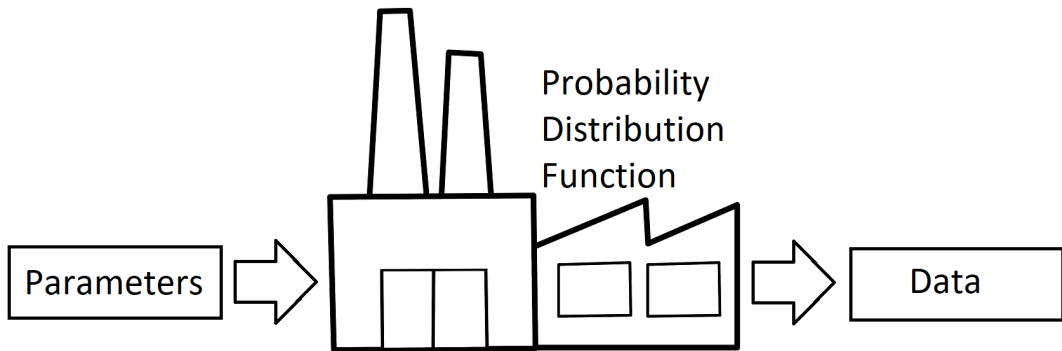
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 - Predictors \rightarrow Linear model

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Making data can be thought of as a *factory*

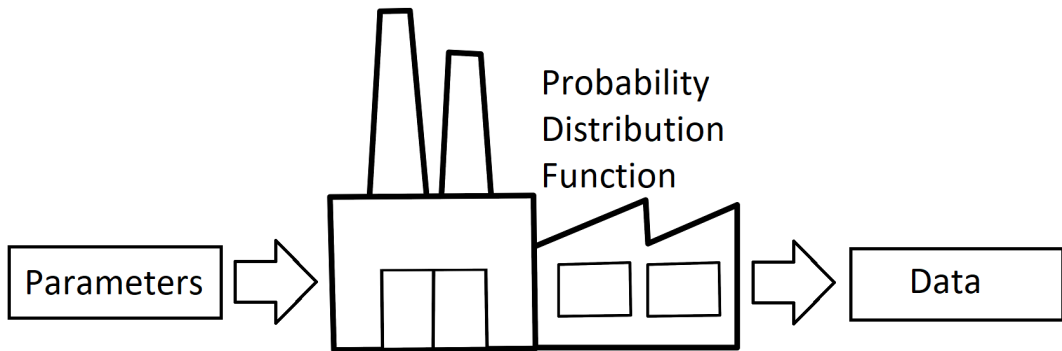
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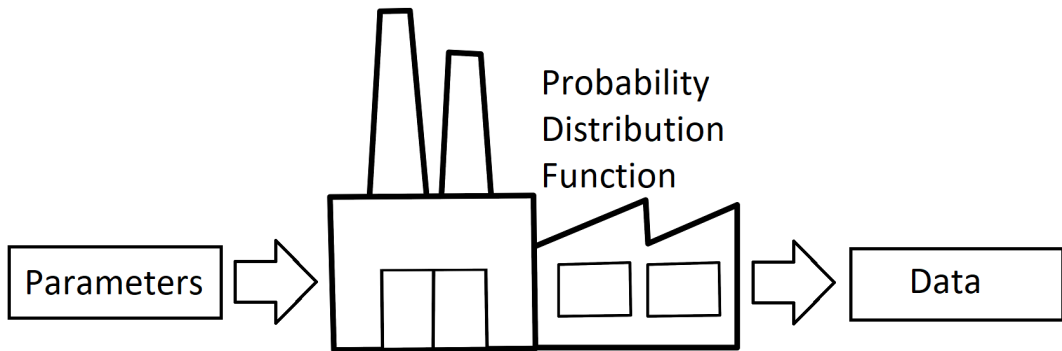
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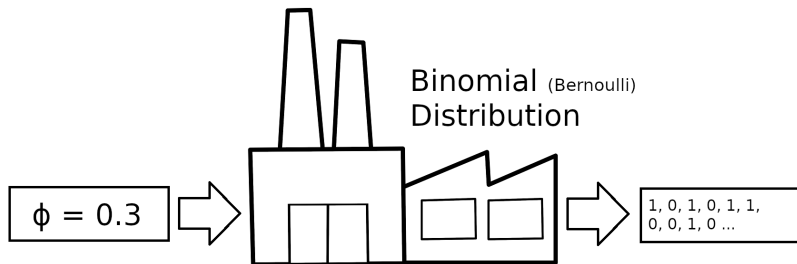
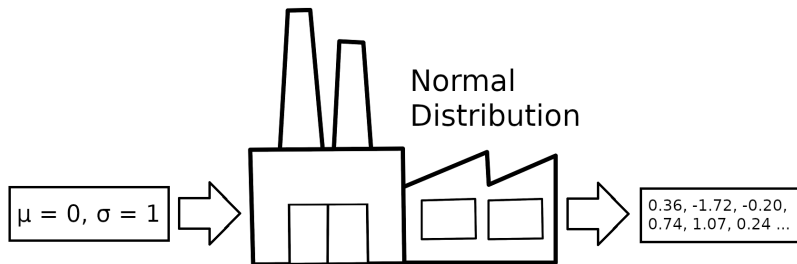
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- Process: **probability function**
- Output: **data** (things made by the process)

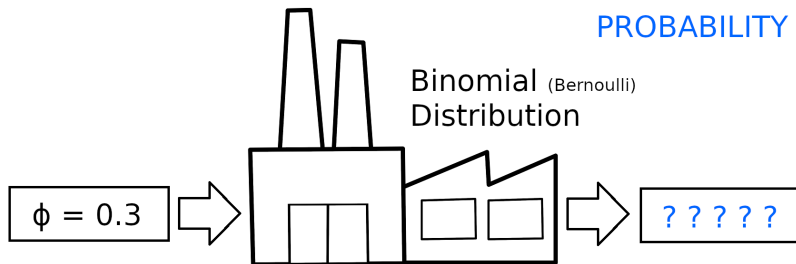


Examples

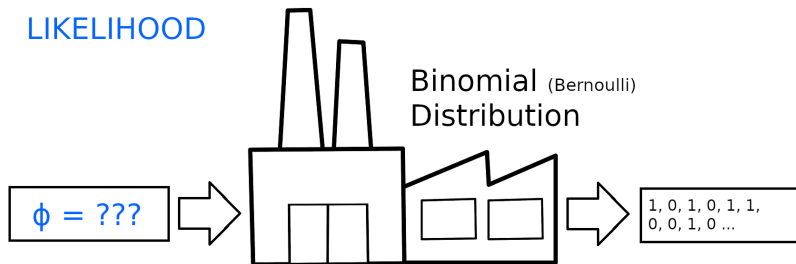


Likelihood vs Probability

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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```

Are we likely to be 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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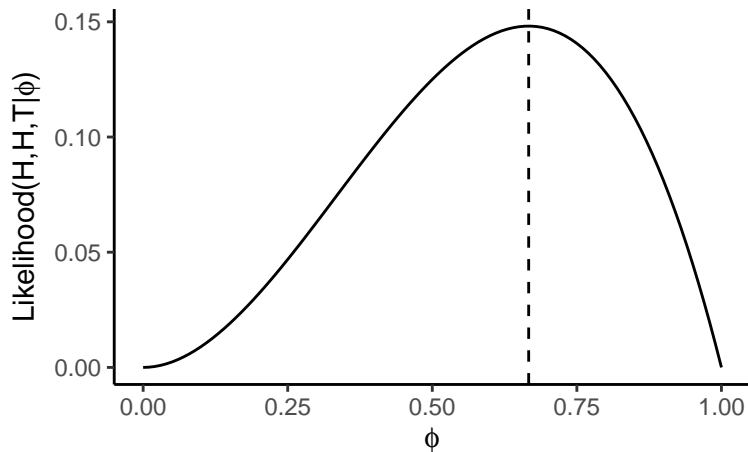
```
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```

```
#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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## AIC: 5.8191
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Wait... our estimate should be 0.666 (2/3), not 0.693!

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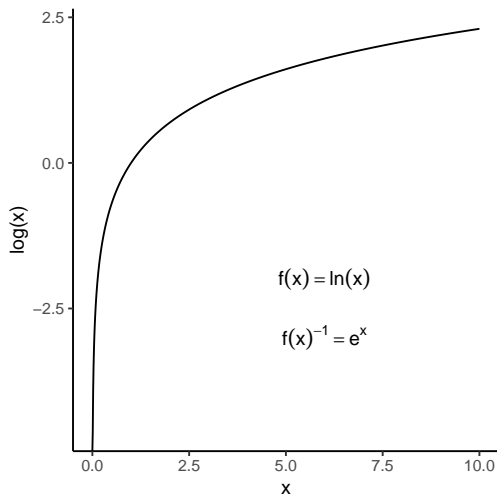
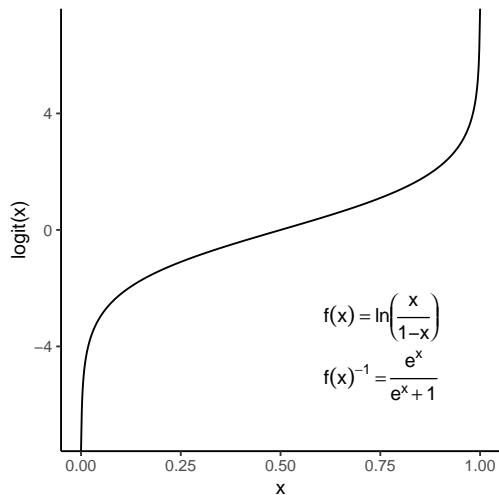
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- $\text{logit}(0.693) = 0.666$, so the GLM actually got it right!

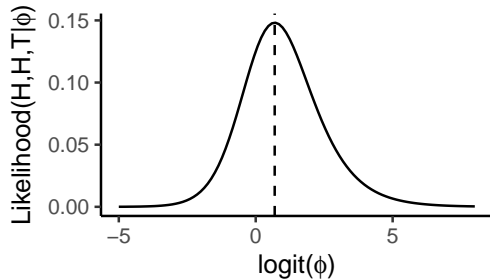
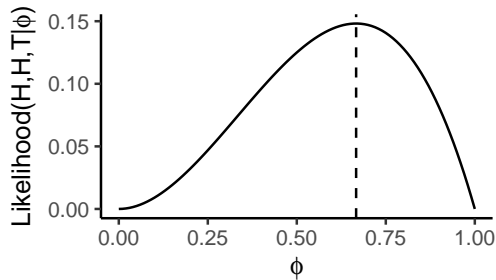
What do these functions look like?



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

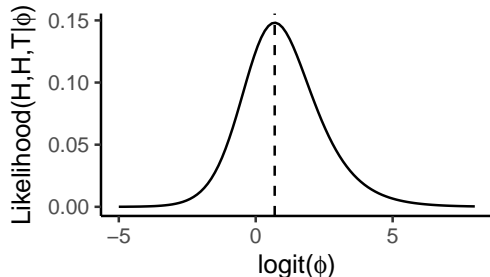
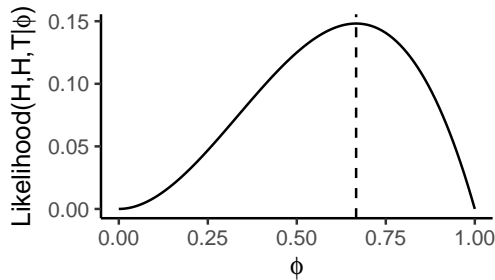
Why do we bother with these link function?

- Likelihood functions are not symmetrical on the regular scale



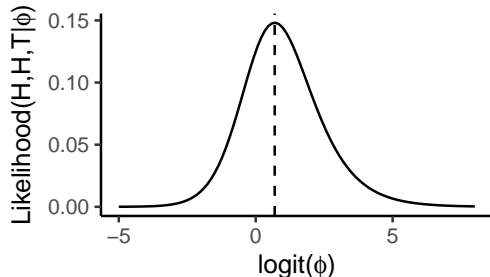
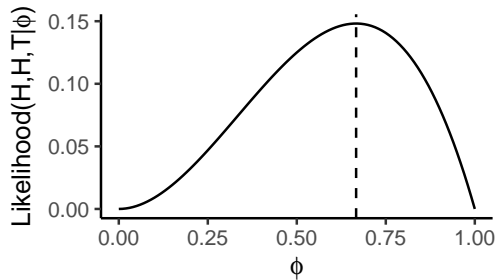
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- On the link-scale, they are closer to a normal distribution
- Makes it easier for R to find the ML estimate (and confidence intervals)



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

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

How do linear models fit into this?

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

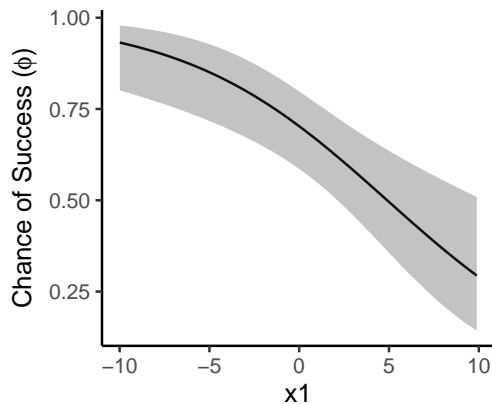
```
# y ~ x, where x is the predictor of y
mod_binomial <- glm(y2 ~ x1 + x2 , data = d1, family = 'binomial') #Fit a binomial GLM
```

```
##
## Call:
## glm(formula = y2 ~ x1 + x2, family = "binomial", data = d1)
##
## 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...

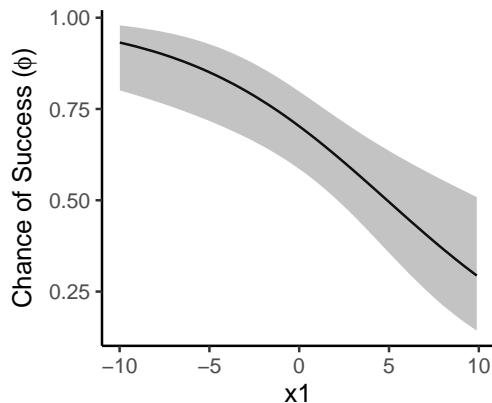
How do I get partial effects plots?

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



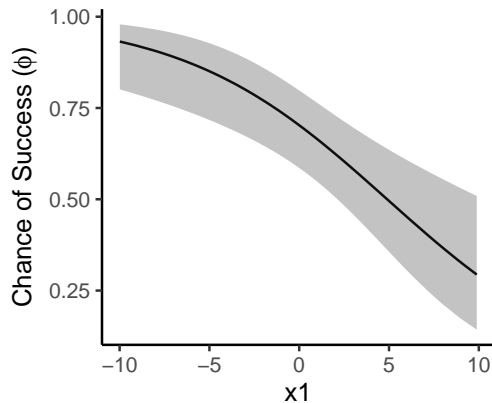
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How do I get partial effects plots?

- `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



A challenger approaches!

- Dr. Roberto Darkley (Robert Barkley's evil nemesis) sent 2 people out to check out some bat roosts in Edmonton and Calgary. One of them dutifully counted bats at each roost, but the other one was really lazy, and just recorded "bats or no bats" (1 or 0).

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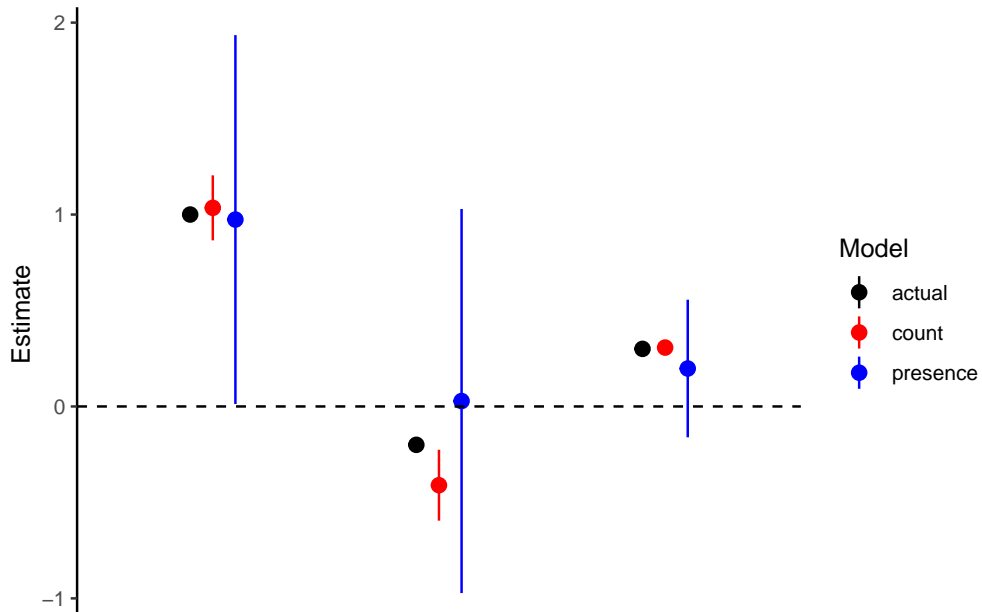
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- How do the models look? Compare the coefficients and see if they are different
 - Bonus: make a partial regression plot of terms in the Poisson GLM

Model results



Part 3: Models behaving badly

Motivation

- Are my model results reliable?

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- Show-and-tell!

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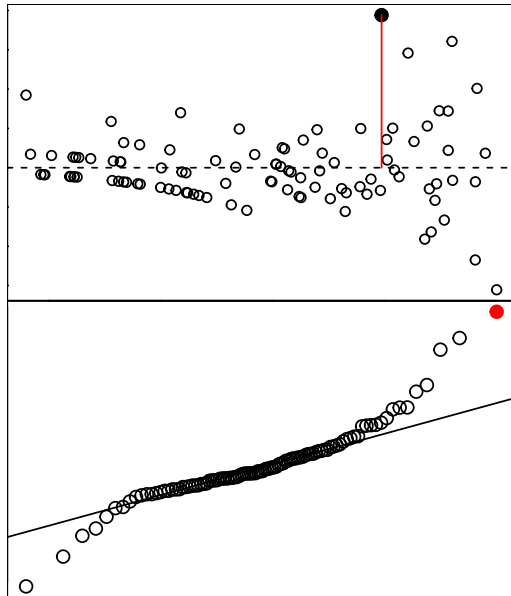
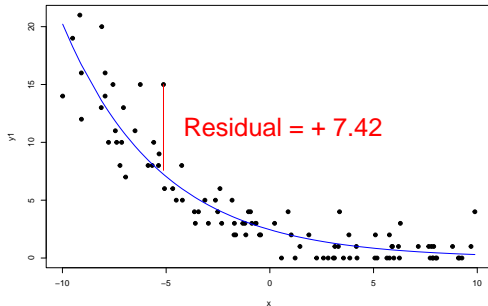
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In addition to *response* (regular) residuals there are:

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Deviance residuals use *likelihood*:

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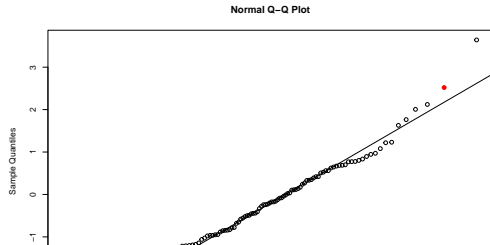
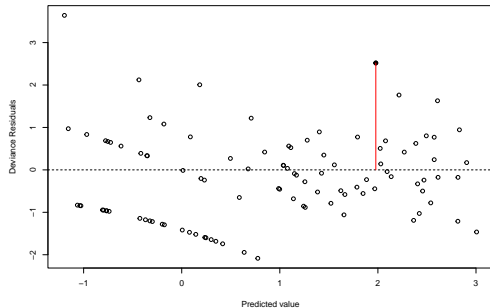
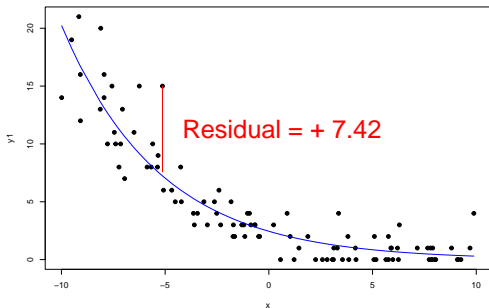
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- For more about the different kinds of residuals, see [here](#)

Solution: use deviance residuals for GLMs

Keep in mind:

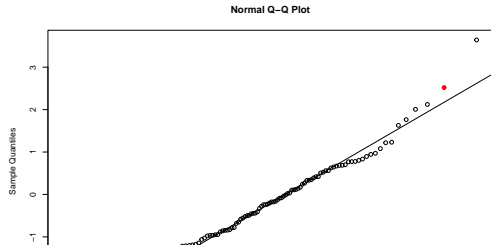
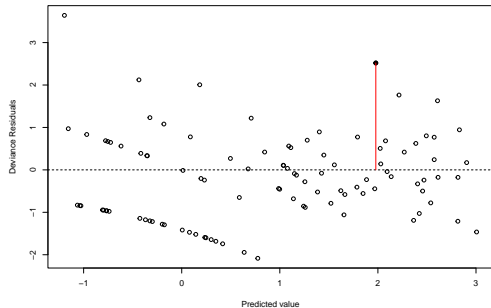
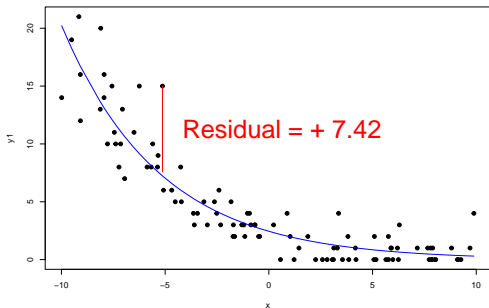
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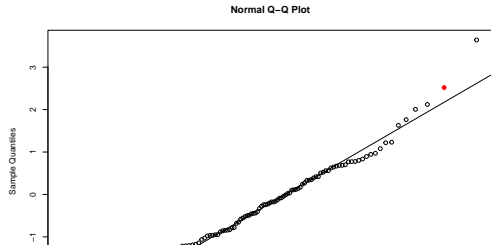
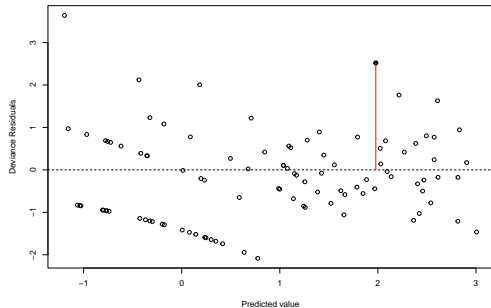
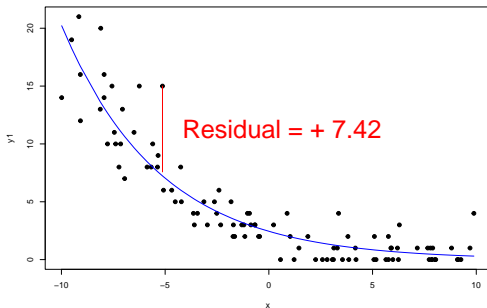
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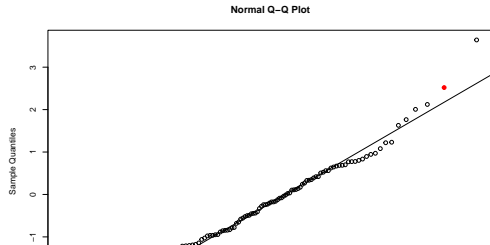
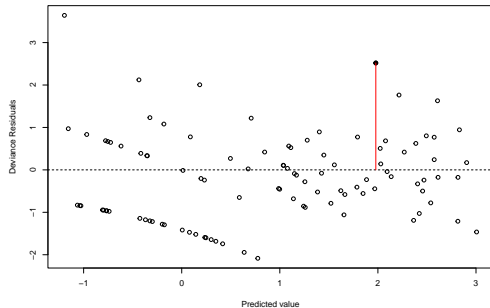
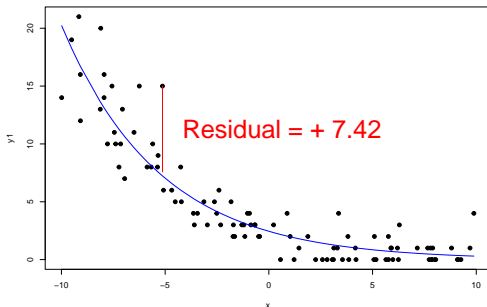
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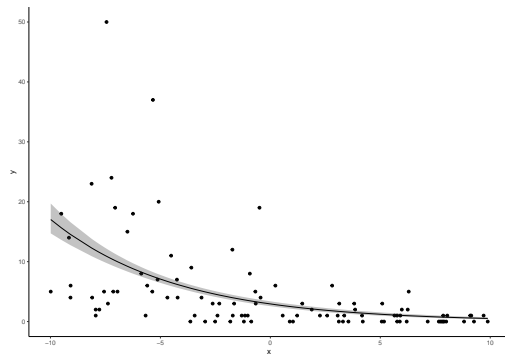
Keep in mind:

- 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

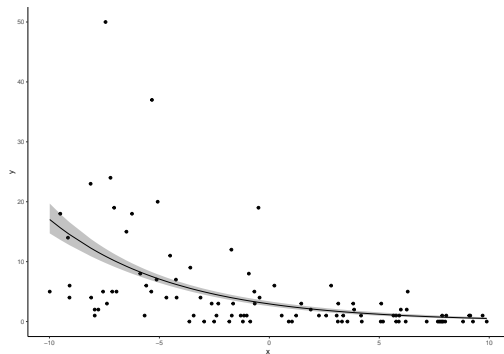
- Binomial and Poisson families have **no** variance term (e.g. SD).



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

Problem 2: Overdispersion

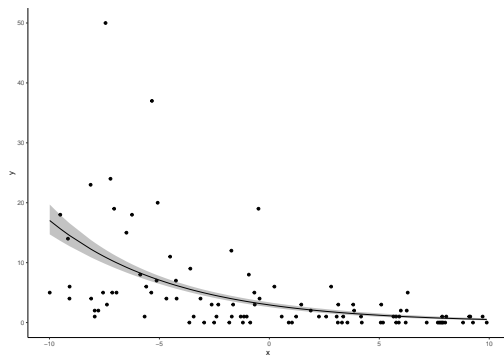
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Problem 2: Overdispersion

- 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

Problem 2: Overdispersion

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

- In Poisson or Binomial models, Residual deviance \div Degrees of Freedom should be ~ 1

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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)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -4.1009  -1.7543  -0.8805   0.4796   8.6102
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  1.07897     0.06871   15.70  <2e-16 ***
## x            -0.17581     0.01069  -16.44  <2e-16 ***
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##
## (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
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##
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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

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

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Solutions for overdispersion

Try the following (in this order):

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

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 - ① Fixed effects
 - ② Random effects
- ② Try distributions that account for overdispersion
 - ① Negative Binomial, Beta Binomial, Zero-inflated Poisson²

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

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- ④ Design a better study :(

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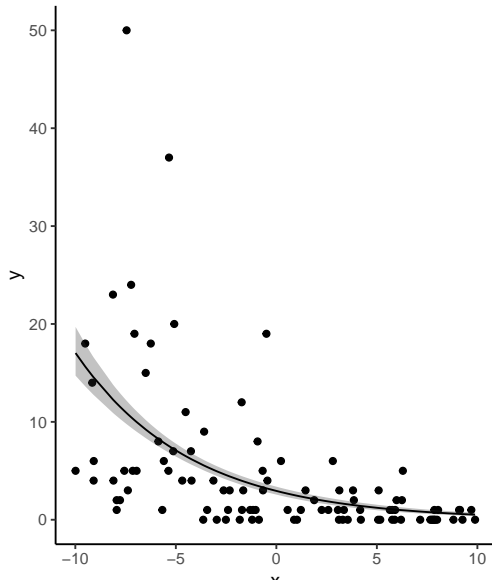
Negative Binomial Regression

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

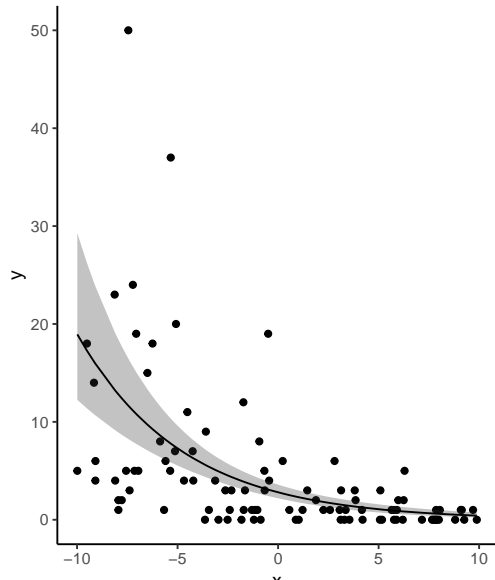
```
##
## Call:
## glm.nb(formula = y2 ~ x, data = d1, init.theta = 1.075023363,
##       link = log)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.9829  -1.0492  -0.3989   0.3831   2.4289
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  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
##
```

Negative Binomial Regression

Poisson regression



Negative Binomial Regression

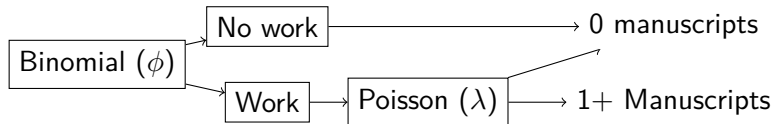


Zero-inflation: drunk monks

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:

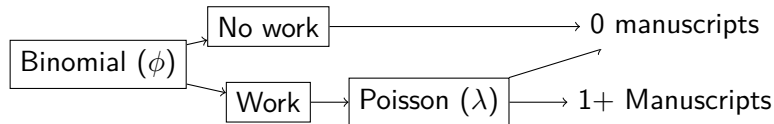


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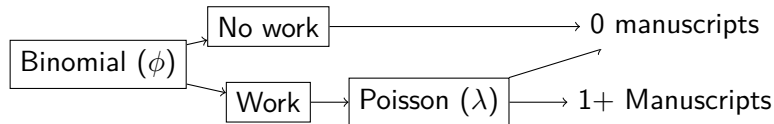


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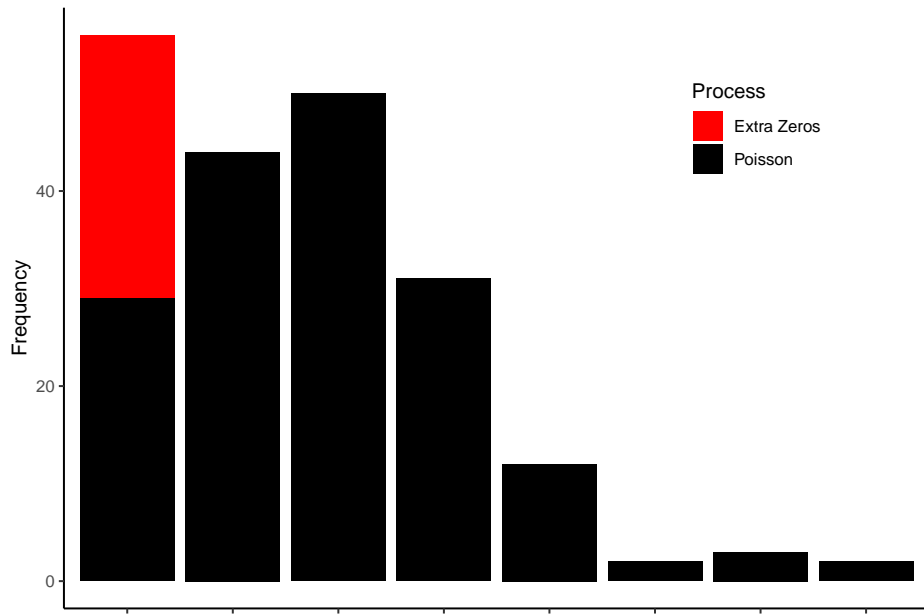
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- ② Some days they decide to try out the beer that's been brewing in the cellar! No manuscripts get made on those days.
- ③ The number of manuscripts made (per day) follows a *zero-inflated Poisson distribution*

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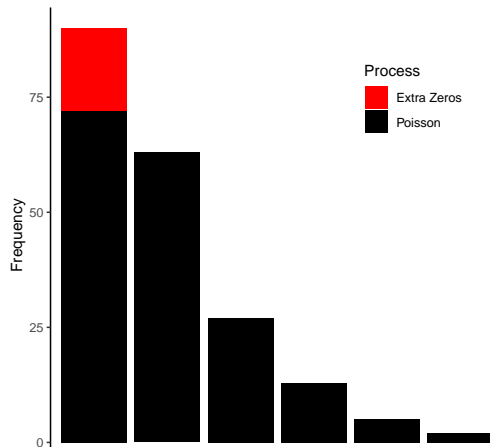
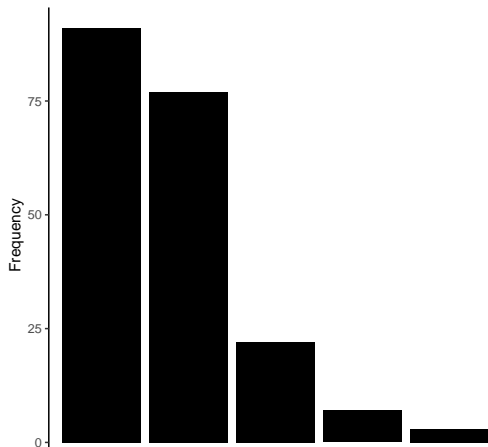


Zero-inflation: graphical model



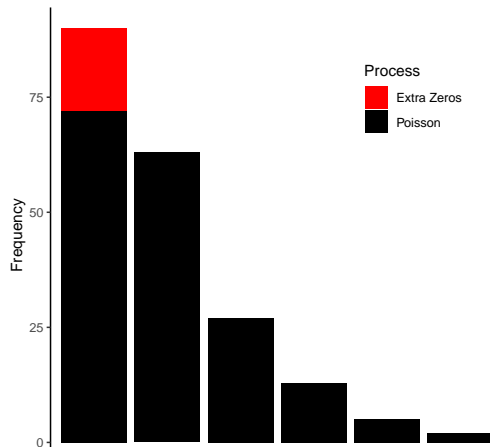
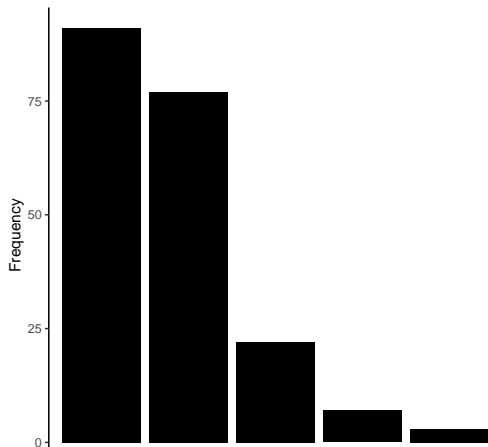
Problem: hard to fit

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- 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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ML vs REML

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Solution:

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

Other useful things about GLMs!

- Binomial GLMs with >1 trial

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

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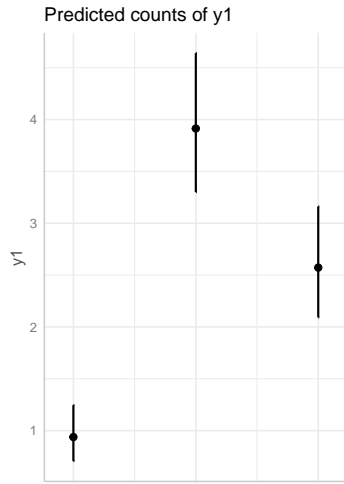
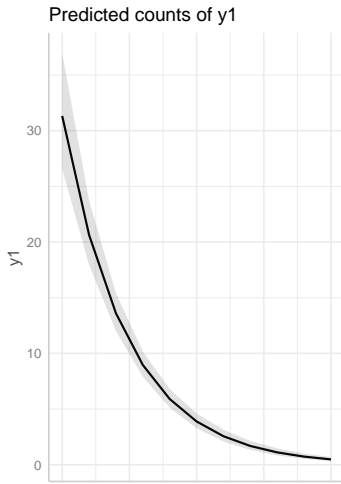
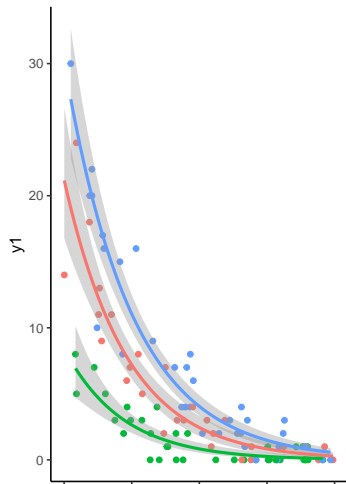
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- See [here](#), [here](#) or [here](#) for more info on R^2
- Try `rsquaredglmm()` from `piecewiseSEM` or `r.squaredGLMM()` from `MuMIn`

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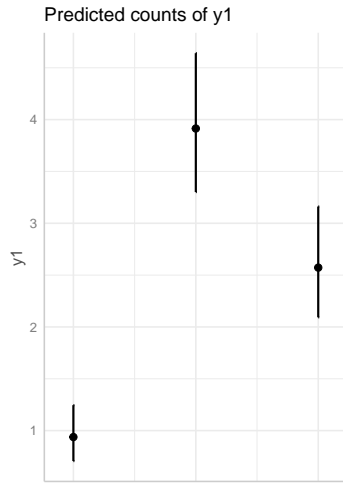
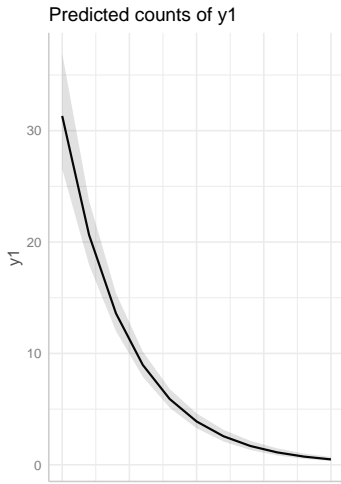
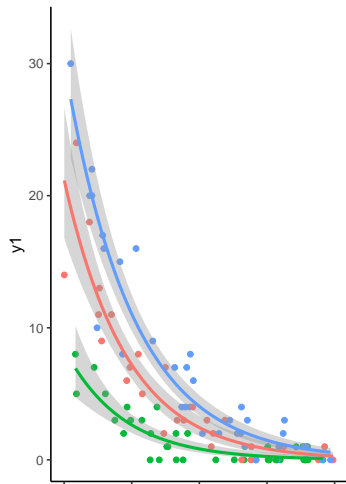
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- `library(ggeffects)` and `library(effects)` work for partial effects plots, but...
- Residuals are tricky to display, unless you plot them on the link scale

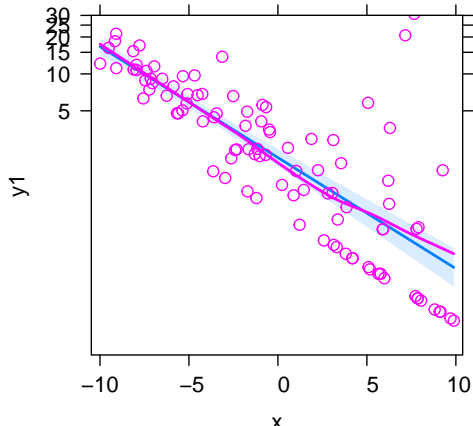


Partial effects plots

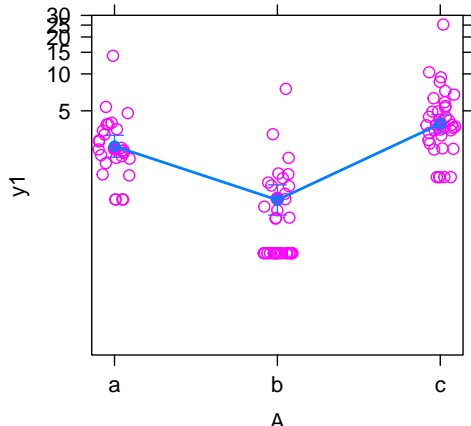
- Plots from effects use *working residuals* (not on the link scale)

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

x effect plot



A effect plot



Show-and-tell!

