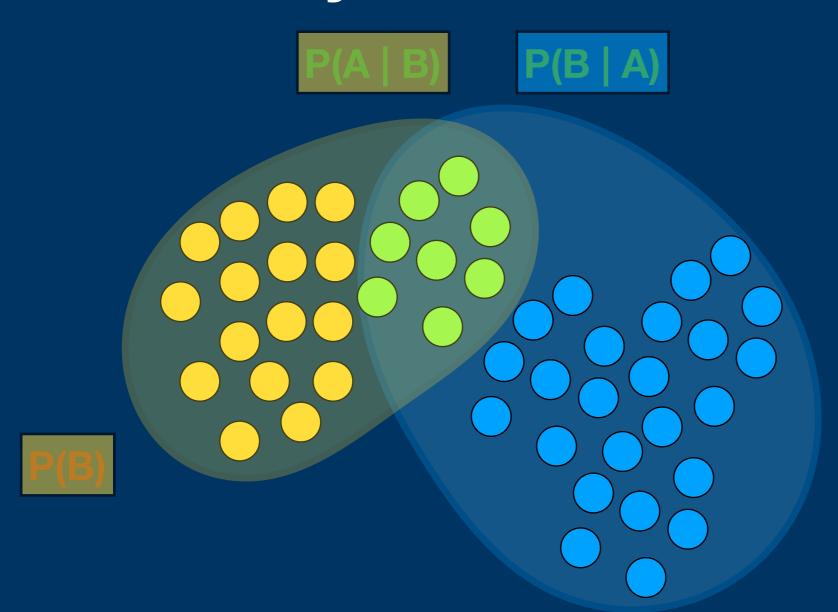


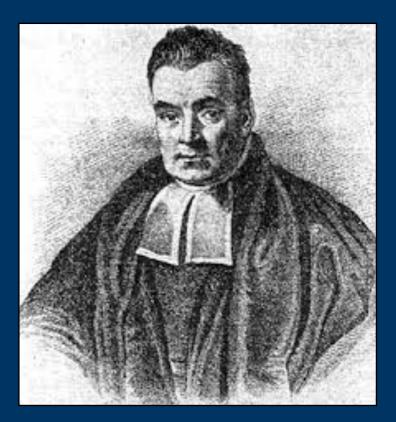




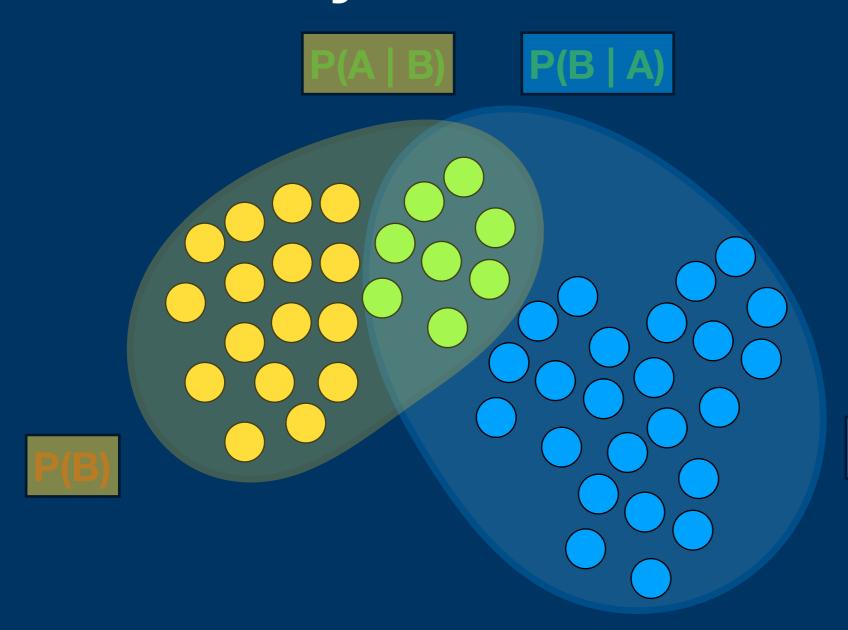
Bayesian statistics in ecology

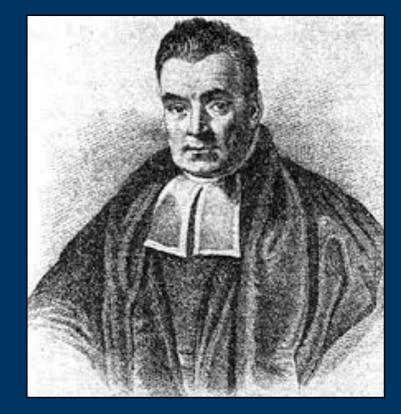
Part 1 – Prerequisites Bayes theorem





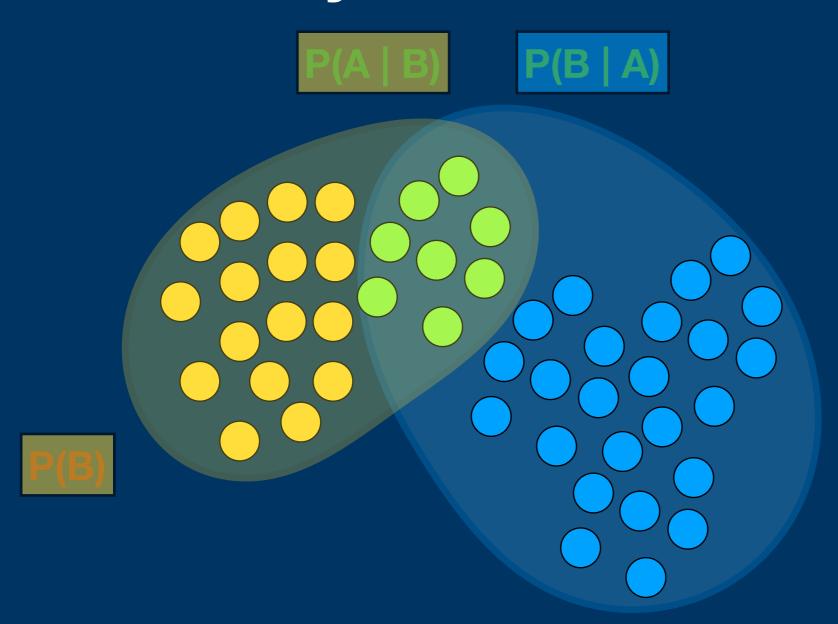
T. Bayes, 1761

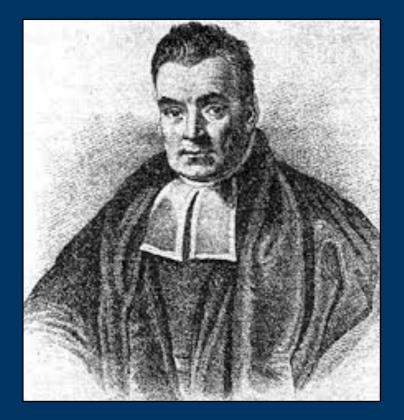




T. Bayes, 1761

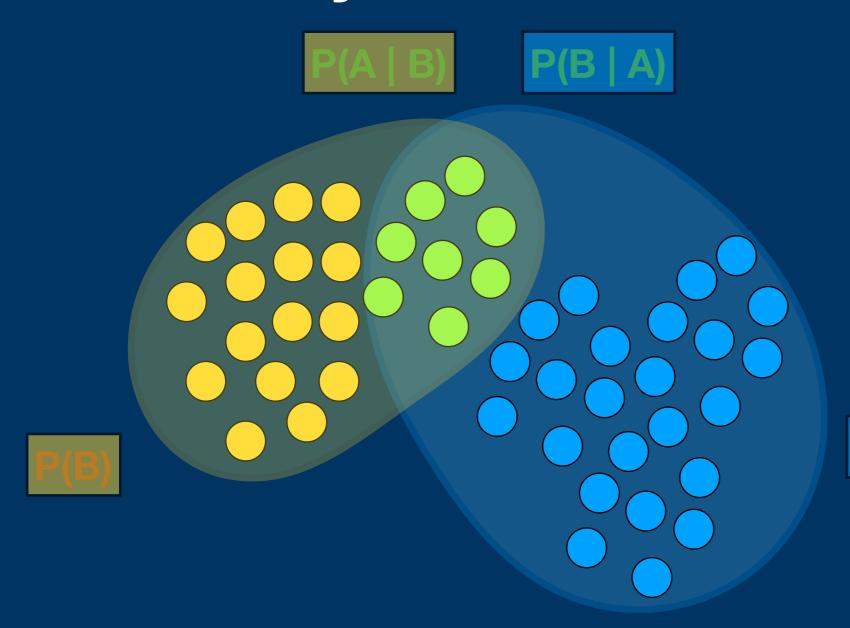
$$P(A \cap B) = P(B \mid A) \cdot P(A)$$



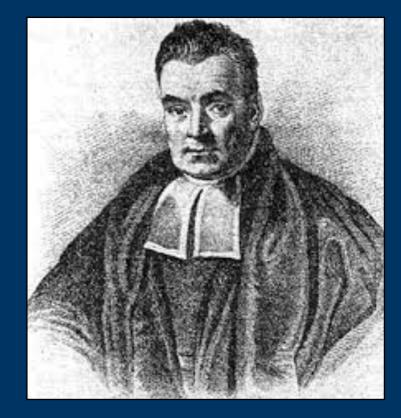


T. Bayes, 1761

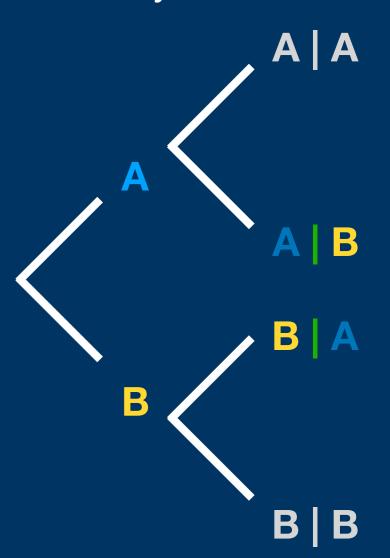
$$P(A \cap B) = P(B \mid A) \cdot P(A)$$
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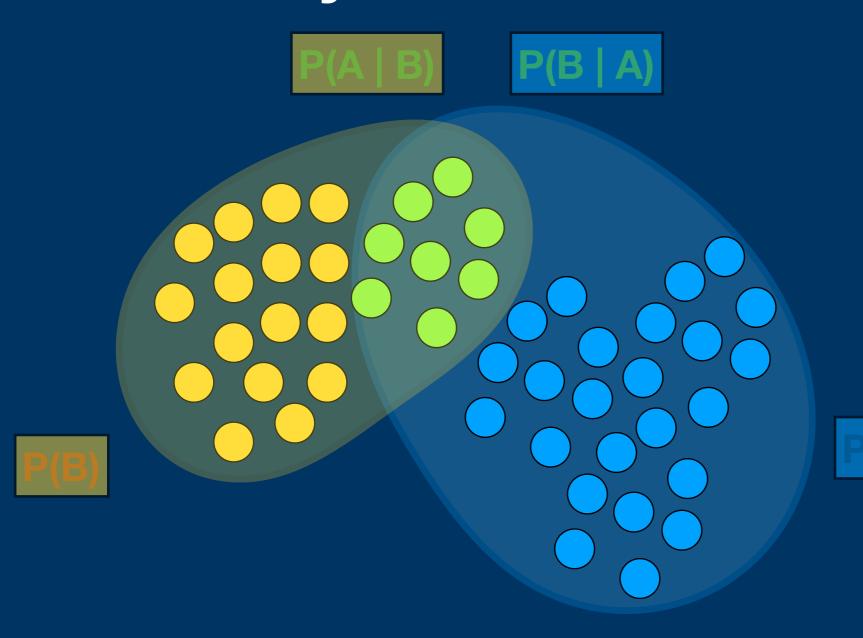


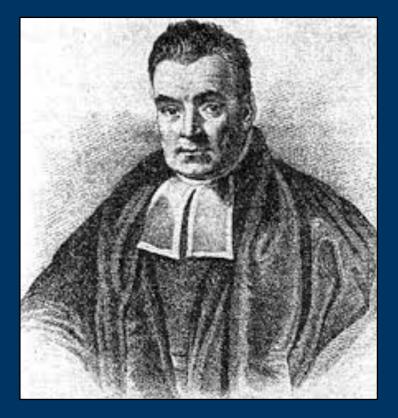
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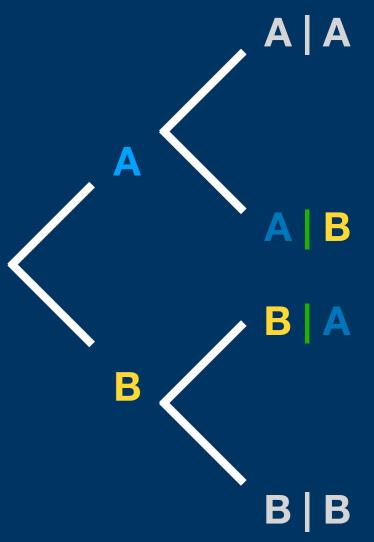
T. Bayes, 1761



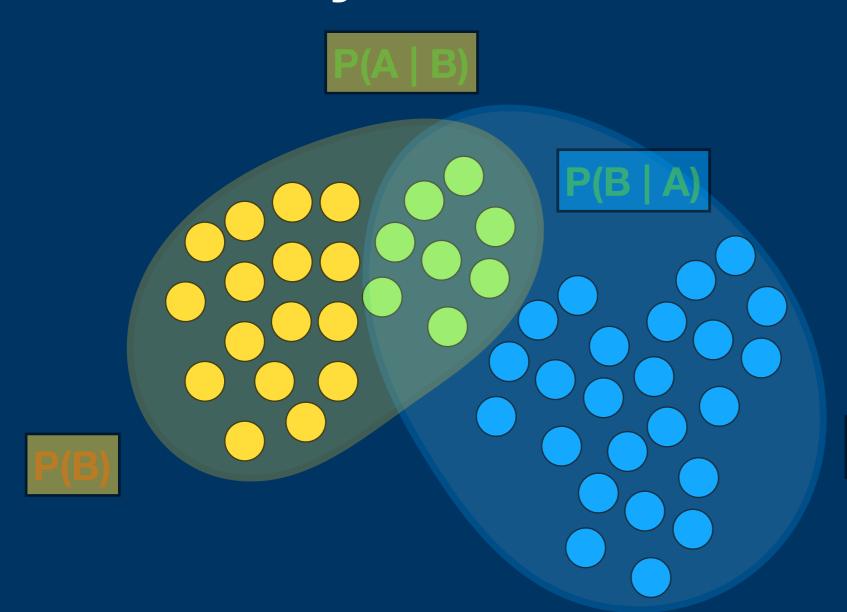




T. Bayes, 1761

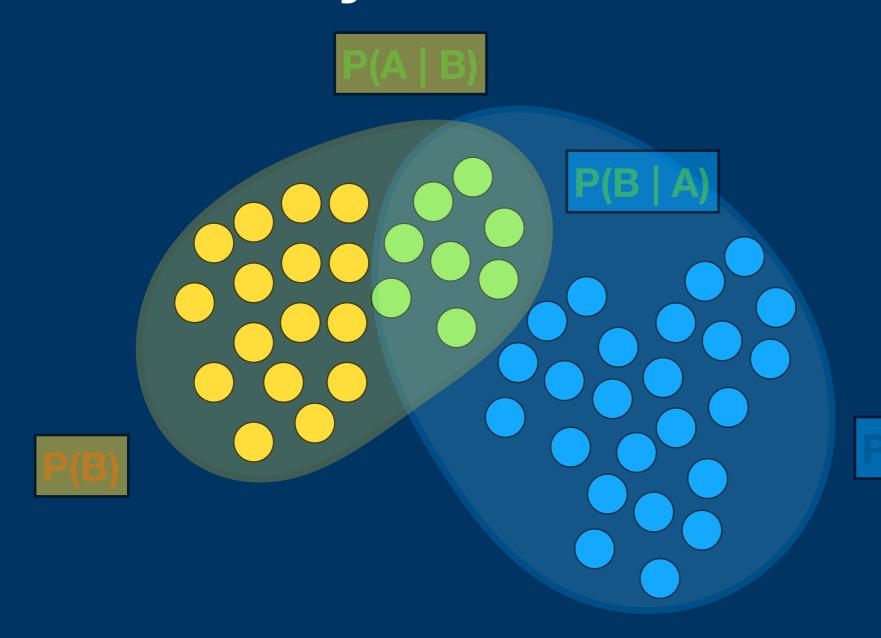


 $P(A) \cdot P(B \mid A) = P(B) \cdot P(A \mid B)$





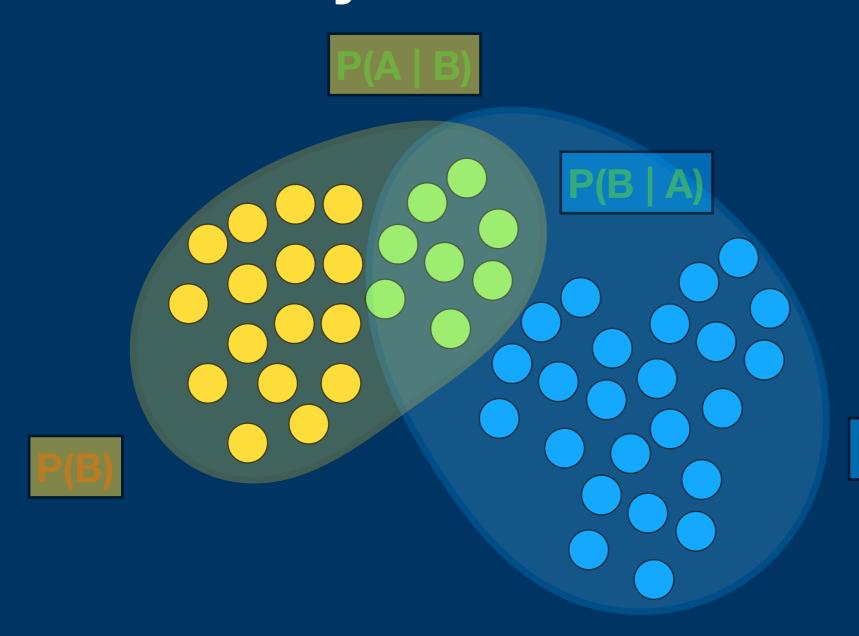
P.-S. Laplace, 1774





P.-S. Laplace, 1774

$$P(A) \cdot P(B \mid A) = P(B) \cdot P(A \mid B)$$





P.-S. Laplace, 1774

$$P(A) \cdot P(B \mid A) = P(B) \cdot P(A \mid B)$$

$$P(B \mid A) = \frac{P(B) \cdot P(A \mid B)}{P(A)}$$

Frequentist vs. Bayesian

Frequentist

Likelihood of the results within H₀

P(x | H₀)

if $P(x \mid H_0) < 0.05$ we reject H_0

R. Fisher, 1930's

Bayesian

Credibility of H₀ within the results

 $P(H_0 \mid x)$

-Too complex

-Too subjective

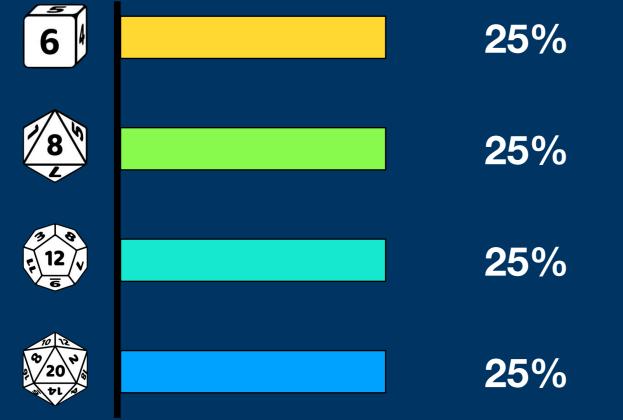
$$P(H_0 \mid x) = \frac{P(H_0) \cdot P(x \mid H_0)}{P(x)}$$



With the frequentist approach

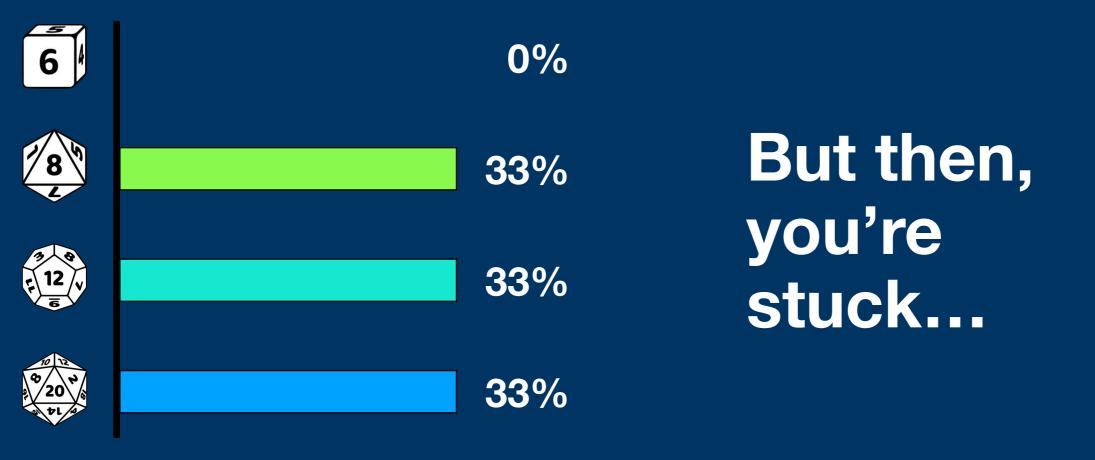


With the frequentist approach





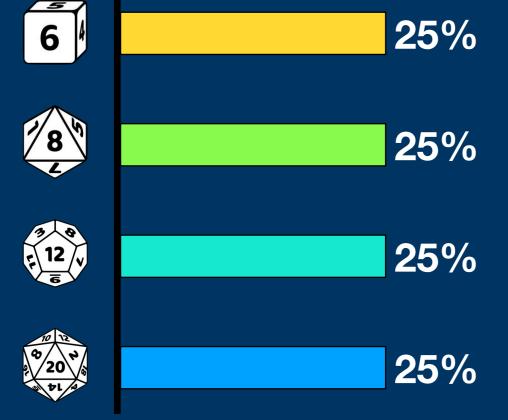
With the frequentist approach





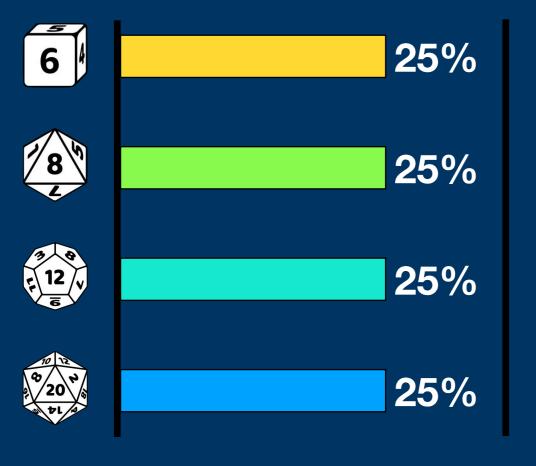






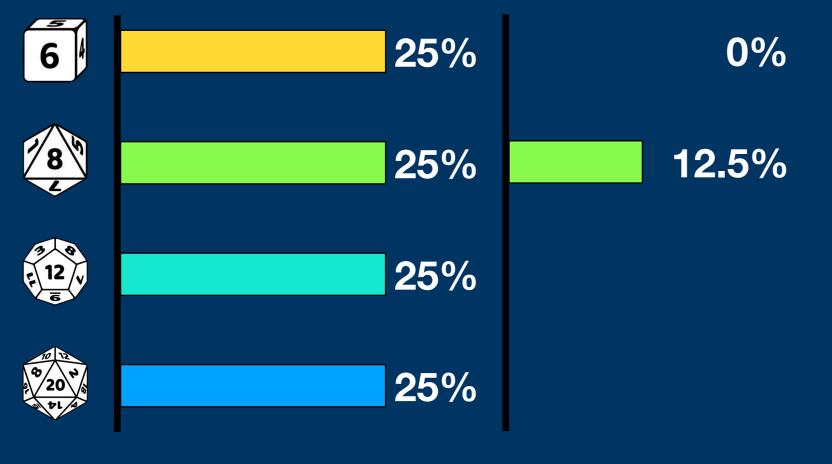


With the bayesian approach

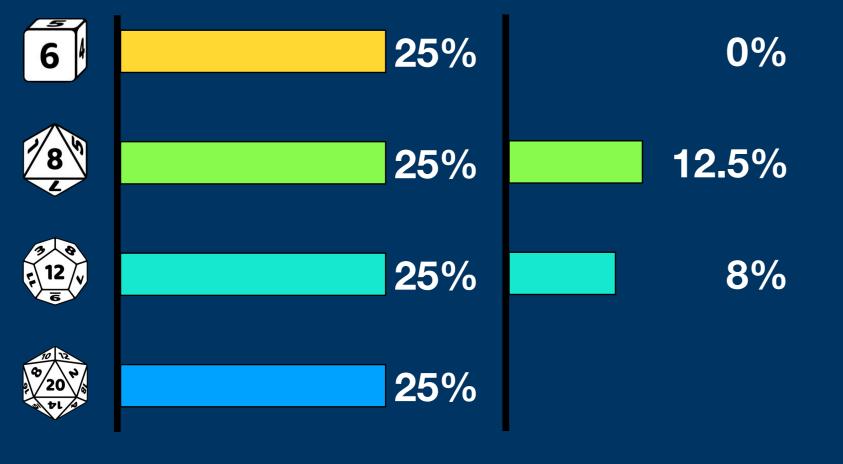


0%

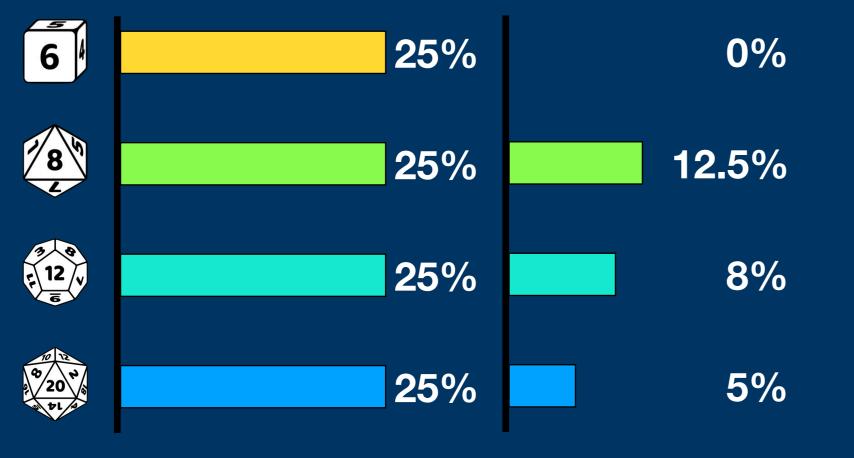




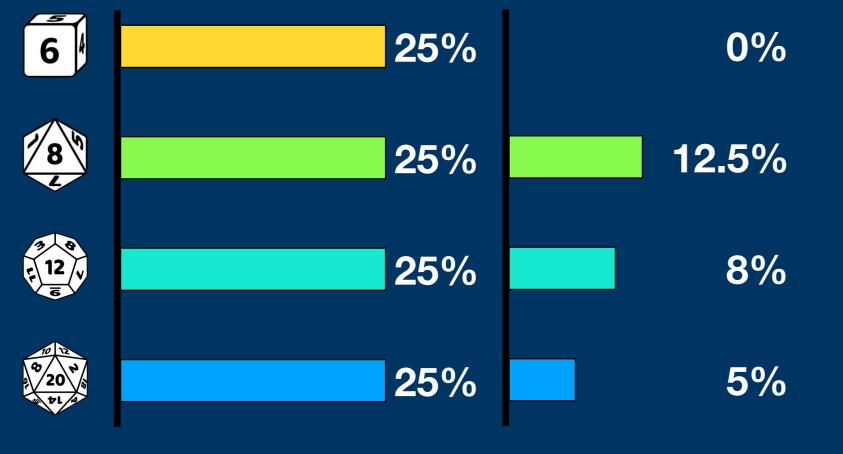




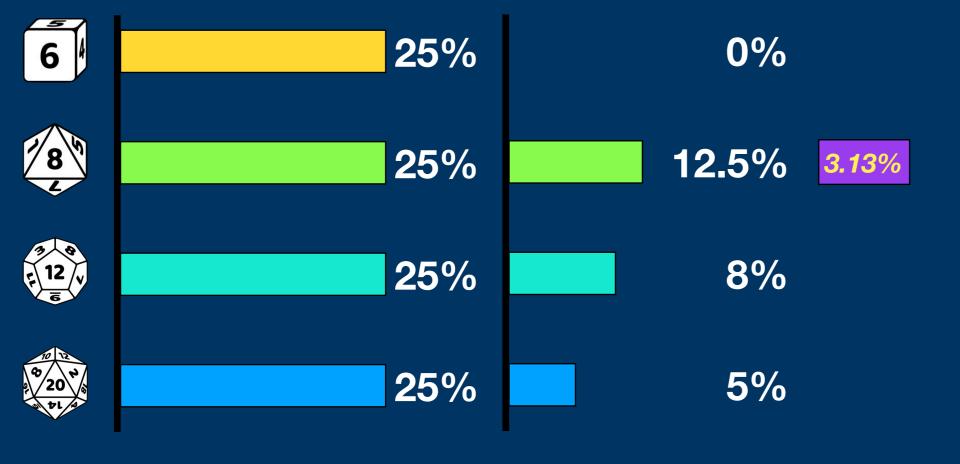




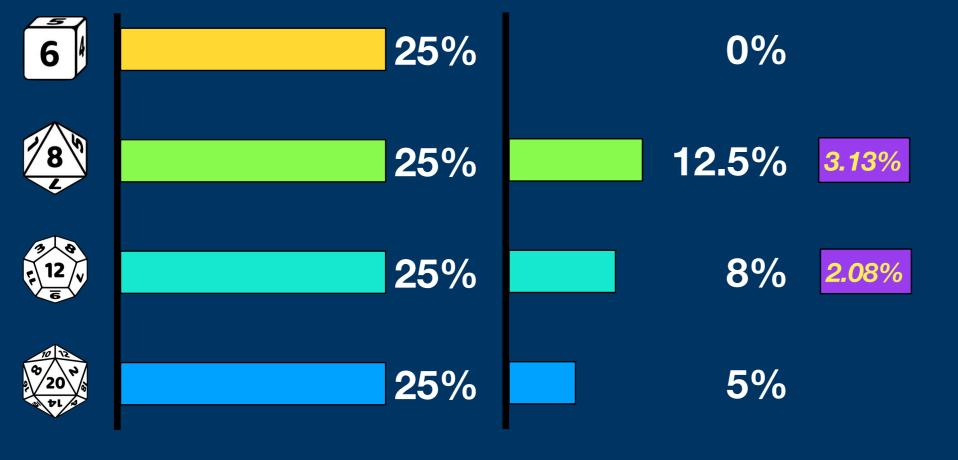
$$P(H_0 \mid x) = \frac{P(H_0) \cdot P(x \mid H_0)}{P(x)}$$



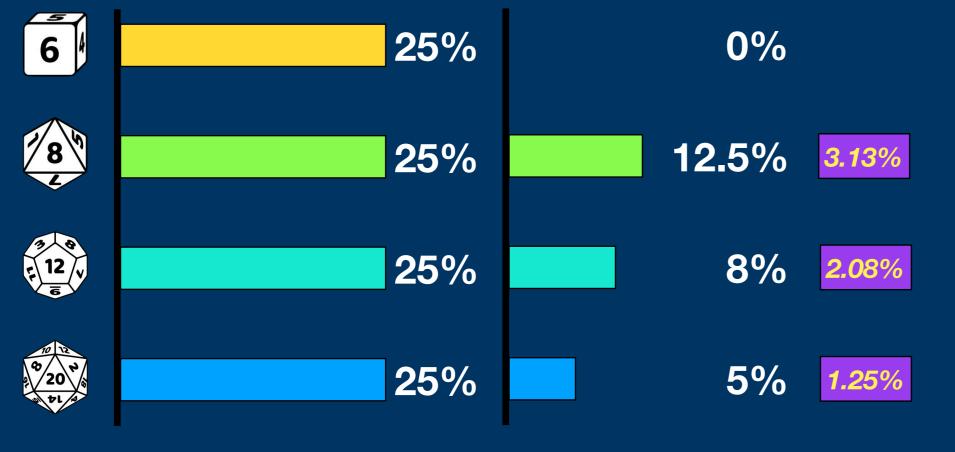
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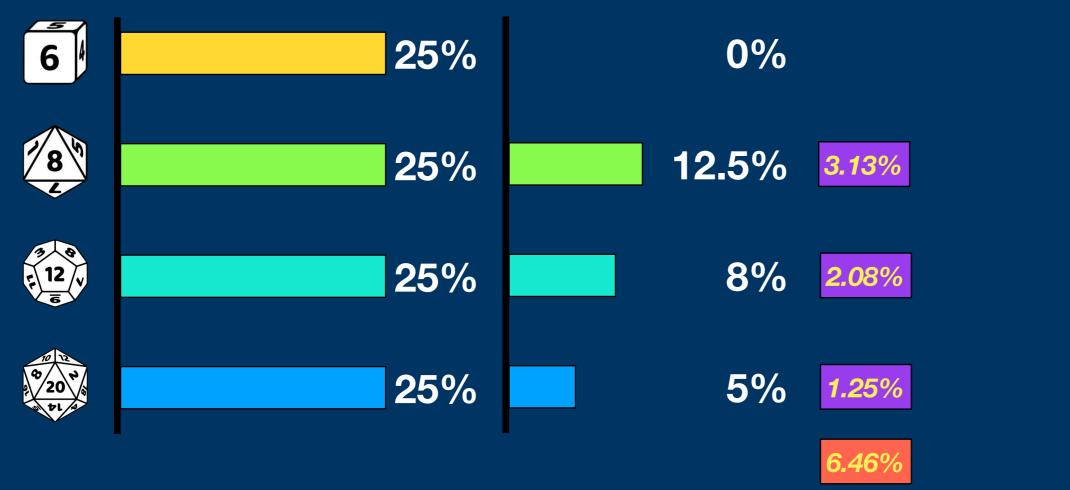
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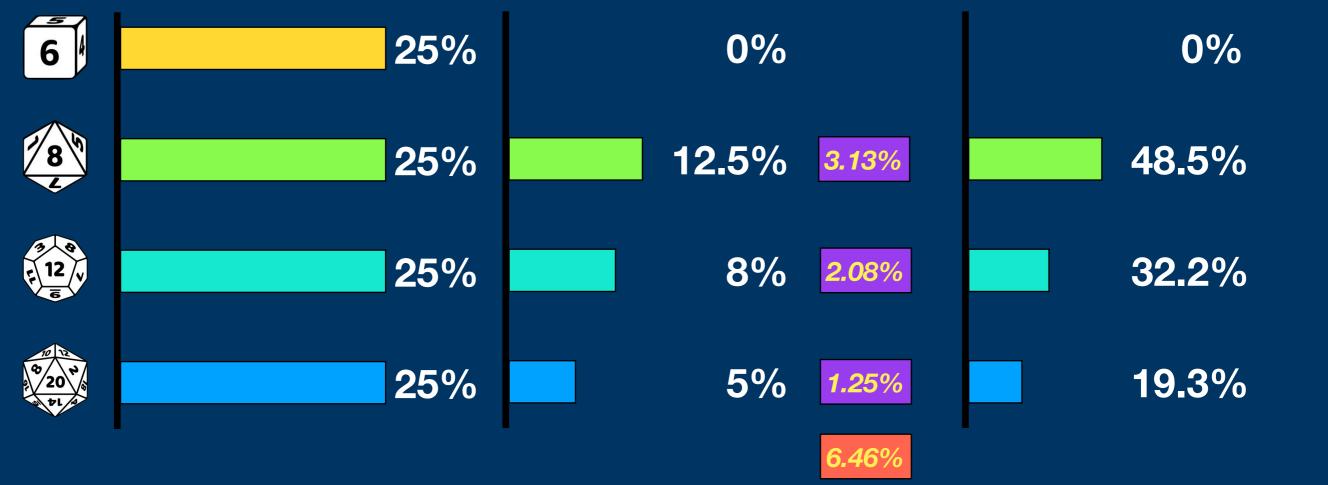
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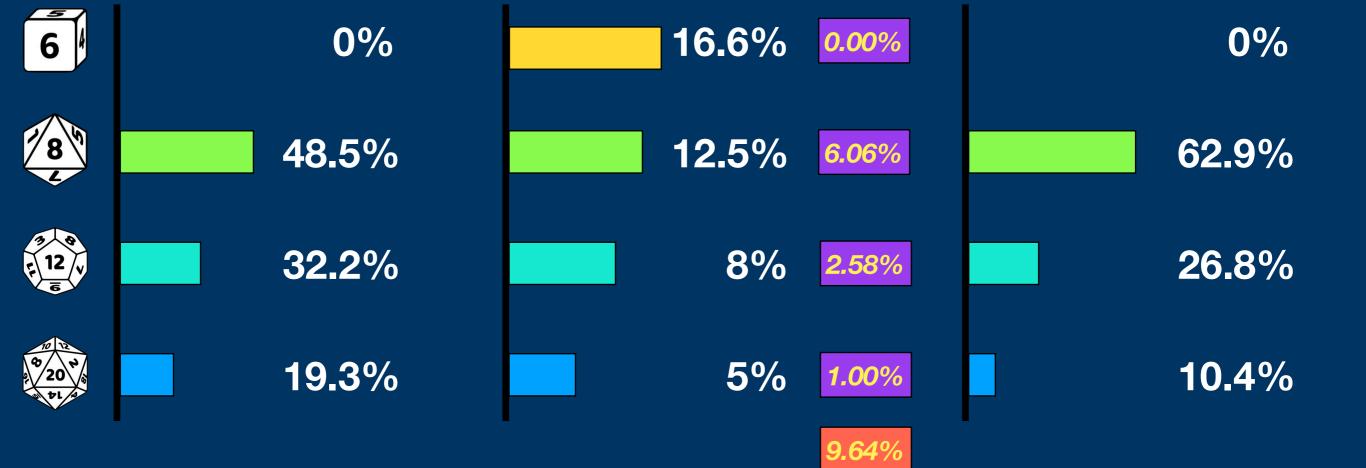








6 8 12 20 then I draw 2

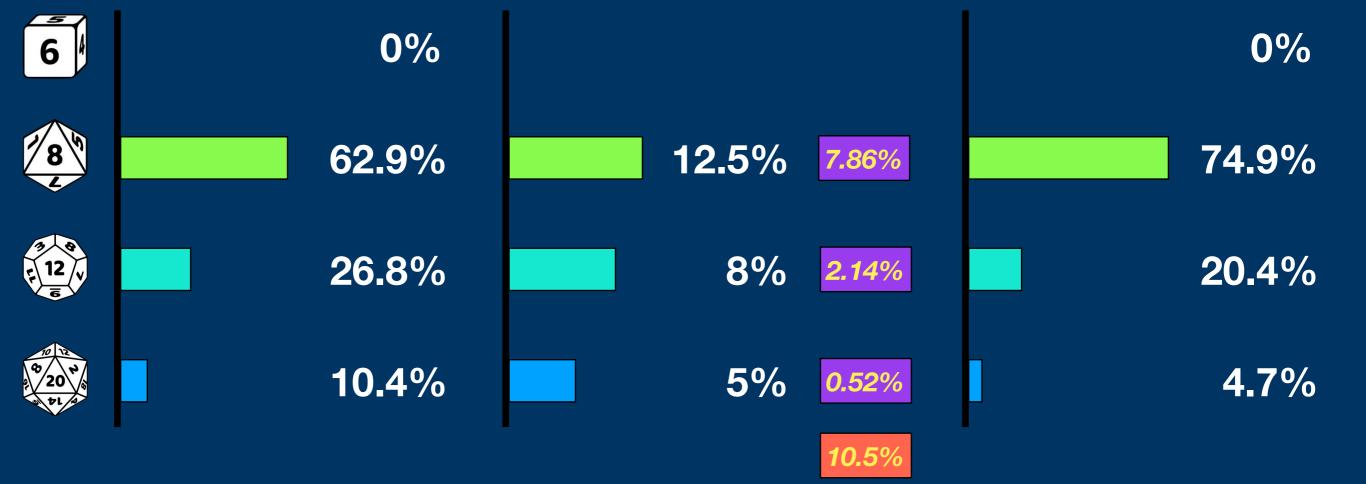








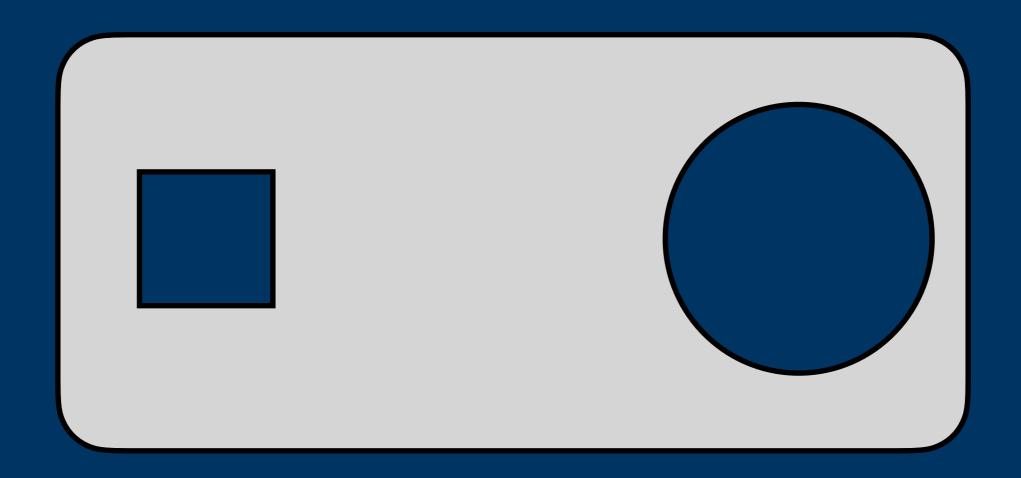




Part 1 – Prerequisites Monte Carlo Markov Chains (MCMC)

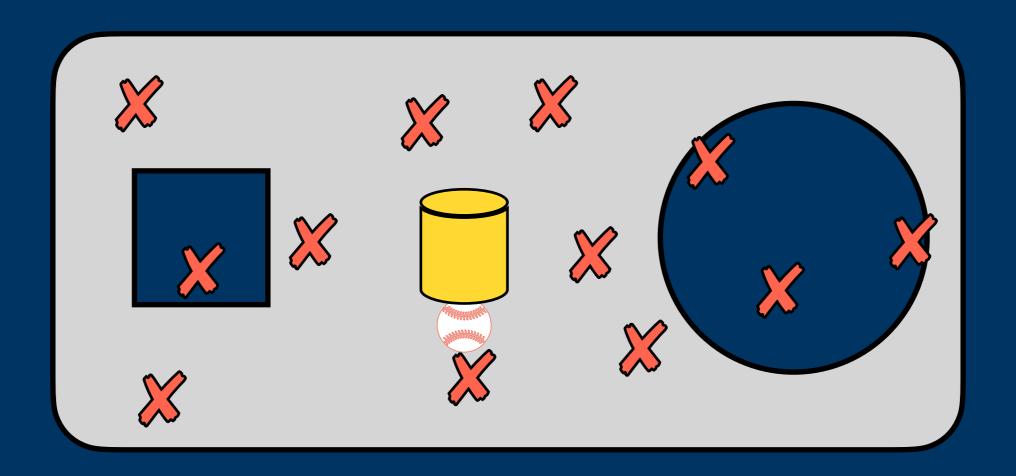
MCMC is synonymous with randomness. It involves simulations that evolve randomly. The term originates from Monaco, known for its casinos and gambling.

Consider the following scenario: A table with two holes — a round one and a square one — where we randomly throw a ball several times.

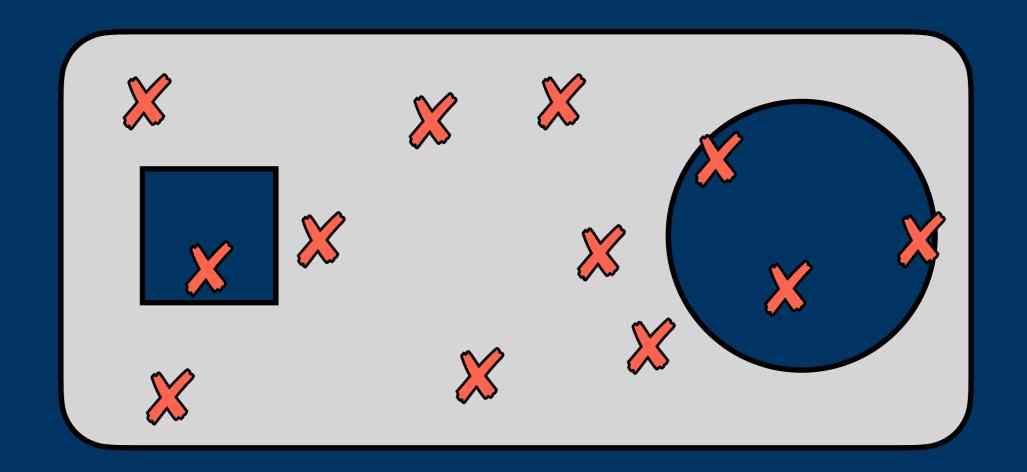


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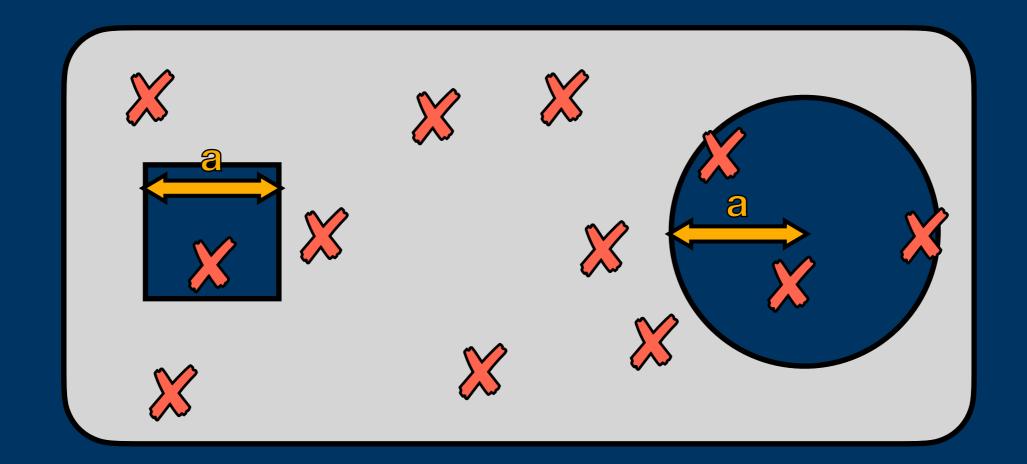


If we calculate the ratio of the number of balls inside each geometric shape, we will find: $\frac{1}{2} = \pi$

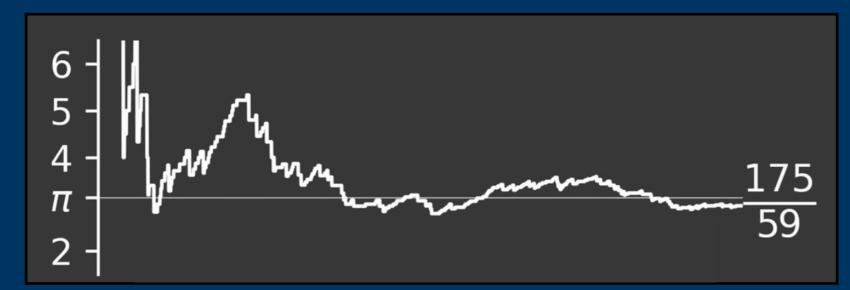


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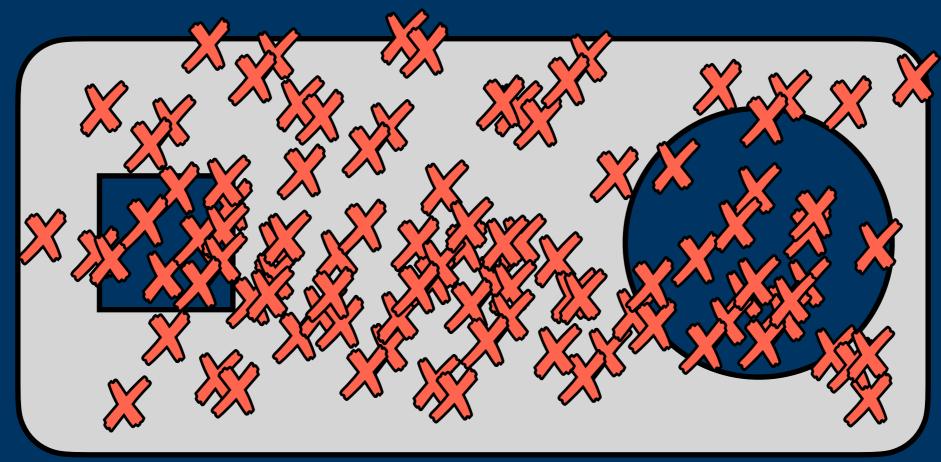
$$= \pi \cdot a^2$$



If we repeat this experiment a huge number of times, we can make a trace plot of our results:



Law of large numbers



Part 2 – Applications in Biology

Case study – impact of alcohol on heart

A data frame with 21 observations on 5 variables:

country:

alcohol: liters alcohol from wine, per capita

deaths: deaths per 100,000

heart: heart disease dths per 100,000 **liver:** liver disease dths per 100,000

country	alcohol	deaths	heart	liver
Australia	2,5	785	211	15,3
Austria	3,9	863	167	45,6
Belg/Lux	2,9	883	131	20,7
Canada	2,4	793	191	16,4
Denmark	2,9	971	220	23,9
Finland	0,8	970	297	19,0
France	9,1	751	71	37,9
Iceland	0,8	743	211	11,2
Ireland	0,7	1000	300	6,5
Israel	0,6	834	183	13,7
Italy	7,9	775	107	42,2
Japan	1,5	680	36	23,2
Netherlands	1,8	773	167	9,2
New Zealand	1,9	916	266	7,7
Norway	0,8	806	227	12,2
Spain	6,5	724	86	36,4
Sweden	1,6	743	207	11,2
Switzerland	5,8	693	115	20,3
UK	1,3	941	285	10,3
US	1,2	926	199	22,1
West Germany	2,7	861	172	36,7

Is there a risk if I drink too much wine?

Case study – impact of alcohol on heart

A data.frame with 21 observations on 5 variables:

country:

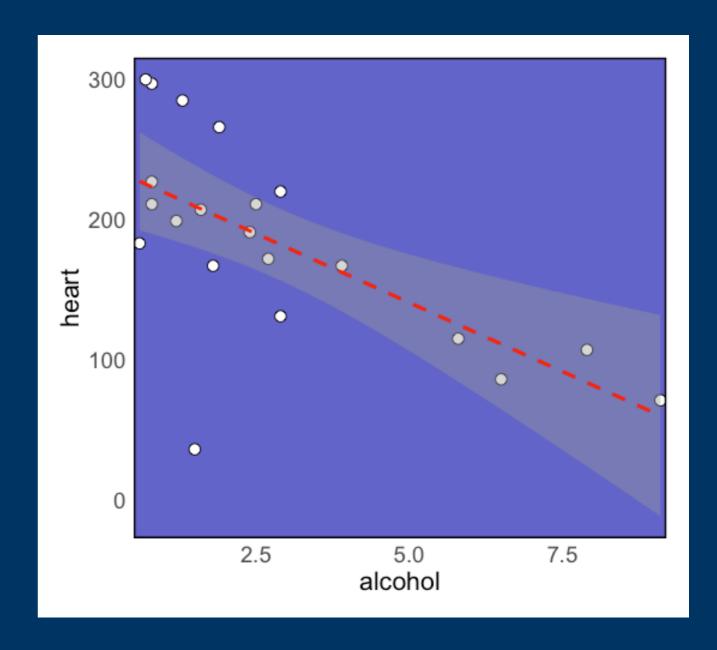
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UK	1,3	941	285	10,3
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Is there a risk if I drink too much wine?



With the frequentist approach

```
> summary(lm(heart ~ alcohol, data = wooldridge::wine))
Call:
lm(formula = heart ~ alcohol, data = wooldridge::wine)
Residuals:
    Min
                   Median
              10
                               30
                                       Max
-173.623 -16.528 -0.655
                           23.346
                                    74.631
Coefficients:
           Estimate Std. Error t value Pr(>|t|)
(Intercept) 239.147
                        19.032 12.565 1.19e-10 ***
alcohol
                        5.121 -3.843
        -19.683
                                        0.0011 **
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Residual standard error: 56.3 on 19 degrees of freedom
Multiple R-squared: 0.4374, Adjusted R-squared: 0.4078
F-statistic: 14.77 on 1 and 19 DF, p-value: 0.001096
```

Easy code (only one line)

With the frequentist approach

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Easy code (only one line)

My estimates with the corresponding errors

With the frequentist approach

```
Easy code (only
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                                                                 one line)
Call:
lm(formula = heart ~ alcohol, data = wooldridge::wine)
Residuals:
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              10
                                      Max
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                                                                 My estimates with the
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                                                                 corresponding errors
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                        5.121 -3.843
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                                                               My R<sup>2</sup>
Multiple R-squared: 0.4374, Adjusted R-squared: 0.4078
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```

With the frequentist approach

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                                                                 one line)
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Residuals:
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                  Median
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            239.147
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                                                                  Even my p-value
```

With the frequentist approach

As stated before, It's easy to compute. We quickly conclude (while omitting to mention the limited sample size of only 21 observations) that French , followed by Italians and Spanish can continue to drink without any risk and we submit our findings for publication in *Nature*.

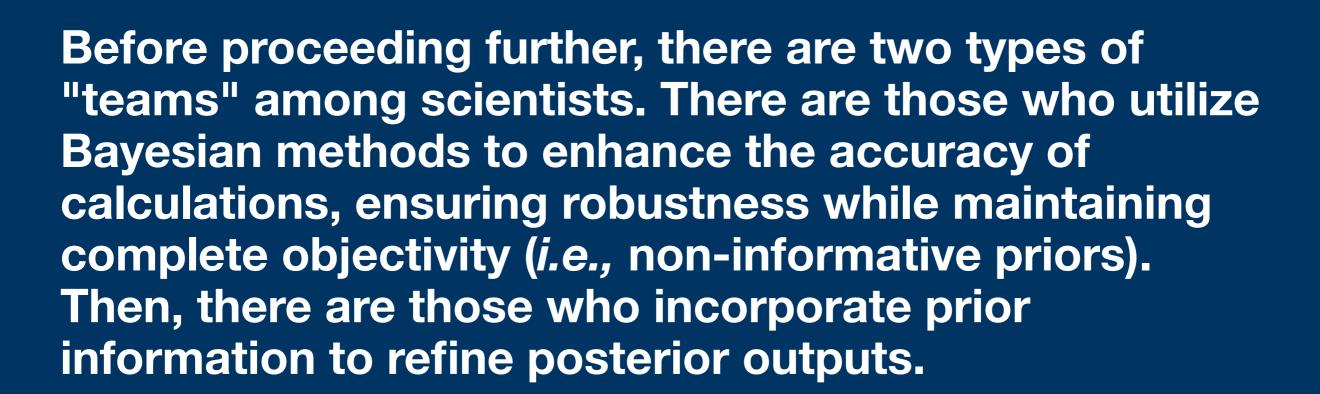
With the bayesian approach

As stated before, It's easy to compute. We quickly conclude (while omitting to mention the limited sample size of only 21 observations) that French , followed by Italians and Spanish can continue to drink without any risk and we submit our findings for publication in *Nature*.

 $b \sim r + (m \mid s)$

But you've been rejected because you did not consider a major previous study...

With the bayesian approach



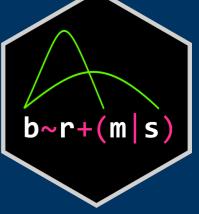
 $b \sim r + (m \mid s)$

In our case, we align with the latter group of scientists. We have been advised by the editor about a study stating that the slope found in a previous study was more likely -15 with a standard error of 5.

With the bayesian approach

```
reg ← brms::brm(formula = heart ~ alcohol, data = wooldridge::wine,
chains = 3, iter = 20000, warmup = 2500, cores = 3,
prior = prior(normal(-15, 5), class = "b", coef = "alcohol"))
```

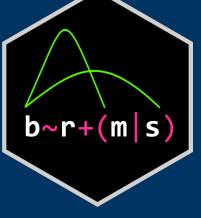
With the bayesian approach



Exact same line of code as previously!

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With the bayesian approach

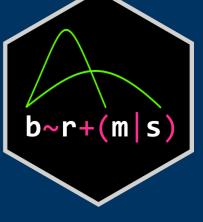


Exact same line of code as previously!

```
The number of MCMC we want (2 to 5
recommended)

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With the bayesian approach



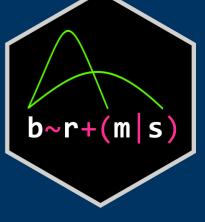
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The number of MCMC we want (2 to 5 recommended)

The number of calculs you want by chain

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With the bayesian approach



Exact same line of code as previously!

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The number of MCMC we want (2 to 5 recommended)

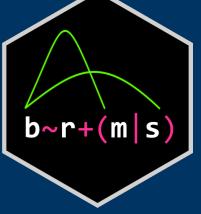
The number of calculs you want by chain

The number of calculation you want by chain

The number of calculation
```

The number of calculs you want to discard at the beginning

With the bayesian approach



Exact same line of code as previously!

The number of MCMC we want (2 to 5 recommended)

The number of calculs you want by chain

```
reg 

brms::brm(formula = heart - alcohol, data = wooldridge::wine, chains = 3, iter = 20000, warmup = 2500, cores = 3, prior = prior(normal(-15, 5) class = "b", coef = "alcohol"))
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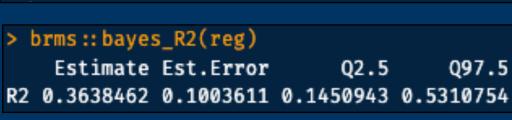
The number of calculs you want to discard at the beginning

The prior formulation for the slope b from the variable "alcohol"

 $b \sim r + (m \mid s)$

With the bayesian approach

```
> reg
 Family: gaussian
 Links: mu = identity; sigma = identity
Formula: heart ~ alcohol
  Data: wooldridge::wine (Number of observations: 21)
 Draws: 3 chains, each with iter = 20000; warmup = 2500; thin = 1;
         total post-warmup draws = 52500
Population-Level Effects:
          Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
                                                      46557
Intercept
           232.92
                      16.04
                              200.74
                                       264.09 1.00
                                                               34962
           -17.29 3.62 -24.25 -10.02 1.00
alcohol
                                                      44605
                                                               36800
Family Specific Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
        57.73
                   9.45
                           42.66
                                    79.39 1.00
                                                           35356
sigma
                                                  41533
Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).
```



With the bayesian approach

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                            42.66
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sigma
                                                   41533
                                                            35356
Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).
```

The total number of draws

```
> brms::bayes_R2(reg)
    Estimate Est.Error Q2.5 Q97.5
R2 0.3638462 0.1003611 0.1450943 0.5310754
```

With the bayesian approach

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 Links: mu = identity; sigma = identity
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                               200.74
                                        264.09 1.00
alcohol
            -17.29
                               -24.25
                       3.62
                                        -10.02 1.00
                                                       44605
                                                                36800
Family Specific Parameters:
      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk ESS Tail ESS
         57.73
                    9.45
                            42.66
                                     79.39 1.00
sigma
                                                   41533
                                                            35356
Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).
```

The total number of draws
CI stands for credible interval and not confident interval

```
> brms::bayes_R2(reg)
    Estimate Est.Error Q2.5 Q97.5
R2 0.3638462 0.1003611 0.1450943 0.5310754
```

With the bayesian approach

```
> reg
 Family: gaussian
  Links: mu = identity; sigma = identity
Formula: heart ~ alcohol
   Data: wooldridge::wine (Number of observations: 21)
  Draws: 3 chains, each with iter = 20000; warmup = 2500; thin = 1;
         total post-warmup draws = 52500
Population-Level Effects:
          Estimate Est.Error 1-95% CI u-95% CI Rhat
                                                                34962
                                                       46557
Intercept
            232.92
                       16.04
                               200.74
                                        264.09 1.00
alcohol
            -17.29
                               -24.25
                        3.62
                                        -10.02 1.00
                                                       44605
                                                                 36800
Family Specific Parameters:
      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk ESS Tail ESS
                                     79.39 1.00
         57.73
                    9.45
                            42.66
sigma
                                                   41533
                                                            35356
Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
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The total number of draws
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 $b \sim r + (m \mid s)$

R_{hat} means it has converged

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With the bayesian approach

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Population-Level Effects:
          Estimate Est.Error 1-95% CI u-95% CI Rhat
                                                                 34962
                                        264.09 1.00
                                                       46557
Intercept
            232.92
                       16.04
                               200.74
alcohol
            -17.29
                               -24.25
                        3.62
                                        -10.02 1.00
                                                       44605
                                                                 36800
Family Specific Parameters:
      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk ESS Tail ESS
         57.73
                    9.45
                            42.66
                                     79.39 1.00
sigma
                                                   41533
                                                             35356
Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1)
```

```
The total number of draws
CI stands for credible interval and not confident interval
```

 $b \sim r + (m \mid s)$

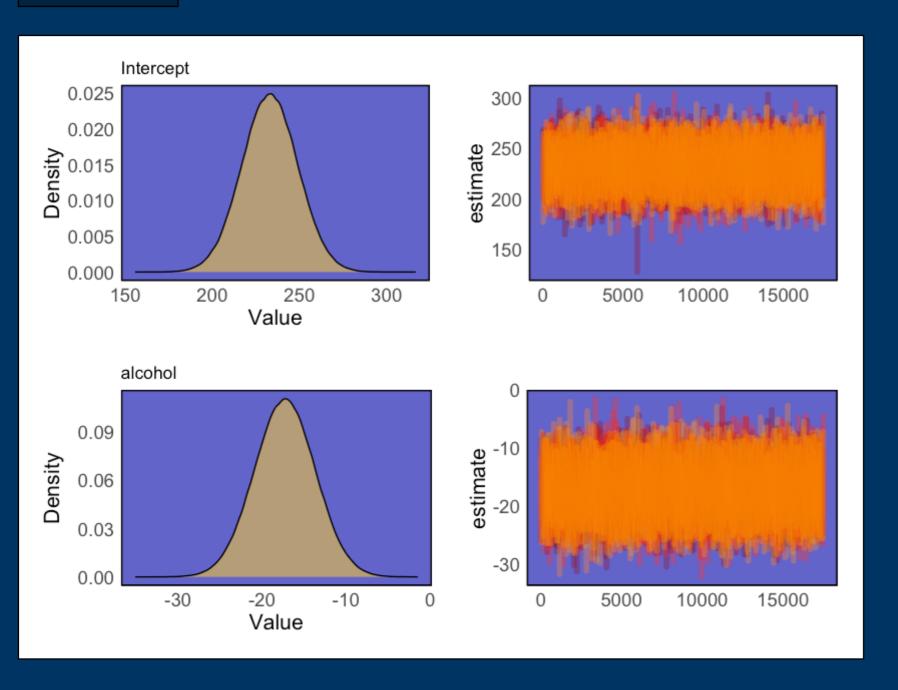
R_{hat} means it has converged

Now you have a distrib. for your R²

 $b\sim r+(m|s)$

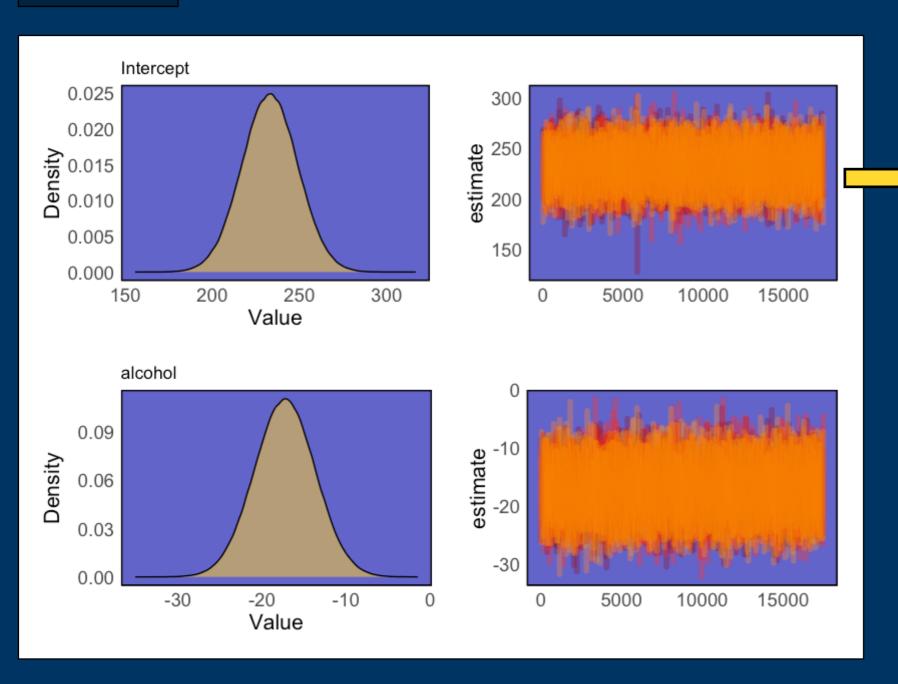
With the bayesian approach

> plot(reg)



With the bayesian approach

> plot(reg)

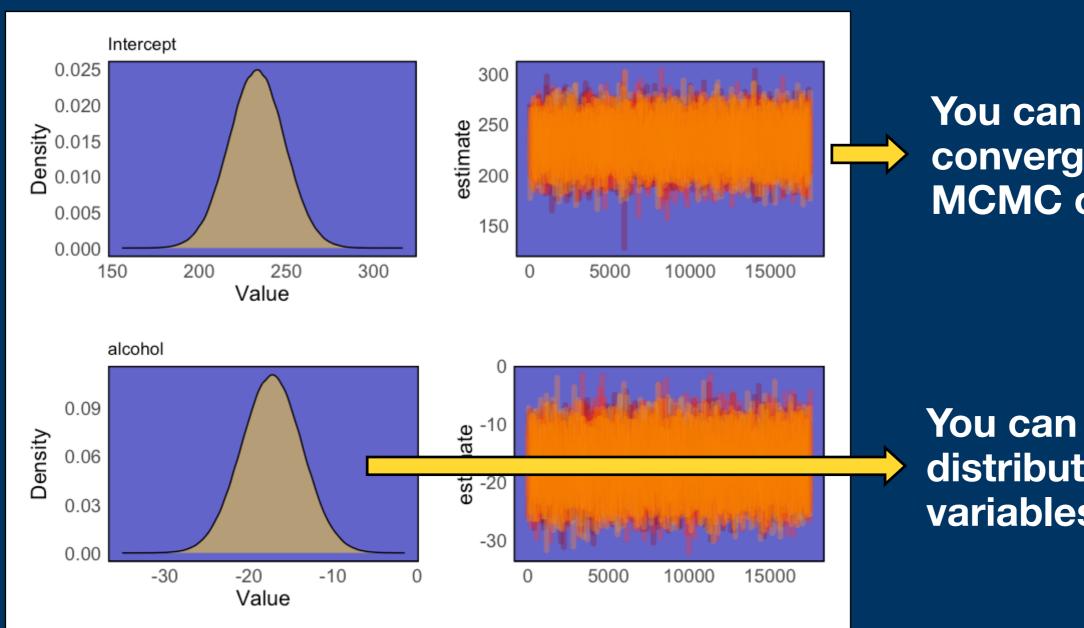


You can see the convergence of your MCMC chains

 $b \sim r + (m|s)$

With the bayesian approach

> plot(reg)

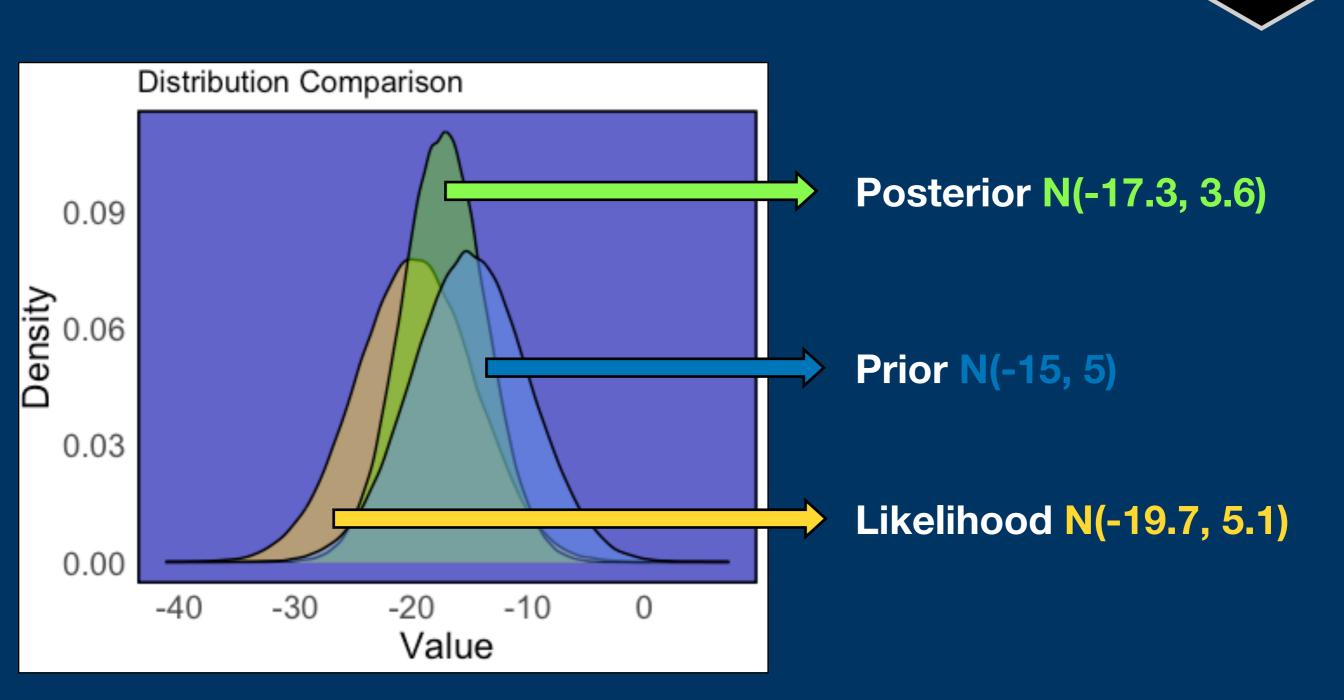


You can see the convergence of your MCMC chains

 $b \sim r + (m \mid s)$

You can also see the distribution of your variables

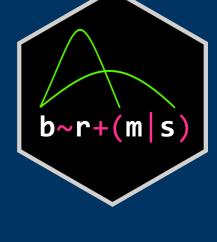
With the bayesian approach



With the bayesian approach

Now you're able to confirm that French ■, followed by Italians ■ and Spanish ■, are safe and you can resubmit for publication in *Nature*. Kudos!

With the bayesian approach

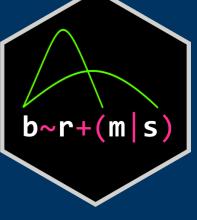


Now, imagine you want to argue that wine is harmful. Your goal is to completely shut down wine shops. You've realized that you can incorporate prior information that could alter the conclusion.

For instance, instead of using a prior distribution of N(-15, 5), you switch it to N(+15, 5).

With the bayesian approach

```
> reg
 Family: gaussian
 Links: mu = identity; sigma = identity
Formula: heart ~ alcohol
   Data: wooldridge::wine (Number of observations: 21)
 Draws: 3 chains, each with iter = 20000; warmup = 2500; thin = 1;
        total post-warmup draws = 52500
Population-Level Effects:
          Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
                                       213.89 1.00
                                                               30686
Intercept 174.00
                       21.66
                              128.93
                                                       33901
alcohol
             3.60
                       4.92 -5.72
                                       13.46 1.00
                                                       29457
                                                               34014
Family Specific Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk ESS Tail ESS
sigma
        80.88
                   15.37
                            56.17
                                   115.66 1.00
                                                  27885
                                                            33377
Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).
> brms::bayes_R2(reg)
     Estimate Est.Error
                                02.5
                                         097.5
R2 0.02777283 0.03003607 4.026603e-05 0.1057474
```

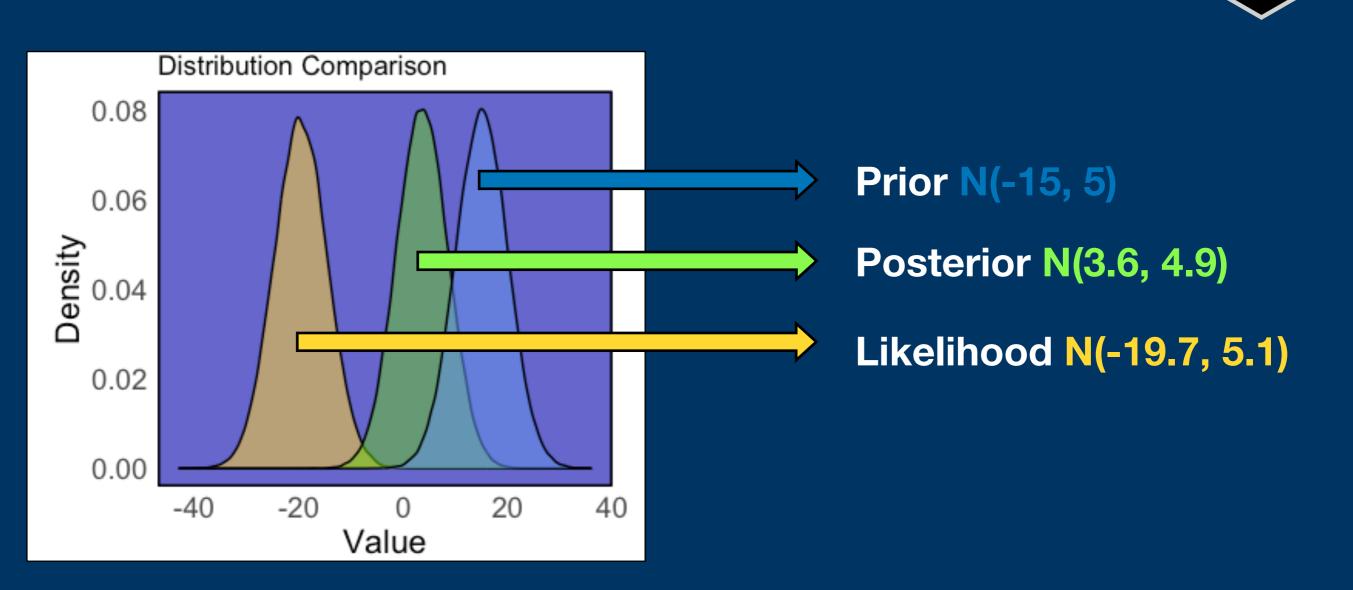




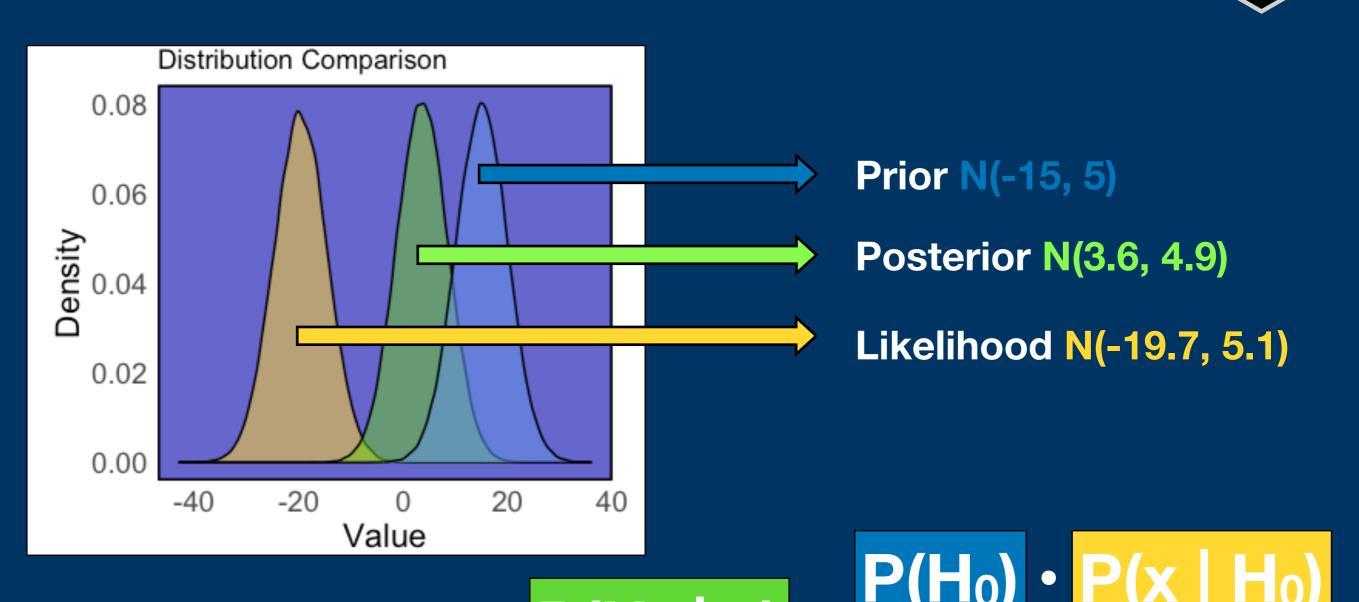
Fortunately, your credible interval is both negative and positive

Explain only 2%

With the bayesian approach



With the bayesian approach



Moving forward

With the bayesian approach

In this case, we had few data (n= 21 obs). Fortunately, our 95% credible intervals include both negative and positive values, which does not allow us to conclude that drinking wine is harmful. It is important to note that this conclusion is not solely driven by theory but rather emphasizes the importance of setting priors appropriately. With more data, it becomes increasingly difficult to bias your conclusions.

Another option, which I personally prefer, is to use non-informative priors (such as uniform distributions, large standard errors, or Student's t-distributions).

Presenting a plot showing the likelihood, prior, and posterior distributions helps illustrate how the data are treated.

Moving forward

With the bayesian approach

There are plenty of distributions you can use. It will depends directly about your data.

Some ideas here:

Species cover are understood between 0 and 100%, most of the time it would be a <u>beta distribution</u> we need to use

Species counts refers to Poisson distribution

Multiple choices refers to multinomial (if 2, Binomial) distribution

You can have a look here: https://rdrr.io/cran/brms/man/brmsfamily.html







Thank you for your attention!