# Needles in a Haystack: Reevaluating COVID-19 Vaccine Efficacy in Emergency Use Authorization Trials Using Frequentist and Bayesian Statistical Methods

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## 1 Abstract

The Pfizer COVID-19 vaccine was issued with fewer tests than normal due to circumstances deemed worthy by the Federal Drug Administration to send out Emergency Use Authorization. Although fewer tests are needed in this process, it is still important to ensure safety and efficacy of the vaccine. This analysis replicates a former study by Polack et al. investigating vaccine efficacy using Bayesian inference and Frequentist statistical methods. We found that the Pfizer vaccine efficacy was approximately 95% in both methods, which is much higher than the required 30% FDA rate. Using different assumptions in Bayesian modeling, we say that even in the most pessimistic circumstances the vaccine showed to be consistently exceeding FDA expectations. This re-analysis demonstrates that even during Emergency Use Authorization roll-out, the vaccine was statistically effective, rendering it to be a crucial portion of the COVID-19 relief effort.

## 2 Keywords

Beta Binomial, Parametric bootstrap, Maximum Likelihood Estimation, Vaccine Efficacy

## 3 Introduction

COVID-19 is a disease that comes from the SARS-CoV-2 virus, first emerging in late 2019. The first cases originated in Wuhan, China, and quickly spread worldwide, eventually leading the World Health Organization to classify it as a global pandemic (Hao et al., 2020). The zoonotic property of COVID-19 (infection comes from contact with other people) and the world's slow adaptation to it propelled its initial rapid spread. Countries began to go on lockdown starting with China in January of 2020. This was followed by most other countries declaring lockdown or restriction on social interaction (Koh, 2020). Non-essential businesses were closed, and most operations were moved online, affecting the economic and social lives of most people across the world. Many countries implemented mask mandates and social distancing measures to contain the COVID-19 outbreak - we still see the effects of this today, as the use of masks has now become standard practice in countries where it was not before the pandemic. International travel, mask mandate violations, and social distancing violations contributed to the spread of COVID-19 and its variants, such as Delta and Omicron.

Although short-term solutions such as social distancing and mask mandates helped contain COVID-19's spread, the long-term solution of vaccines helped the most in allowing life to return to how it was prior to the pandemic. Globally, vaccine roll-out began in early 2021, although the United States Federal Drug Administration gave the Pfizer and Moderna mRNA vaccine emergency approval in December 2020 for use by essential workers (Chirico, Teixeira da Silva, Tsigaris & Sharun, 2020). Due to the brevity of the situation, these vaccines were approved with less testing than is typically required to ensure that a vaccine is safe and effective. One of the studies conducted to gain emergency authorization was the Polack et al. study, a crucial component of the COVID recovery effort.

We analyzed the data from the Polack et al. (2020) study related to the BNT162b2 vaccine distributed by Pfizer and BioNTech- commonly referred to as the Pfizer vaccine. Pfizer and BioNTech successfully received a US FDA Emergency Use Authorization to begin distributing the two-dose

vaccine. In lieu of the shelter-in-place and amount of deaths caused by COVID-19, the FDA decided to forgo the typical testing process in favor of quickly finding and distributing cures to COVID-19. The researchers found an efficacy rate of the vaccine to be 95 percent and were more than 99.99 percent confident the true vaccine efficacy rate was greater than the FDA criterion of 30 percent efficacy. We want to test the efficacy of the BNT162b2 COVID-19 vaccine for ourselves in order to confirm the safety and success rate of distribution. Testing is important for determining the safety of medical tools, and review of statistical methods used to determine safety is crucial for improving future testing. Follow-up study replication helps to improve future testing methods and ensure the safety of more people. We want to replicate and assess the efficacy rate of the vaccine and test it against the FDA criterion.

| Group | Cases | Sample_size |
|---|---|---|
| BNT162b2 | 0.05% (8) | 99.95% (17,411) |
| Placebo | 0.92% (162) | 99.08% (17,511) |
| Total | 0.48% (170) | 99.52% (34,922) |

Figure 1: Percentages of data showing split between placebo and vaccine group, and participants who contracted COVID-19.

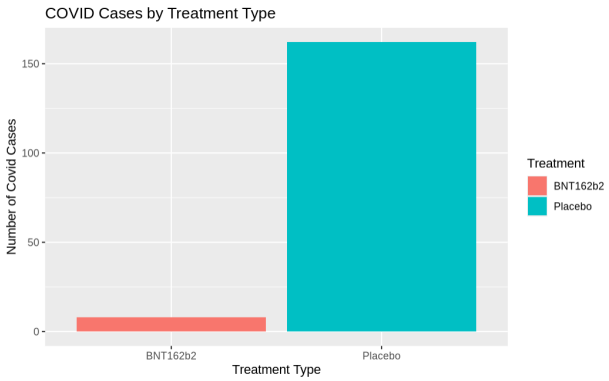


Figure 2: Bar graph of COVID cases grouped by treatment type.

We see in Fig. 1 that in the Polack data, 0.05 percent of people with the vaccine contracted COVID-19 and 0.92 percent of people with the placebo contracted COVID-19. In Fig. 2, we can see the clear split in Covid cases between the two groups that will be analyzed. Based on these initial visualizations, we can see that there is quite a large difference between the Covid cases in the

vaccine and in the placebo group. Therefore, we expect to see a high vaccine efficacy rate similar to the study, meaning that the vaccine will be safe to distribute for use at a much higher margin than the FDA criterion. We assume our results may differ slightly due to our use of Bayesian statistics, but should follow the same trend as the Polack paper.

# 4 Statistical Methods

The data we analyzed came from a double-blind, placebo-controlled, efficacy study. 43,448 participants were randomly assigned to receive either the BNT162b2 vaccine or a placebo. The study stopped once 170 people were infected with COVID-19. Among those vaccinated, 8 infections were reported, while 162 infections occurred in the placebo group. Our analysis estimates the rate parameter of SARS-CoV-2 infections among individuals inoculated with Pfizer's BNT162b2 and, by extension, evaluates vaccine efficacy using Frequentist and Bayesian approaches. We used a single binomial model to estimate the vaccine efficacy, our parameter of interest. X was the random variable defined as the number of vaccinated individuals infected with COVID-19 out of the 170 infected cases. We assumed $X \sim Binom(170, \pi)$ where $\pi = P(Vaccinated|Infected)$. This model is held under the following assumptions: a fixed number of trials ($n = 170$), a constant rate parameter, independent trials, and binary infection outcomes (infected or not infected). We know $\psi = \frac{1-2\pi}{1-\pi}$ where $\infty < \psi < 1$. We used $\psi$ to solve for $\pi$ such that $\pi = \frac{\psi-1}{\psi-2}$. $\psi$ is our parameter of interest because the FDA requires that the vaccine efficacy is greater than 30%, this is what we will be testing. Therefore, the null hypothesis is $H0 : \psi = 0.3$ and the alternative hypothesis is $H1 : \psi \geq 0.3$.

## 4.1 Likelihood Inference

### 4.1.1 Maximizing $\psi$

To find the maximum likelihood vaccine efficacy rate $\psi_0^{mle}$, we took the likelihood function of the binomial rate parameter $\hat{\pi}_0^{mle}$ for a binomial random variable $X \sim Binom(n, \hat{\pi}_0^{mle})$ which follows

$$L(\pi) = \binom{n}{x}(\pi)^x(1-\pi)^{n-x}$$

where $n$ denotes the sample size and $x$ is an instance of the random variable $X$. We are interested in finding the likelihood estimator for $\psi$, the vaccine efficacy, so we used the transformation $\pi = \frac{\psi-1}{\psi-2}$ and obtained

$$L(\psi) = \binom{n}{x}(\frac{1-\psi}{2-\psi})^x(\frac{1}{2-\psi})^{n-x}$$

Taking the natural log of our likelihood function, we obtained

$$\ell(\psi) = ln\binom{n}{x} + xln(1-\psi) - xln(2-\psi) + (n-x)ln(1) - (n-x)ln(2-\psi)$$

To maximize the function $\ell(\psi)$, we took the first derivative with respect to $\psi$ and obtained,

$$\frac{d\ell(\psi)}{d\psi} = \frac{-x}{1-\psi} + \frac{n}{2-\psi}$$

Setting the derivative equal to zero and solving, we obtain the formula that maximizes $\psi$, such that,

$$\hat{\psi}_0^{mle} = \frac{n-2x}{n-x}$$

We checked the second derivative and found it to be negative proving that $\hat{\psi}_0^{mle}$ is a maximum estimation (Appendix Likelihood Estimation).

### 4.1.2 Confidence Interval Estimation of $\psi$

We applied two methods to compute the confidence interval estimate of $\psi$: a large sample Wald confidence interval and a parametric bootstrap.

To construct the large-sample confidence interval for $\psi$, we applied the generalized central limit theorem, which states that for large $n$, $\hat{\psi}_0^{mle} \approx Norm(\psi_0, \sqrt{\frac{1}{nI(\psi)}})$ where the Fisher Information is $I(\psi) = E[-\frac{d^2}{d\psi^2}\ell_\psi(X)]$. To calculate the Fisher Information, we took the negative of the second derivative of $\ell(\psi)$ which we computed $-\frac{d^2\ell(\psi)}{d\psi^2} = \frac{X}{(1-\psi)^2} - \frac{n}{(2-\psi)^2}$. Since $X$ follows a binomial distribution, its expected value is $E[X] = n\pi$. However, to express the Fisher information in terms of $\psi$, we apply the transformation $\pi = \frac{1-\psi}{2-\psi}$ and substitute the transformed maximum likelihood estimator, $\hat{\pi}_0^{mle}$ into our expectation. Using this substitution and the linearity of expectation we

obtained

$$I(\psi) = \frac{n}{(1-\psi)(2-\psi)} - \frac{n}{(2-\psi)^2}$$

The large sample, $(1-\alpha)$ Wald confidence interval of $\psi_0$ will therefore be

$$\psi_0^{mle} \pm z_{\frac{\alpha}{2}} \sqrt{\frac{1}{nI(\psi)}}$$

In our second method to calculate the confidence interval of $\psi$, we performed $1,000$ iterations of the bootstrap resampling to estimate the distribution of $\psi$.

### 4.1.3 P-value Calculations

We also applied two different methods to calculate the p-value for our test: a chi-square distribution-based approach and an empirical p-value method.

To calculate the value using a chi squared distribution, we used the null and alterative hypothesis $H_0 : \psi = 0.3$ and $H_1 : \psi \geq 0.3$ and calculated the likelihood ratio $\Lambda = \frac{L(\hat{\psi}_0^{mle})}{L(\psi_0^{null})}$ as our test statistic. We then applied the transformation $W = 2ln(\Lambda)$. We applied this transformation so that $W \sim X_1^2$. With this transformation, we calculated $P(W > W^*)$ where $W^*$ is our test statistic under the transformation to obtain our p-value.

We also performed an nonparametric empirical p-value calculation

$$\hat{p} = \frac{\sum_{i=1}^{B} 1(W^* > W_{obs})}{B}$$

using $150,000$ resampling repetitions.

## 4.2 Bayesian Inference

For the Bayesian method, prior assumptions were made and used with the results of the study to update our assumptions. Our beta prior is $X_\pi \sim Binom(n, \pi)$ $g(\pi) = Beta(a, b)$ and the beta model is $f(X|\pi) \approx Binomial(n, \pi)$. The posterior is $h(\pi|x) = Beta(a+x, n-x+b)$. Our significant parameter of interest is $\psi = \frac{1-2\pi}{1-\pi}$.

We tested all prior assumptions against the FDA guideline that the efficacy must be greater

than 0.3 for the vaccine to be deemed effective.

$$P(\psi \geq 0.3) = P(\frac{1-2\pi}{1-\pi} \geq 0.3) = P(\pi \leq \frac{7}{17})$$

$$P(\psi \geq 0) = P(\frac{1-2\pi}{1-\pi} \geq 0) = P(\pi \leq \frac{1}{2})$$

For the optimistic and pessimistic priors, we set different apriori beliefs to be equal to $P(\pi \leq \frac{1}{2})$ and $P(\pi \leq \frac{7}{17})$. We found the a and b for $\pi$ where the percentiles chosen from the apriori beliefs are $\frac{1}{2}$ and $\frac{7}{17}$. Replicating the Pfizer results, we already knew the a and b values and used the prior given to find the apriori beliefs.

Then, we found the posterior median for $\pi$, and converted it to $\psi$. We found the posterior intervals at the 95% level, at the 0.025 and 0.975 tails of the beta posterior distribution. We then found the posterior interval for $\pi$ and converted it to $\psi$ using $\psi = \frac{1-2\pi}{1-\pi}$. Finally, we tested against the null hypothesis.

## 5 Results

Our main goal is to determine whether the efficacy of our vaccine is above the FDA guideline of 30%. Taking the data we know from the sample, we first found the sample estimate of the relative risk $\hat{RR}$ and vaccine efficacy. We found $\hat{\pi}_{BNT} = \frac{8}{17{,}411} = 0.000459$ which is the proportion of Covid cases in the vaccinated group and $\hat{\pi}_p = \frac{162}{17{,}511} = 0.00925$ which is the proportion of Covid cases in the placebo group.

Using these values, we found the relative risk $\hat{RR}$ of the vaccine trials.

$$\hat{RR} = \frac{\hat{\pi}_{BNT}}{\hat{\pi}_p} = \frac{0.000459}{0.00925} = 0.04967$$

Using the relative risk, we can calculate vaccine efficacy.

$$1 - \frac{\hat{\pi}_{BNT}}{\hat{\pi}_p} = 1 - 0.04966 = 0.9514$$

The vaccine efficacy calculated for the sample is approximately 95%, which is much higher than the FDA requirement of 30%.

| Analysis Results | | | |
|---|---|---|---|
| **Method** | **Vaccine Efficacy Estimate** | **P-Value** | **95% Confidence Interval** |
| Frequentist | $\psi = 0.9506$ | $2.8222 \times 10^{-28}$ -($X^2$ test), 0-(empirical) | [0.9479, 0.9533] (Wald), [0.9103, 0.9820] (bootstrap) |
| Bayesian | $\psi = 0.7523$ | Pessimistic: $1.931788 \times 10^{-13}$ | [0.6661909, 0.8196993] |
| | $\psi = 0.9184$ | Optimistic: 0 | [0.8644559, 0.9548464] |
| | $\psi = 0.9486$ | Pfizer: 0 | [0.9035199, 0.9762552] |

Table 1. Comparison of Bayesian and Frequentist results.

### 5.1 Likelihood Inference

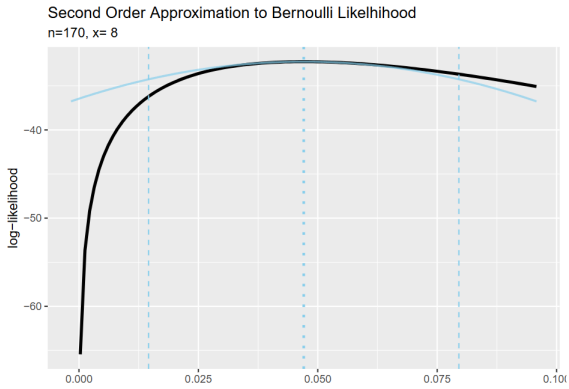


Figure 3: Taylor Approximation to Log-likelihood

We evaluated the efficacy of the vaccine using maximum likelihood methods. The estimated vaccine efficacy was $\psi_0 = 0.9506$, indicating a 95.06% reduction in disease risk among vaccinated individuals compared to the unvaccinated group.

To assess the statistical significance, we computed two p-values. The chi-square test yielded a p-value of $2.822210^{-28}$, demonstrating extremely strong evidence against the null hypothesis. Furthermore, an empirical p-value obtained through resampling was 0, further supporting the

evidence against the null hypothesis.

Confidence intervals were calculated using the Wald and bootstrap methods. The Wald 95% confidence interval was $[0.9479, 0.9533]$, suggesting a highly precise estimate. The bootstrap confidence interval was wider at $[0.9103, 0.9820]$, reflecting the potential variability in the estimate, but still demonstrating strong vaccine efficacy.

## 5.2 Bayesian Inference

We investigated what model would be best for the data and making inferences on the vaccine efficacy. To model this data, we used a single binomial random variable X. To decide on our apriori beliefs, we first calculated the prior elicitation of a and b using the uniform distribution to see if the vaccine meets FDA guidelines.

$$P(\psi \geq 0.3) = P(\frac{1-2\pi}{1-\pi} \geq 0.3) = P(\pi \leq \frac{7}{17})$$

### 5.2.1 Pessimistic Prior

A pessimistic set of beliefs for a prior is a good starting point, as if our vaccine efficacy still comes out looking good, then we have even more reason to believe that it is high above the FDA regulations. For our first prior, we selected the following beliefs:

$$P(\psi \geq 0.3) = 0.05 \text{ and } P(\psi \geq 0) = 0.5$$

These beliefs look as follows when written in terms of $\pi$:

$$P(\pi \leq \tfrac{7}{17}) = 0.05 \text{ and } P(\pi \leq \tfrac{1}{2}) = 0.5$$

Using these beliefs, we found a and b to both be 43.03. This means our prior is Beta(43.03, 43.03) and our posterior is Beta(43.04+8, 170-8+43.03).

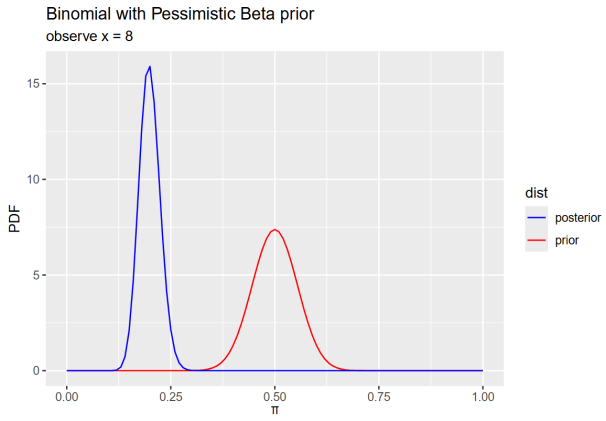


Figure 4: Pessimistic beta prior and posterior distribution plot

The posterior median for $\pi$ is approximately 0.1985. We transformed the median into $\psi$ which became 0.7523. We then calculated the confidence interval and are 95% sure $\psi$ is between [0.6661909, 0.8196993]. Finally, we found the p-value for the probability of seeing results as or more extreme than ours when the null hypothesis $H0 : \psi = 0.3$ is true to be 1.931788e-13, indicating a significant result.

### 5.2.2 Optimistic Prior

We wanted to test a more optimistic assumption compared to the pessimistic one, so we selected the following beliefs:

$$P(\psi \geq 0.3) = P(\pi \leq \tfrac{7}{17}) = 0.5 \text{ and } P(\psi \geq 0) = P(\pi \leq \tfrac{1}{2}) = 0.75$$

Using these beliefs, we found $a = 6.24$ and $b = 8.77$, making our prior Beta(6.24, 8.77) and the posterior to be Beta(6.24+8, 170-8+8.77).

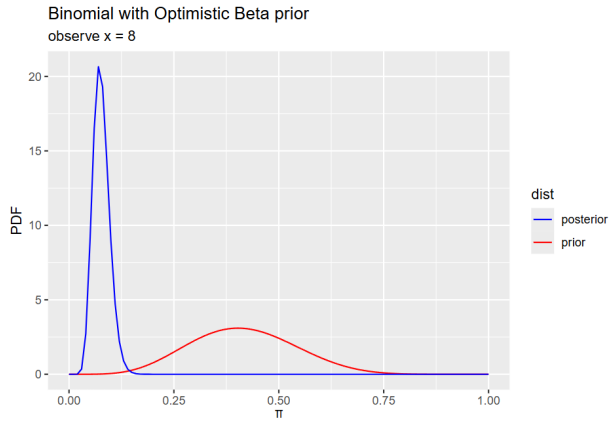


Figure 5: Optimistic beta prior and posterior distribution plot

We found the posterior median for $\pi$ and transformed it to the median into $\psi$, which was 0.9184. We then calculated the confidence interval obtained the result that we are 95% sure $\psi$ is between [0.8644559, 0.9548464] based on our selected prior. We found a p-value extremely close to 0, indicating a significant result.

### 5.2.3 Pfizer Prior

We wanted to replicate the priors and results used in the research paper. We know they used a prior of Beta(0.700102, 1). Their posterior was Beta(0.700102+8, 170-8+1). We found the values x and y they used for their prior where $P(\psi \geq 0.3) = x$ and $P(\psi \geq 0) = y$ checked that they were accurate. We found that:

$$P(\psi \geq 0.3) = P(\pi \leq \tfrac{7}{17}) = 0.53729 \text{ and } P(\psi \geq 0) = P(\pi \leq \tfrac{1}{2}) = 0.6155$$

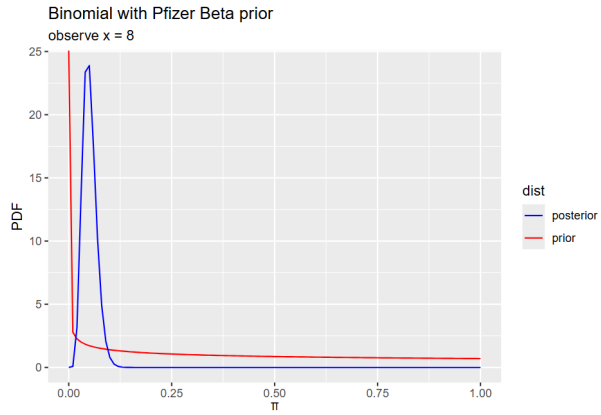


Figure 6: Phizer beta prior and posterior distribution plot

We found the posterior median for $\pi$ and transformed it for the median into $\psi$, which was 0.9486. We then calculated the confidence interval and are 95% sure $\psi$ is between [0.9035199, 0.9762552] based on the prior selected. We found a p-value extremely close to 0, indicating a significant result. This matched with the results of the study.

# 6 Discussion

Using maximum likelihood estimation, we found that the estimate of $\psi$ was 0.9506. This is almost exactly what Pfizer found to be their estimate, only being slightly larger than theirs. This means that our maximum likelihood estimation procedure is comparable to the results that the Pfizer study got, and we can conclude that the vaccine is effective and safe for public use with a high margin above the minimum requirement of 30%. All priors from Bayesian estimation rejected the Null Hypothesis $H0 : \psi = 0.3$ because of the very low p values. As we were more pessimistic in our prior beliefs, we found lower and larger confidence intervals. The Pfizer prior had the highest confidence interval. We assume that the prior chosen by Pfizer was optimistic because they wanted to assume the drug would do well. Their chosen values were $P(\psi \geq 0.3) = 0.53729$ and $P(\psi \geq 0) = 0.6155$ and are very calculated. They may have wanted a certain result where the p-value is very close to zero and a confidence interval where the lowest point is above 90, which ensures the vaccine looks highly efficient. Comparing our optimistic prior to Pfizer's we see that the prior they used is more optimistic than ours, resulting in a higher estimate. Even with our more pessimistic beliefs we still found the vaccine to be effective by FDA standards. By Bayesian estimation for all three priors we assume that $\psi \geq 0.3$ and by the FDA is efficient.

Using likelihood inference, we are able to use straightforward computation based on our observed data, which gives us an objective view on how the data behaves and what the vaccine efficacy is. The presence of a relatively large sample size is also an advantage, as it allows us to use Frequentist methods. The use of Bayesian inference is both a strength and weakness when it comes to statistical re-evaluation of the presented data. The use of priors allows for flexibility in certainty of testing and for testing the limits of our data's significance. However, due to this flexibility, different priors must be examined to understand the efficacy of the vaccine and how its predicted value fluctuates with the assumptions that are made. This is computationally intense and takes time to complete.

Further investigation may be done to include other factors that may be affecting vaccine efficacy. A prominent issue following the initial Covid outbreak was subsequent outbreaks of different and stronger strains. An interesting direction would be to compare how vaccine efficacy differs based on the Covid strain to learn to effectively treat more people. Another point of interest is the duration of immunity after receiving the approved vaccine. Researchers could investigate how long people show immunity after receiving not only the Pfizer vaccine, but other vaccines with different efficacy rates, and comparing them to gain more knowledge on the relationship between vaccinations and immunity rates. Finally, investigating the long-term effects of this vaccine is important to gain knowledge on next steps and future prevention. A longitudinal study may be done to investigate long-term side effects after receiving this vaccine, and well as subsequent booster doses to examine the long-term effects of those as well.

# 7 References


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# 8 Appendix

## 8.1 Code for Intro Plots

```
covid_df_long = data.frame(Treatment = c("Placebo", "BNT162b2"), Count = c(162, 8))

ggplot(data = covid_df_long, aes(x = Treatment, y = Count, fill = Treatment)) +
  geom_col() +
  labs(title = "COVID Cases by Treatment Type", x = "Treatment Type", y = "Number of Covid Cases")
```

## 8.2 Likelihood Inference Code

### 8.2.1 $\psi$ MLE and Large Sample Confidence Interval

```
#obtaining psi_mle
n = 170
x_i = 8
psi_mle = (n - 2*x_i) / (n - x_i)
pi_mle = (1 - psi_mle) / (2 - psi_mle)
E_X = 170*pi_mle
fisher_info = (-1) * ((n / (2 - psi_mle)^2) - (E_X / (1 - psi_mle)^2))
z_div_2 = qnorm(p = 1 - alpha/2)

ci_lower = psi_mle - z_div_2 * sqrt(1/(n * fisher_info))
ci_upper = psi_mle + z_div_2 * sqrt(1/(n * fisher_info))
print(c("CI[psi]", ci_lower, ci_upper))

#verified fisher_info equals generalized_fisher
```

### 8.2.2 Likelihood Estimation Second Derivative Test

$$\frac{d\ell(\psi)}{d\psi} = \frac{x}{1-\psi} + \frac{-n}{2-\psi}$$

$$\frac{d^2\ell(\psi)}{d\psi^2} = \frac{-x}{(1-\psi)^2} - \frac{n}{(2-\psi)^2}$$

$$0 = \frac{-x}{(1-\psi)^2} - \frac{n}{(2-\psi)^2}$$

$$\frac{-x}{(1-\psi)^2} = \frac{n}{(2-\psi)^2}$$

### 8.2.3 Bootstrap Confidence Interval

```r
#Bootstrap
set.seed(123)
generate_bootstrap <- function(X, n, B, conf_level = 0.95) {
  psi_hat <- (n - 2*X) / (n - X)
  pi_hat <-  (1 - psi_hat) / (2 - psi_hat)
  boot_psi <- data.frame(psi = numeric(B))

  for (i in 1:B) {
    boot_sample <- rbinom(1, size = n, prob = pi_hat)
    boot_psi$psi[i] <- (n - 2 * boot_sample) / (n - boot_sample)
  }
  return (boot_psi)
}

boot_df <- generate_bootstrap(X=8, n=170, B = 1000)
lower_bound = quantile(x = boot_df$psi, probs= 0.025)
upper_bound = quantile(x = boot_df$psi, probs= 0.975)
print(c(lower_bound, upper_bound))
```

### 8.2.4 $\chi^2$ P-Value

```r
#PVALUE
n=170
x_i=8
psi_null = 0.3
L_psi_mle = choose(n,x_i) * (((psi_mle - 1)/(psi_mle - 2))^x_i) * (1 - (psi_mle - 1)/(psi_mle - 2)) ^(n-x_i)
L_psi_null = choose(n,x_i) * (((psi_null - 1)/(psi_null - 2))^x_i) * (1 - (psi_null - 1)/(psi_null - 2)) ^(n-x_i)
alpha_ratio = L_psi_mle / L_psi_null
w_obs = 2 * (log(L_psi_mle / L_psi_null))
pval_chi = pchisq(w, df=1, lower.tail = FALSE)
```

### 8.2.5 Empirical P-Value

```
#Empirical Pvalue
set.seed(414)
B = 150000
generate_empirical <- function(n, psi_null){
  pi_null = (1-psi_null) / (2-psi_null)
  W_df <- data.frame(W_star = numeric(B))

  for(i in 1:B){
    x <- rbinom(n = 1, size = 170, prob=pi_null)
    psi_star = (n - 2*x) / (n - x)
    L_psi_star = choose(n,x) * (((psi_star - 1)/(psi_star - 2))^x) * (1 - (psi_star - 1)/(psi_star - 2))^(n-x)
    L_psi_null = choose(n,x) * (((psi_null - 1)/(psi_null - 2))^x) * (1 - (psi_null - 1)/(psi_null - 2))^(n-x)
    W_df$W_star[i] <- 2 * (log(L_psi_star / L_psi_null))
  }

  return(W_df)
}

W_df <- generate_empirical(n=170, psi_null =0.3)
pvalue_empirical <- sum(W_df$W_star >= w_obs) / B
```

## 8.3 Bayes Estimation Code

### 8.3.1 Pessimistic Prior

```
library(LearnBayes)
beta.select(quantile1 = list(p = 0.05, x = 7/17),
                           quantile2 = list(p = 0.5, x = 0.5))
```

```
## [1] 43.03 43.03
```

```
posterior_median_pi = qbeta(0.5, shape1 = 43.03 + 8, shape2 = 170 - 8 + 43.03)

posterior_median_si = (1 - (posterior_median_pi * 2)) / ((1 - posterior_median_pi))
cat("Posterior Median Psi using Pessimistic Beliefs", posterior_median_si)
```

```
## Posterior Median Psi using Pessimistic Beliefs 0.7523308
```

```
pi_ci = qbeta(p = c(0.975, 0.025), shape1 = 43.03 + 8, shape2 = 170 - 8 + 43.03)
ci_bay = (1 - (pi_ci * 2)) / ((1 - pi_ci))
cat("95% CI for Psi Using Pessimistic Beliefs", ci_bay)
```

```
## 95% CI for Psi Using Pessimistic Beliefs 0.6661909 0.8196993
```

```
pval = 1 - pbeta(7/17, shape1 = 43.03 + 8, shape2 = 170 - 8 + 43.03)
cat("P-value for Psi Using Pessimistic Beliefs", pval)
```

```
## P-value for Psi Using Pessimistic Beliefs 1.931788e-13
```

### 8.3.2 Optimistic Prior

```
beta.select(quantile1 = list(p = 0.5, x = 7/17),
                             quantile2 = list(p = 0.75, x = 0.5))
```

```
## [1] 6.24 8.77
```

```
posterior_median_pi = qbeta(0.5, shape1 = 6.24 + 8, shape2 = 170 - 8 + 8.77)

posterior_median_si = (1 - (posterior_median_pi * 2)) / ((1 - posterior_median_pi))
cat("Posterior Median Psi Using Optimistic Beliefs", posterior_median_si)
```

```
## Posterior Median Psi Using Optimistic Beliefs 0.9183971
```

```
pi_ci = qbeta(p = c(0.975, 0.025), shape1 = 6.24 + 8, shape2 = 170 - 8 + 8.77)
ci_bay = (1 - (pi_ci * 2)) / ((1 - pi_ci))
cat("95% CI for Psi Using Optimistic Beliefs", ci_bay)
```

```
## 95% CI for Psi Using Optimistic Beliefs 0.8644559 0.9548464
```

```
pval = 1 - pbeta(7/17, shape1 = 6.24 + 8, shape2 = 170 - 8 + 8.77)
cat("P-value for Psi Using Optimistic Beliefs", pval)
```

```
## P-value for Psi Using Optimistic Beliefs 0
```

### 8.3.3 Pfizer Prior

```
posterior_median_pi = qbeta(0.5, shape1 = 0.700102 + 8, shape2 = 170 - 8 + 1)
posterior_median_si = (1 - (posterior_median_pi * 2)) / ((1 - posterior_median_pi))
cat("Posterior Median for Psi Using Pfizer Prior", round(posterior_median_si, 4))
```

```
## Posterior Median for Psi Using Pfizer Prior 0.9486
```

```
pi_ci = qbeta(p = c(0.975, 0.025), shape1 = 0.700102 + 8, shape2 = 170 - 8 + 1)
pi_si = (1 - (pi_ci * 2)) / ((1 - pi_ci))
cat("CI for Psi Using Pfizer Beliefs", pi_si)
```

```
## CI for Psi Using Pfizer Beliefs 0.9035199 0.9762552
```

```
pval = 1 - pbeta(7/17, shape1 = 0.700102 + 8, shape2 = 170 - 8 + 1)
cat("P-value for Psi Using Pfizer Prior", pval)
```

```
## P-value for Psi Using Pfizer Prior 0
```

```r
alpha = 0.700102
beta = 1
a = pbeta(q=7/17, shape1 = alpha, shape2 = beta)
b = pbeta(0.5, shape1 = alpha, shape2 = beta)
cat("A and B for Pfizer Prior", a , b)
```

```
## A and B for Pfizer Prior 0.5372978 0.6155287
```

```r
beta.select(quantile1 = list(p = a, x = 7/17),
                              quantile2 = list(p = b, x = 0.5))
```

```
## [1] 0.7 1.0
```

## 8.4 Prior and Posterior Distribution Graph Code

```
ggplot() +
  geom_function(fun = dbeta,
                mapping = aes(color = "prior"),
                args = list(shape1=0.700102, shape2=1),
               xlim = c(0,1)) +
  geom_function(fun = dbeta,
              mapping = aes(color = "posterior"),
                args = list(shape1 = 0.700102 + 8, shape2 =  170 - 8 + 1),
                xlim = c(0,1)) +
  scale_color_manual(name = "dist", values = c("blue", "red")) +
                       labs(title = "Binomial with Pfizer Beta prior",
                            y = "PDF",
                            x = expression(pi),
                            subtitle = "observe x = 8")
```

```
ggplot() +
  geom_function(fun = dbeta,
                mapping = aes(color = "prior"),
                args = list(shape1=6.24, shape2=8.77),
               xlim = c(0,1)) +
  geom_function(fun = dbeta,
              mapping = aes(color = "posterior"),
                args = list(shape1 = 6.24 + 8, shape2 = 170 - 8 + 8.77),
                xlim = c(0,1)) +
  scale_color_manual(name = "dist", values = c("blue", "red")) +
                       labs(title = "Binomial with Optimistic Beta prior",
                            y = "PDF",
                            x = expression(pi),
                            subtitle = "observe x = 8")
```

```
ggplot() +
  geom_function(fun = dbeta,
                mapping = aes(color = "prior"),
                args = list(shape1=43.03, shape2=43.03),
               xlim = c(0,1)) +
  geom_function(fun = dbeta,
              mapping = aes(color = "posterior"),
                args = list(shape1 = 43.03 + 8, shape2 = 170 - 8 + 43.03),
                xlim = c(0,1)) +
  scale_color_manual(name = "dist", values = c("blue", "red")) +
                       labs(title = "Binomial with Pessimistic Beta prior",
                            y = "PDF",
                            x = expression(pi),
                            subtitle = "observe x = 8")
```