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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- Meet (some of) the exponential family!
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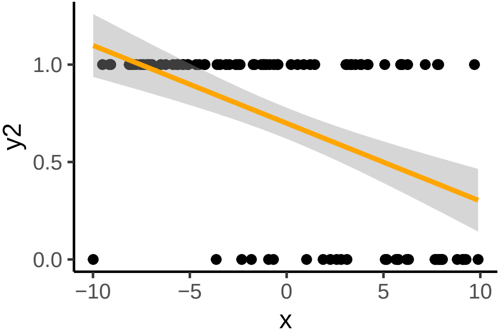
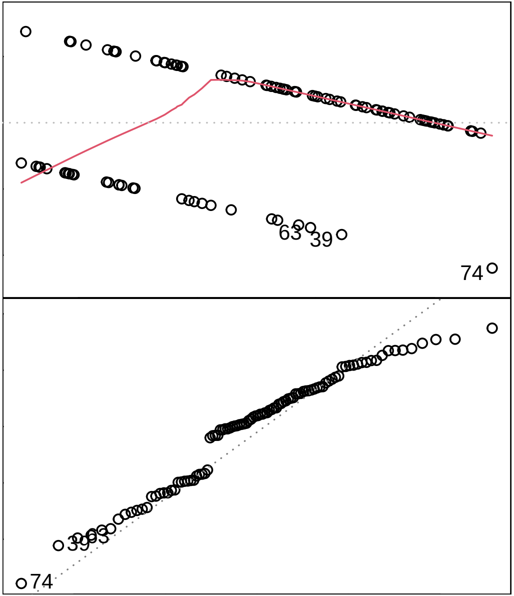
  - Beta-Binomial
  - Negative Binomial
- “Play time”

Christmas gifts for the nerds in your life

Problem: not everything is normal





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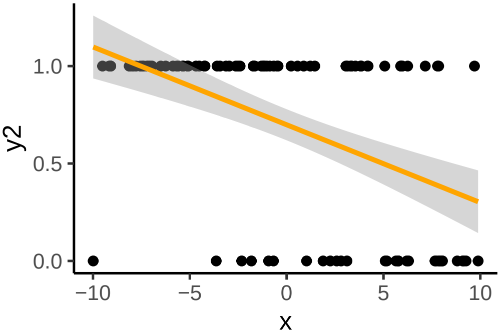
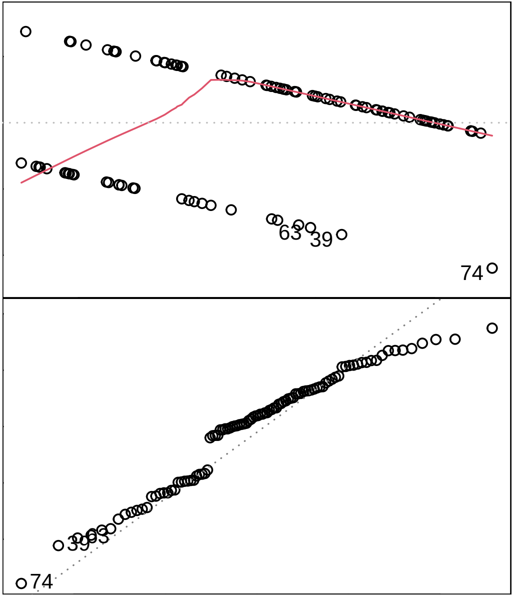
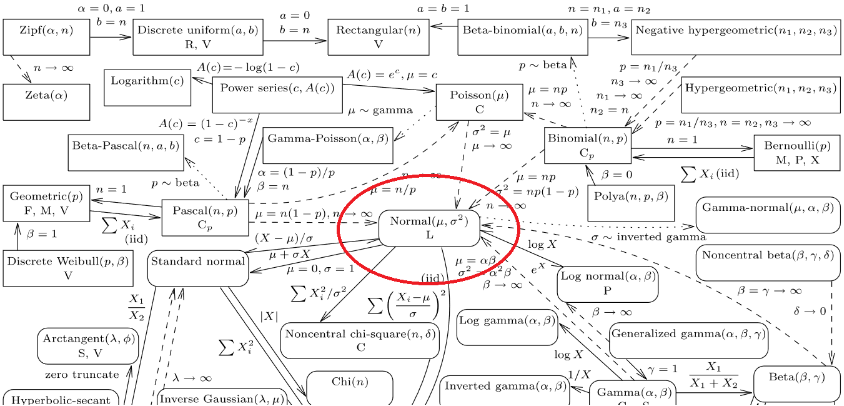




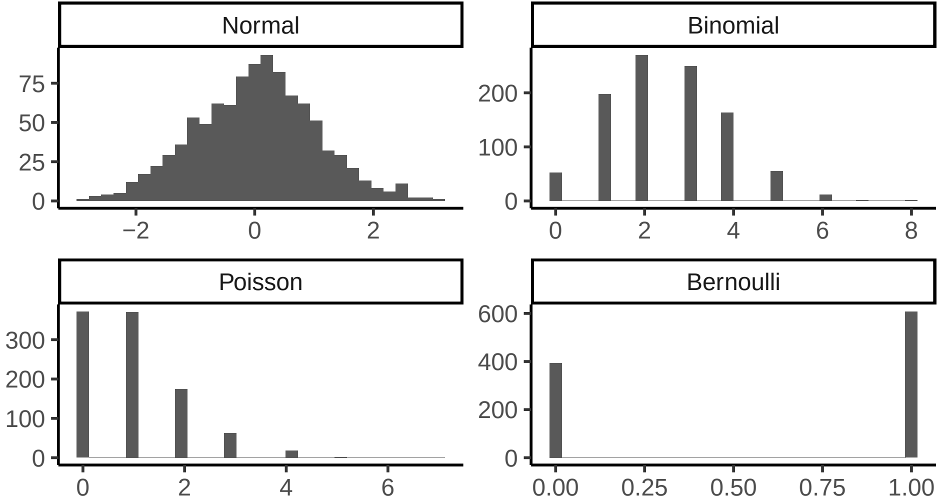
- Some types of data can never be transformed to make the residuals normal
- Solution: **use the distribution that generates the data!**

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

A Galton Board in action:

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?

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

$$= \sim 0.24$$

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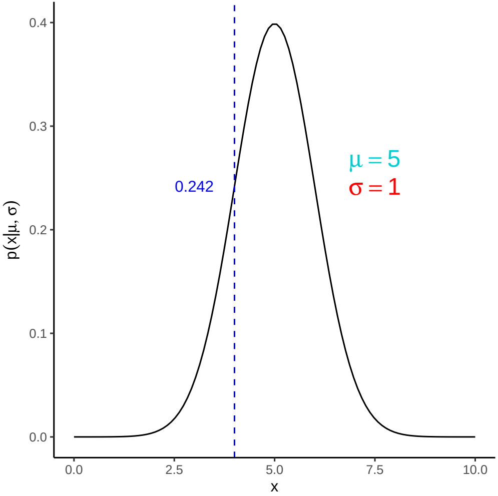
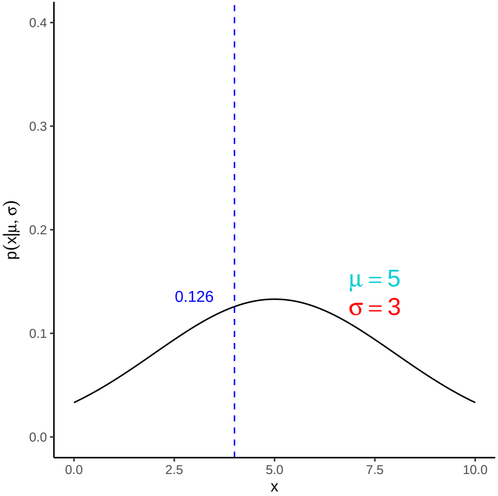
```
#d stands for "density"
dnorm(x=4,mean=5,sd=1)
```

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

The Normal Distribution





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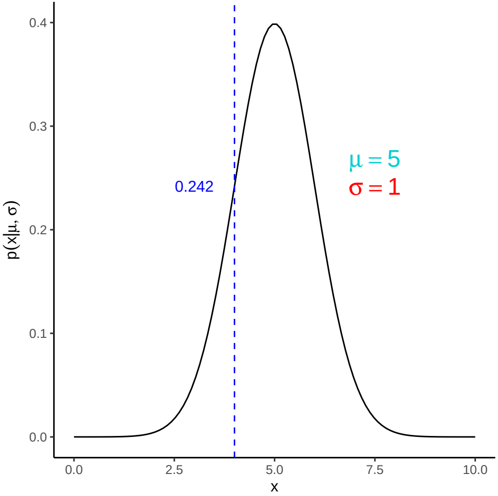

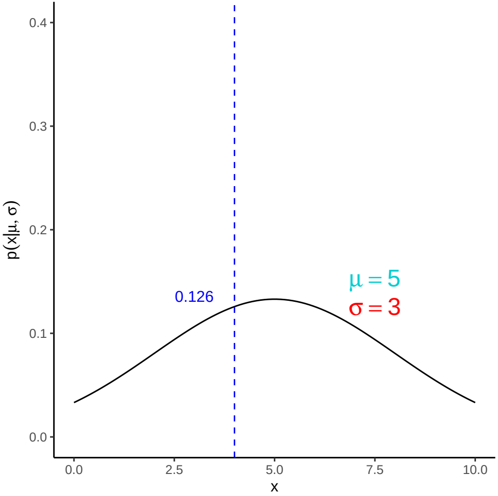

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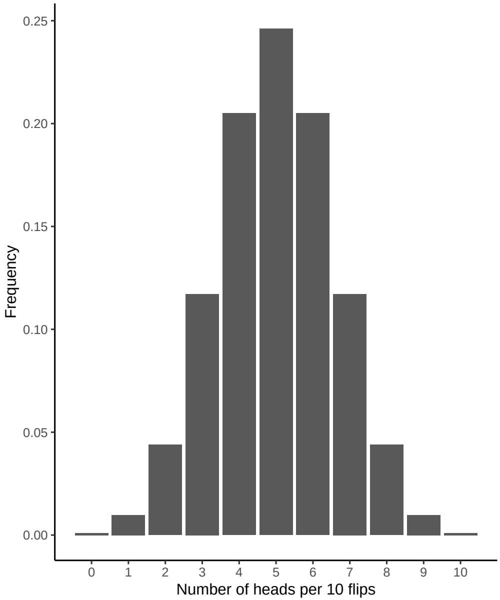
- Left: $\sigma = 1$, Right: $\sigma = 3$

The Binomial Distribution

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



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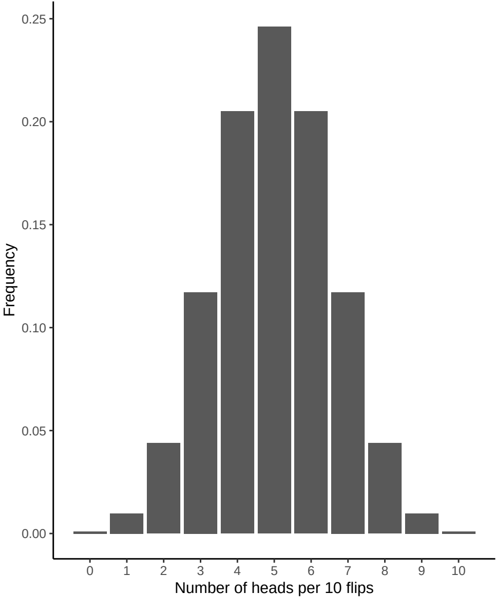

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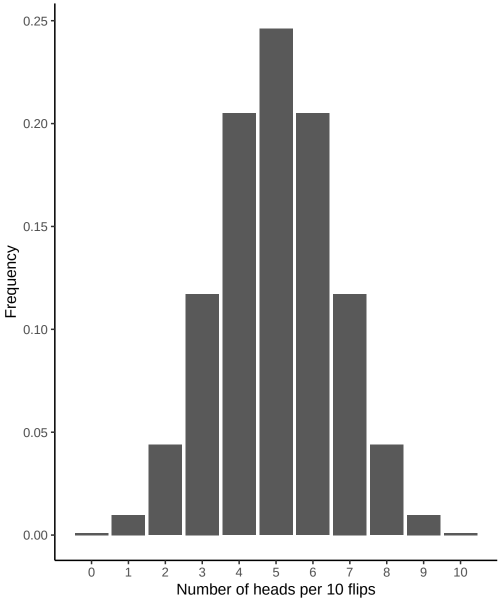

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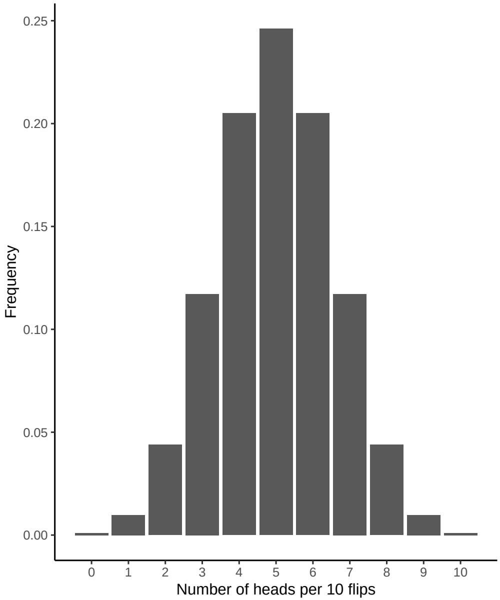

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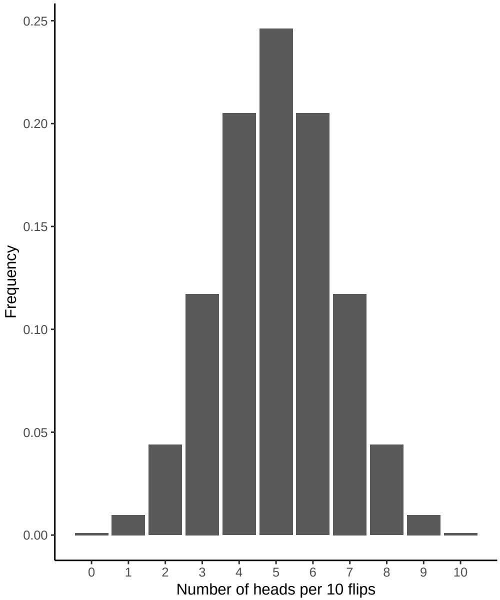

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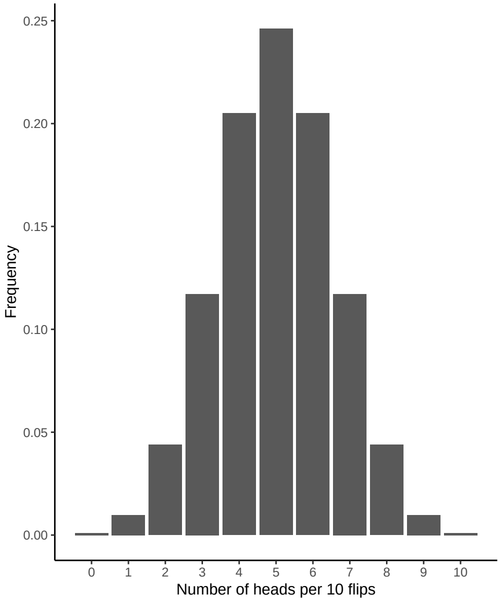

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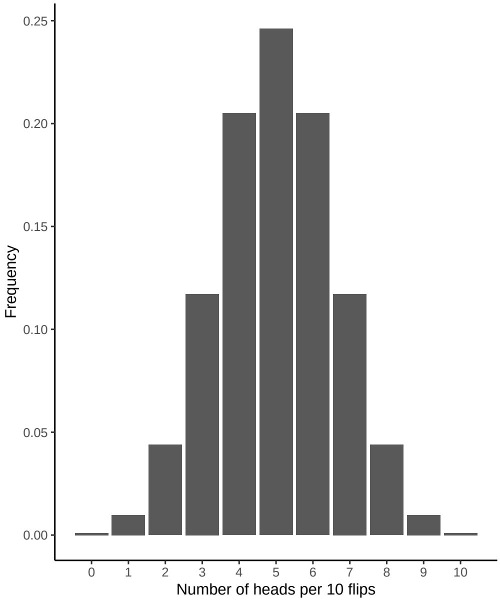
- If N = 1, this is called a *Bernoulli trial*



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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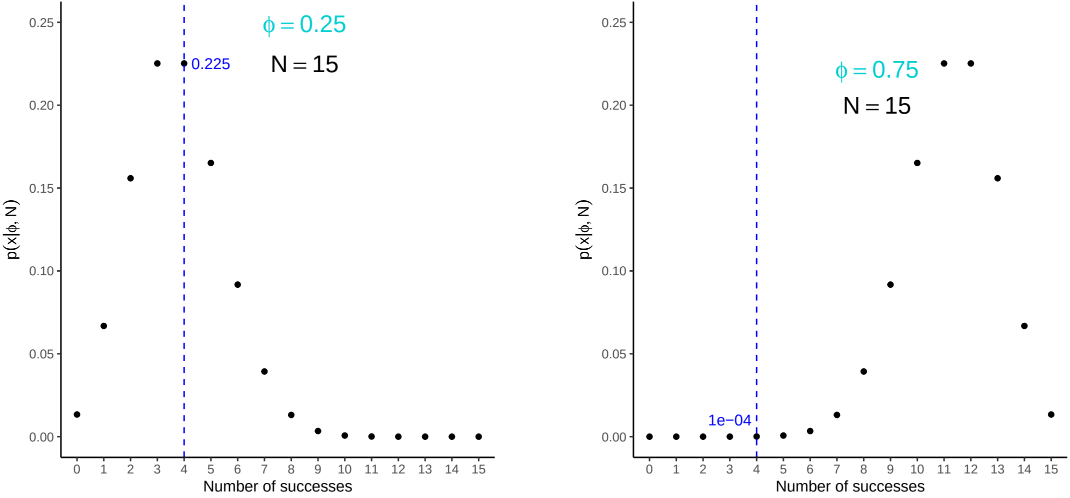

- Probability of x "successes" changes with ϕ and N

The Poisson Distribution

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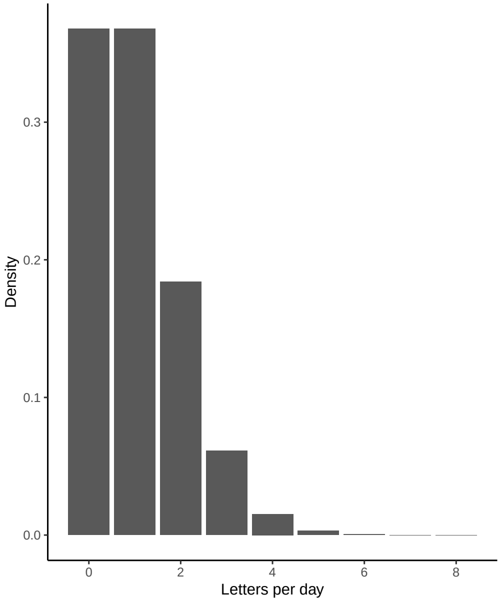

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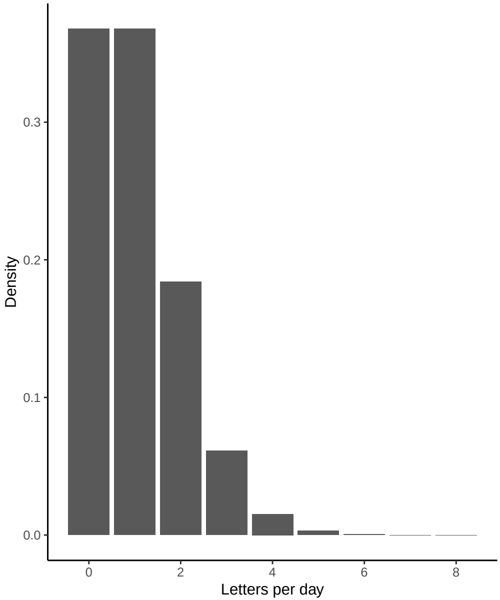

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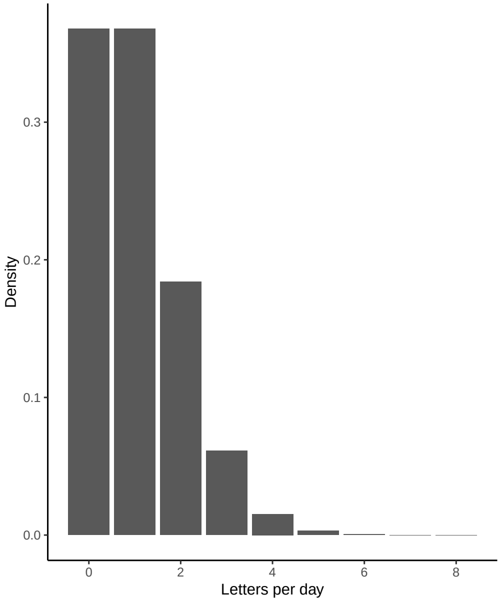

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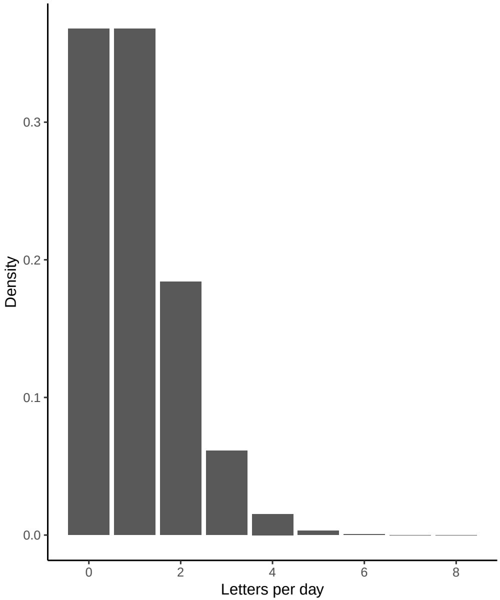

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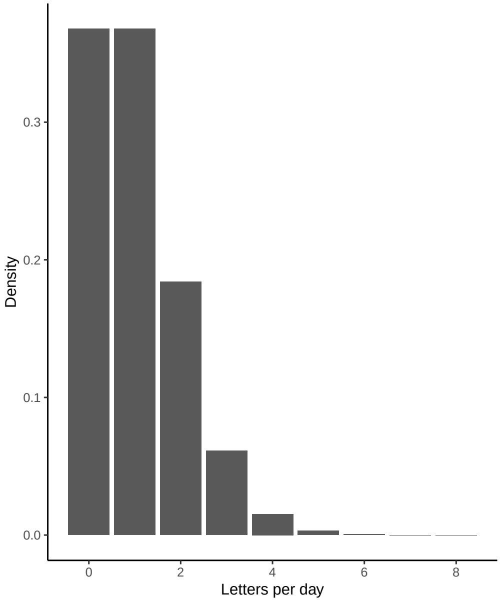

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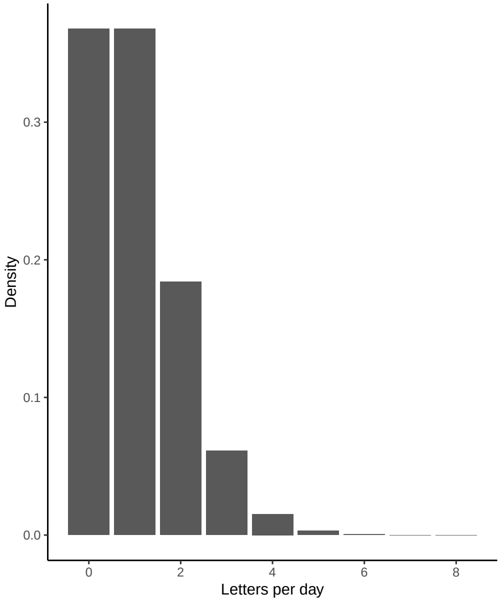

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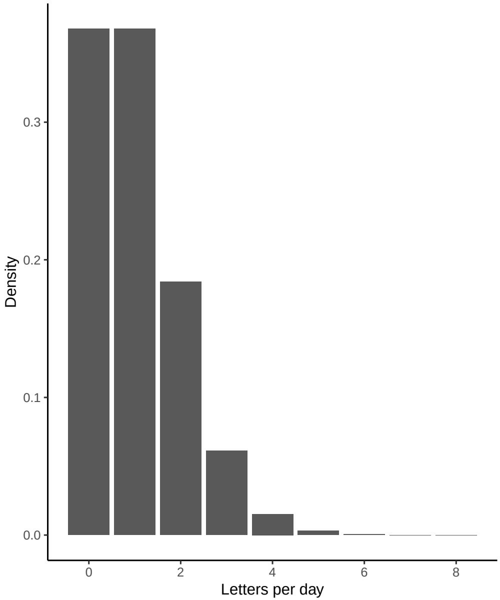
- Equivalent to Binomial distribution, where N is unknown



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

In R, this is easy:

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

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

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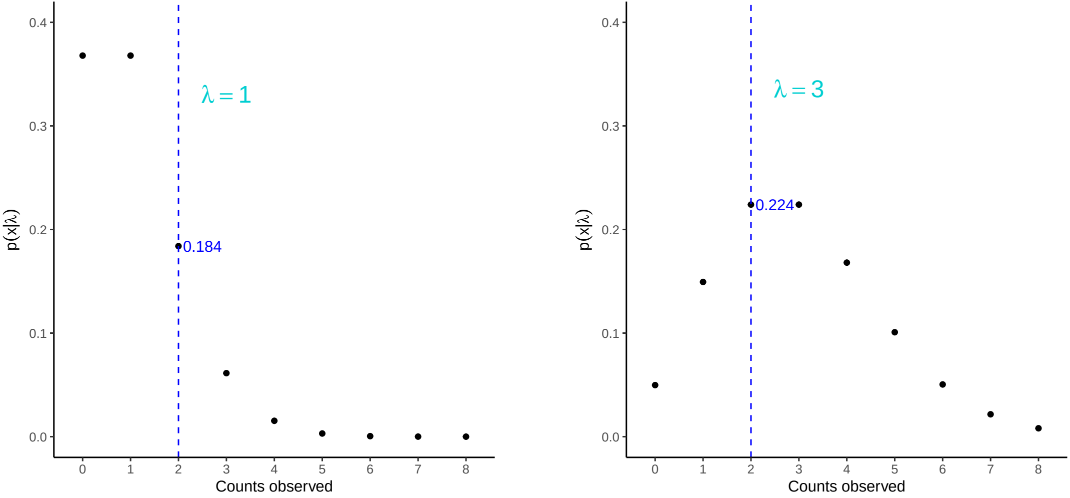

- Probability of x counts changes with λ

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  - *Beta Binomial* and *Negative Binomial* distributions

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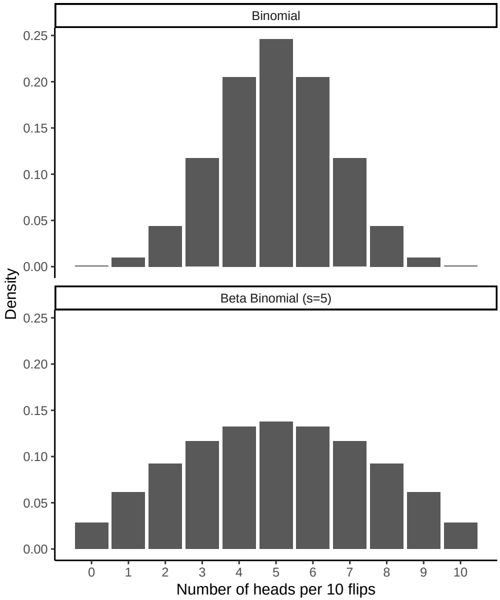
```r
#Extra distributions
library(rmutil)
dbetabinom(x,m=phi,size=N,s=5)
```



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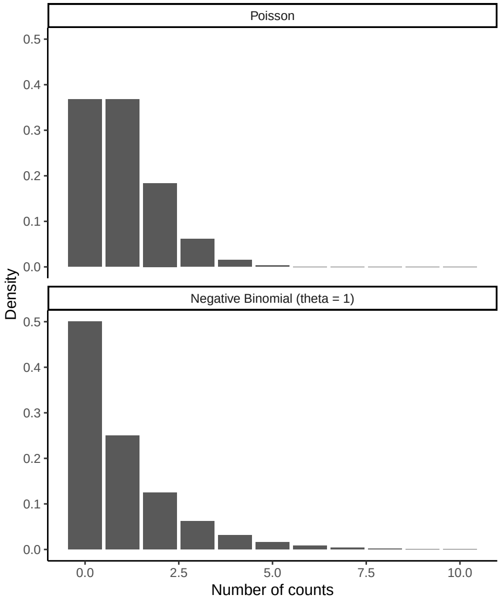
```
#size = theta parameter
dnbinom(x,mu,size=1)
```



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

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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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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

Outline

- Maximum likelihood
    - A way to think about data

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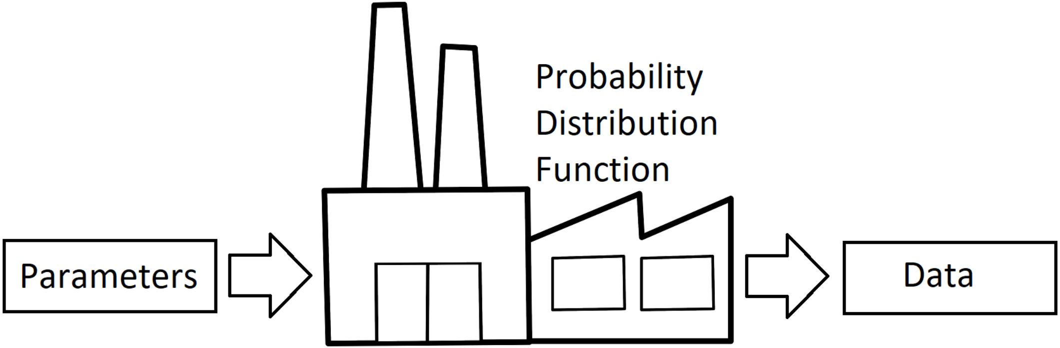
    - Predictors -> Linear model

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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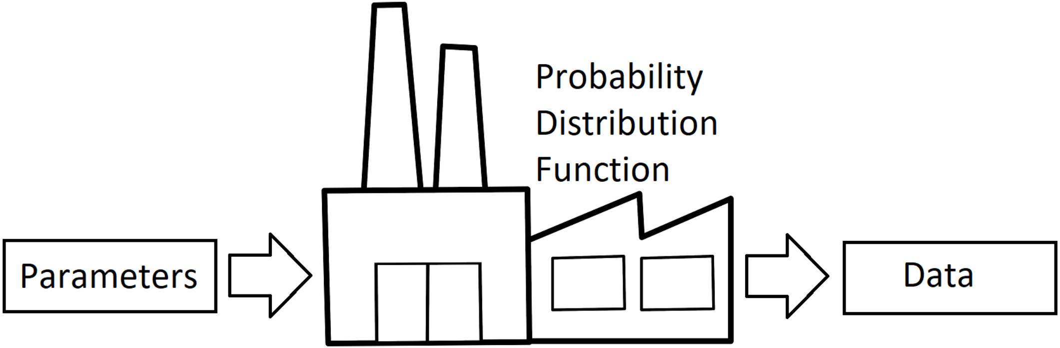
- Process: **probability function**



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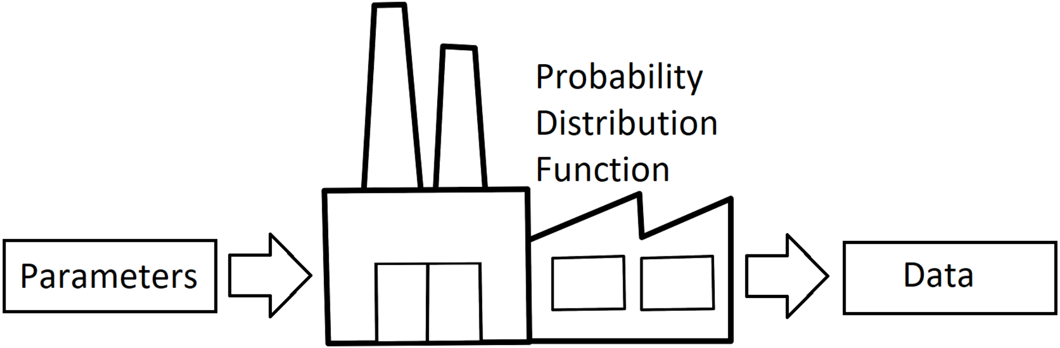
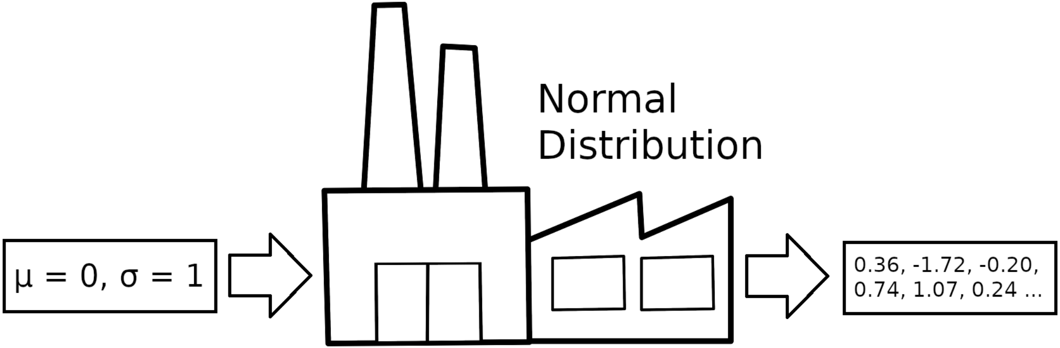
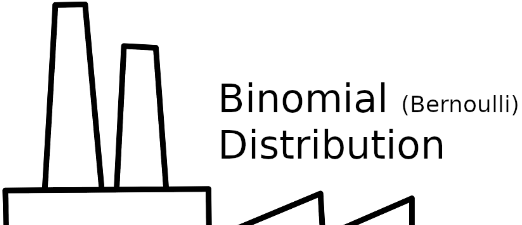
Making data can be thought of as a *factory*

- Input: **parameters** (things that guide the process)
- Process: **probability function**
- Output: **data** (things made by the process)



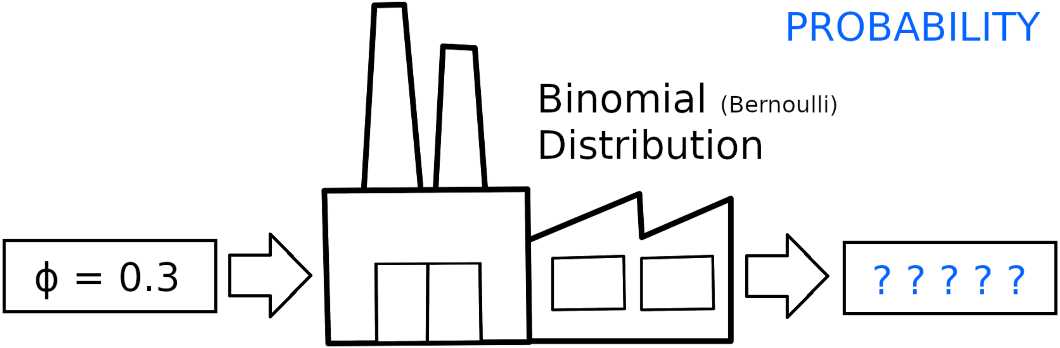
Examples


μ = 0, σ = 1
Normal
Distribution
0.36, -1.72, -0.20,
0.74, 1.07, 0.24 ...

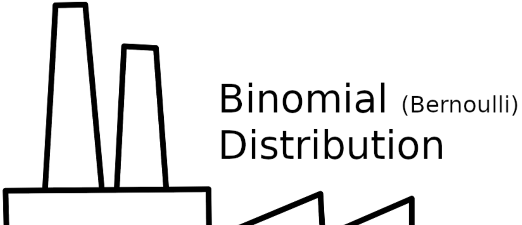

Binomial (Bernoulli)
Distribution

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?"

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

```
## [1] 0.063
```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- "I got 2 heads and a tail. What is the likelihood that $\phi = 0.3$?"

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

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

Likelihood vs Probability (cont.)

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

```
#phi = 0.3
dbinom(1,1,0.3)*dbinom(1,1,0.3)*dbinom(0,1,0.3)
```

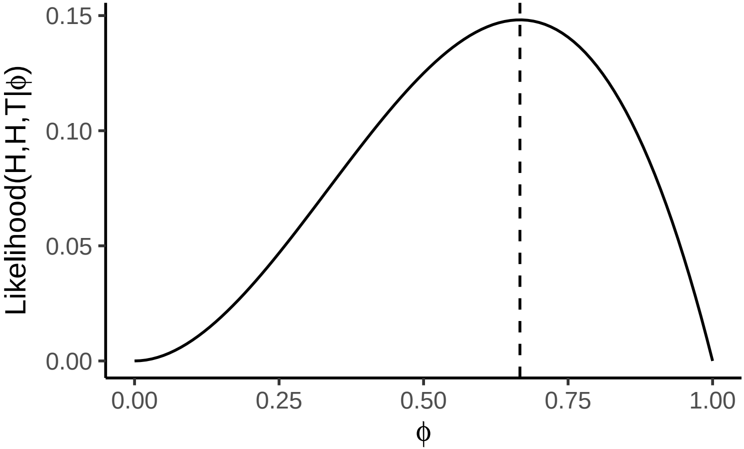
```
## [1] 0.063
```

```
#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

```r
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
## Residual deviance: 3.8191  on 2  degrees of freedom
## AIC: 5.8191
##
## Number of Fisher Scoring iterations: 4
```

Wait... our estimate should be 0.666 (2/3), not 0.693!

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- Some parameters of PDFs have *limits*

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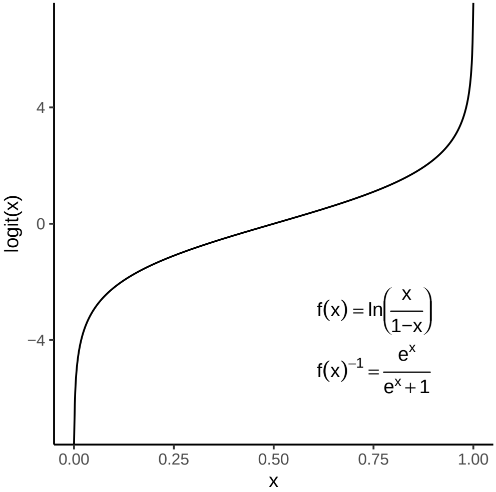
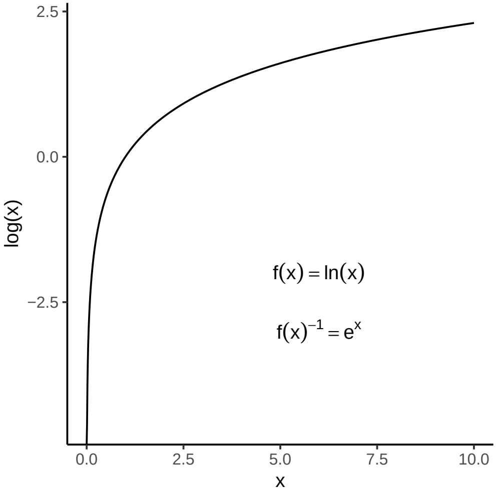
- GLMs use *link functions* to map values onto the appropriate parameter range
  - Normal: Identity (i.e. $\times 1$)
  - Binomial: Logit
  - Poisson/NB: Log
- $\mathit{logit}(0.693) = 0.666$, so the GLM actually got it right!

What do these functions look like?

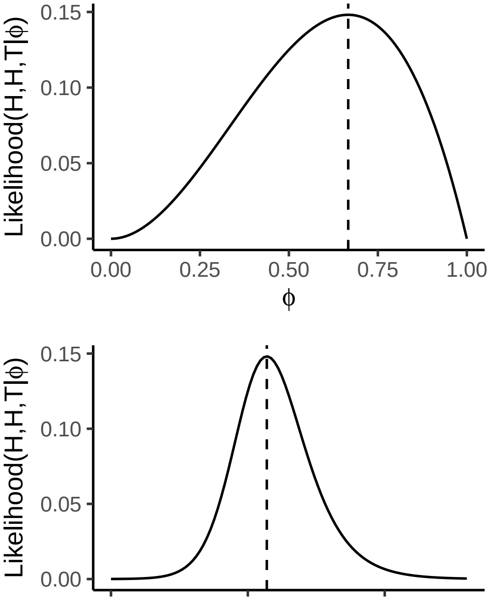




- These functions map parameter values from the appropriate range (0-1 or 0-∞) onto $-\infty$ to $+\infty$

Why do we bother with these link function?

- Likelihood functions are not symmetrical on the regular scale



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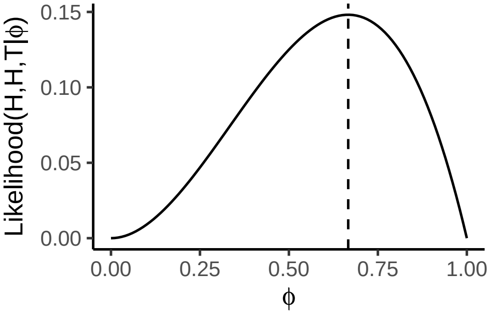
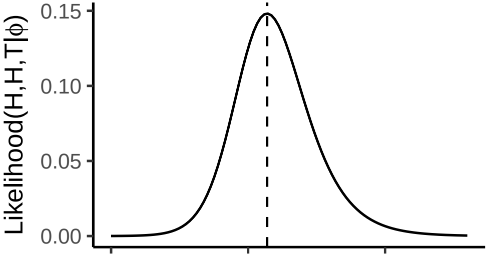
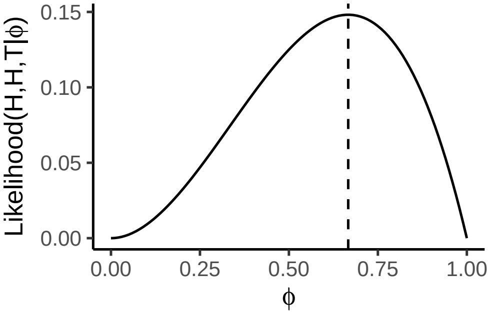
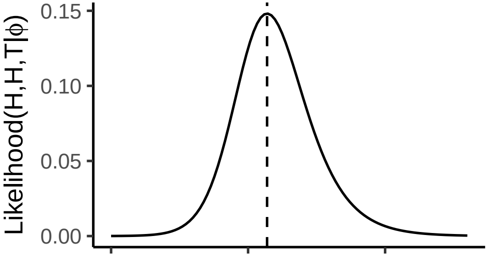




Why do we bother with these link function?

- 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.

$$logit(\hat{\phi}) = b_0 + b_1 x_1 ... + b_i x_i$$
$$flips \sim Binomial(\hat{\phi})$$

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

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1. Expected value (ϕ) fed through a link function
2. Data is fit to a non-normal probability function

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

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`

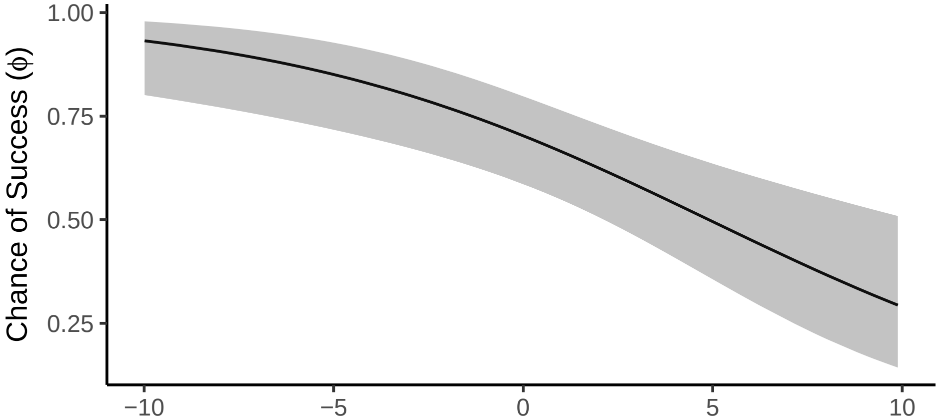
```
# y ~ x, where x is the predictor of y (~1 for just intercept)
mod_binomial <- glm(y2 ~ x1 + x2 , data = d1, family = 'binomial') #Fit a binomial GLM
summary(mod_binomial)
```

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

How do I get partial effects plots?

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

```
ggpredict(mod_binomial, terms='x1 [all]') %>% #Partial effect of x1 term
  ggplot(aes(x, predicted)) + geom_line() +
  geom_ribbon(aes(ymin = conf.low, ymax = conf.high), alpha = 0.3) +
  labs(x = 'x1', y = expression(paste('Chance of Success (',phi,')')))
```



A challenger approaches!

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

Model results