ST502 Project

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Part I

Framingham Heart Study

The Framingham data set contains the systolic blood pressure of 300 smokers and nonsmokers. For this study we will assume the following:

H_0: μ_1 - $\mu_2 = 0$

H_A: μ_1 - $\mu_2 \neq 0$

The null hypothesis being there is no difference in the blood pressure between smokers and non smokers. We believe that there is a difference and this paper will prove if we have enough evidence to reject the null hypothesis.

Normality of Data

Plotting the density of total data (see Appendix I: Figure 1A), we can that it closely follows a normal distribution, Density plots of the split data exhibit similar forms (see Appendix I: Figure 1B). We can also calculate the kurtosis and the skew of the data, which are 3.812, 0.88 for kurtosis and skew respectively, and see that they are quite close to values typically found in normally distributed data. Additionally, the calculated values of sample standard deviation, $\frac{IQR}{1.35}$, and $\frac{MAD}{0.675}$ are 22.89, 22.22, and 21.48. The similarities between the three values indicate that the data is not influenced by outliers. Therefore, we will assume the data and the subsequent split data to be normal.

Statistical Analysis

The goal of this paper is to investigate, through hypothesis testing, whether or not there is enough evidence to reject the null hypothesis. We will conduct the analysis under two conditions; the first assuming equal population variance (using pooled sample variance, S_p) and the second assuming unequal population variance. The results will be presented and any discrepancies between the two outcomes will be discussed.

In order to begin we must first find the difference in mean blood pressure between smoker and non smokers in this dataset. This was calculated to be -9.1577778. Despite this being a non zero number we ar not sure if there is in fact a difference of that this value was due to chance.

In the first analysis we will be assuming equal variances, thereby allowing us to use pooled sample variance (see Appendix I: Equation 1) which was calculated to be 510 using a degree of freedom value 298. Under these conditions the p value was calculated to be 0.0041 which is smaller than α of 0.05 (0.025 for each side of the distribution). In terms of t values, our observed t value of -3.04 is smaller than the t value, -1.97 for a two sided α of 0.05.

Additionally, the 95% confidence limits were calculated for the pooled variance assumption. The observed 95% confidence intervals are -15.08 to -3.23 It can be seen that 0 does not fall into the 95% confidence interval in this case. Therefore the null hypothesis can be rejected.

Based on the aforementioned findings, we can reject the null hypothesis in favor of the alternative hypothesis at an α level of 0.05. In other words, there is significant evidence to support this group of smokers and non smokers have a different range of systolic blood pressure when using pooled variance.

We will now conduct the same analysis as before, but now assuming unequal population variances. In this case the computed sample variances of the two groups are 352.2 for smokers and 562.1) for non smokers. Using equation 3 from Appendix 1, an observed t value of -2.9 is obtained. Comparing that the two sided α of -1.98 with 158 degrees of freedom (as computed using the Satterthwaite Approximation see Appendix I: Equation 4). The observed t value is less than the chosen α value of 0.05, as in the case of pooled sample variance.

Furthermore, the 95% confidence limit in the non pooled case was found to be -15.4 to -2.91. It can be noted that zero is absent from this range, as in the case of the pooled sample variance. In this second scenario, there is sufficient evidence to reject the null hypothesis and to support the alternative at an α level of 0.05.

We have shown that there is sufficient evidence that the blood pressure between smokers and nonsmokers are different. This statement holds true in all cases described in this paper. It should be noted, that while the observed systolic blood pressure values vary between smoker and non smokers, we do not know the underlying cause based on the provided data.

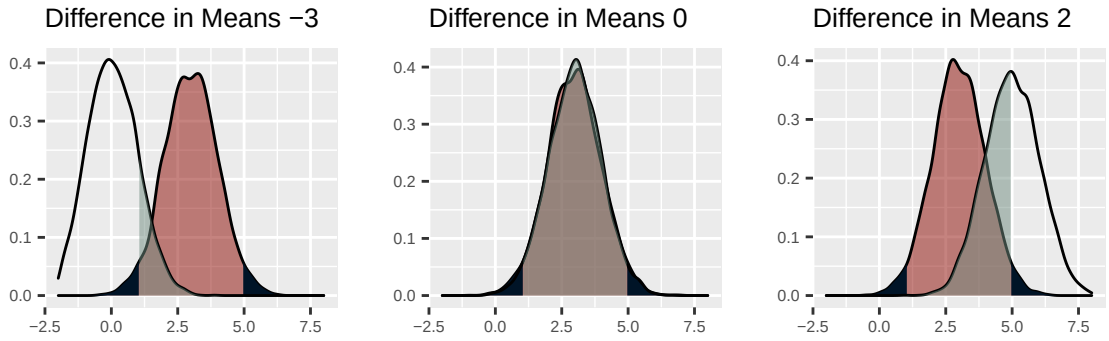
Part II

Introduction

In Part I we were able to see how hypothesis testing allowed to find enough evidence to challenge the "status quo" argument that smoking has no affect on the blood pressure of a person. What we found, through a number of robust statistical methods, that the difference in means, calculated to be 9.1577778, was significant to not have arisen by chance. That within an α of 5%, we are confident that the two groups do exhibit measurable differences. In the following sections, we will explore, through simulated data, the concept of randomness in data and what steps we can take to mitigate that randomness. All simulated date will be generated using the built in rnorm() function in R.

Power of Hypothesis Testing

It is important to briefly discuss the concept of power in hypothesis testing. Power describes the probability of not committing a Type II error, which is to not reject the null hypothesis when there was in actuality enough evidence to do so. The probability of a Type II error is represented by β. Power is the complement to that probability (1 - β). The value of β is the portion of the alternate distribution that is within the null hypothesis non rejection region limits. Below are a number of plots to help depict this concept. In each of the plots the shaded red is the null distribution and its location stays constant (mean = 3). The dark tails represent the rejection region of the null distribution. The outline distribution represents the "true" alternative distribution. Within that distribution is the shaded light blue region which is equal to β. It can be seen that as the difference between the two distributions shrinks the value of β increases and the power shrinks. Power reaches minimum and β reaches maximum when the two distributions are the same.



Simulation Study

Below, various scenarios were simulated by creating 2 normally distributed data sets of various mean, variances, and sample sizes. Each scenario was repeated a thousand times. For each of those repeats a hypothesis test was conducted and the number of times the null hypothesis was rejected was recorded. See Appendix III for results. All hypothesis testing was using pooled and unpooled variance, regardless of the actual values of variance.

The following table includes the values of each parameter used in the simulation:

Parameter	Possible Values
μ_0	0, 4, 5, 6, 10
σ_0^2	1, 4, 9
n_0	10, 30, 70
μ_A	5
σ_A^2	1
n_A	10, 30, 70

It was noted that the smaller difference between the alternative and null mean values were, the less likely the null hypothesis was rejected. Larger values of variance also reduced the number of rejected null hypothesis. In both cases, the more overlap between the two distributions, the less powerful the test. One way that can increase the power of the t-test is to increase the sample size. For a specific example, we can look at test cases #9 and #129. In both cases the

distribution means were 6 and 5 for the null and alternative hypotheses respectively, along with the respective variances of 4 and 1. The only difference between the two cases was the sample size ($n_9 = 10$ and $n_{129} = 70$). This increase in sample size resulted in almost an 4 fold increase in power (286/952 (pooled) or 265/948 (unpooled) rejected nulls). Test cases 69 and 114 use different combinations of, but lower than 70, sample sizes than the aforementioned two. While they exhibited increased signs of power, they did not get as high as test case 129. It stands to reason that large variances and small deltas in mean can be mitigated by increasing the sample size accordingly.

Below are summaries of (1 - β) calculations for test cases #9 and #129:

	Test Case #9	Test Case #129
Min	0.0500009	0.0707365
1st Quantile	0.1169414	0.8610788
Median	0.2979222	0.9652580
Mean	0.3793437	0.8953985
3rd Quantile	0.6114560	0.9947153
Max	0.9999994	0.9999993

The pattern further.....

Appendix I: Equations and Figures

Figures

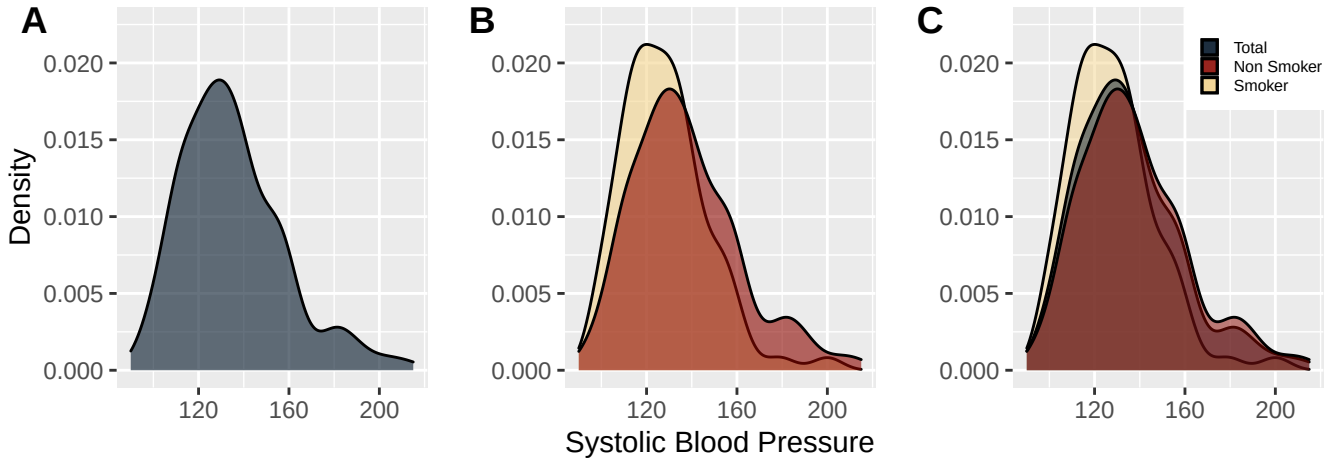


Figure 1: Data plots

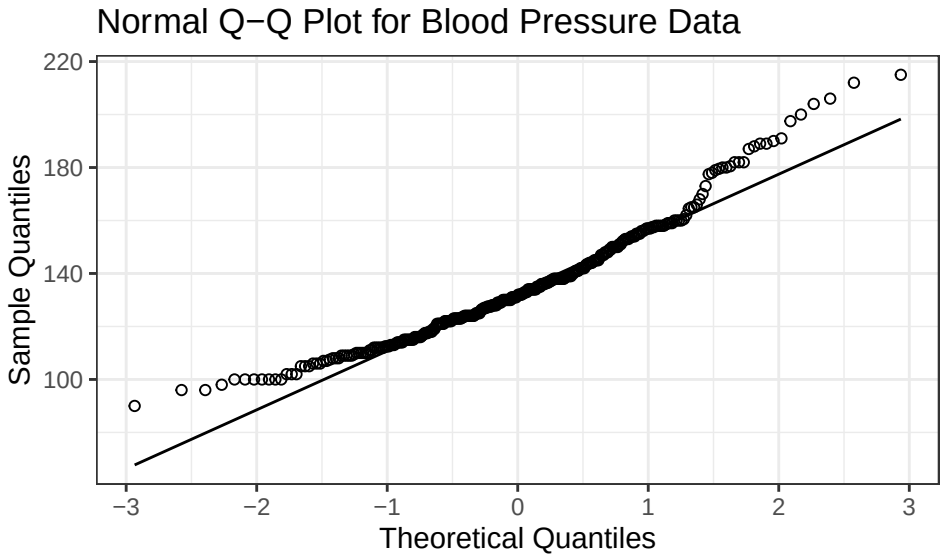


Figure 2: Q-Q Plot

Equations:

Equation 1: Pooled Sample Variance:

$$S_p^2 = \frac{(n_1 - 1)S_1^2 + (n_2 - 1)S_2^2}{n_1 + n_2 - 2}$$

Equation 2: Observed T Statistic (pooled variance):

$$t_{obs} = \frac{\mu_1 - \mu_2}{S_p\sqrt{\frac{1}{n_1} + \frac{1}{n_2}}}$$

Equation 3: Observed T Statistic (distinct variance):

$$t_{obs} = \frac{\mu_1 - \mu_2}{\sqrt{\frac{S_1^2}{n_1} + \frac{S_2^2}{n_2}}}$$

Equation 4: Satterthwaite Approximation:

$$\nu = \frac{\left(\frac{S_1^2}{n_1} + \frac{S_2^2}{n_2}\right)^2}{\frac{\left(\frac{S_1^2}{n_1}\right)^2}{n_1 - 1} + \frac{\left(\frac{S_2^2}{n_2}\right)^2}{n_2 - 1}}$$

Appendix II: Part I Results

	Attribute Value
Data Mean	134.935000
Data Sample Variance	524.085226
Smoker Mean	128.066667
Smoker Variance	352.211712
Nonsmoker Mean	137.224444
Nonsmoker Variance	562.144712
Difference in Mean	-9.157778
Pooled Sample Varance	510.013699
Weighted Pooled Sample Root Variance	3.011131
Weighted Nonpooled Sample Root Variance	9.993684
CI Pooled Lower	-15.080000
CI Pooled Upper	-3.230000
CI Nonpooled Lower	-15.400000
CI Nonpooled Upper	-2.910000

Appendix III: Part II Results

Test Case	μ_1	σ_1^2	n_1	μ_2	σ_2^2	n_2	Test Results Unpooled	Test Results Pooled	Difference in Mean
1	0	1	10	5	1	10	1000	1000	-5
2	4	1	10	5	1	10	578	562	-1
3	5	1	10	5	1	10	54	39	0
4	6	1	10	5	1	10	527	546	1
5	10	1	10	5	1	10	1000	1000	5
6	0	4	10	5	1	10	1000	1000	-5
7	4	4	10	5	1	10	268	259	-1
8	5	4	10	5	1	10	43	55	0
9	6	4	10	5	1	10	271	265	1
10	10	4	10	5	1	10	1000	1000	5
11	0	9	10	5	1	10	992	995	-5
12	4	9	10	5	1	10	126	156	-1
13	5	9	10	5	1	10	53	50	0
14	6	9	10	5	1	10	133	200	1
15	10	9	10	5	1	10	992	999	5
16	0	1	30	5	1	10	1000	1000	-5
17	4	1	30	5	1	10	723	776	-1
18	5	1	30	5	1	10	49	52	0
19	6	1	30	5	1	10	731	740	1
20	10	1	30	5	1	10	1000	1000	5
21	0	4	30	5	1	10	1000	1000	-5
22	4	4	30	5	1	10	523	260	-1
23	5	4	30	5	1	10	43	6	0
24	6	4	30	5	1	10	549	281	1
25	10	4	30	5	1	10	1000	1000	5
26	0	9	30	5	1	10	1000	1000	-5
27	4	9	30	5	1	10	338	82	-1
28	5	9	30	5	1	10	57	3	0
29	6	9	30	5	1	10	349	87	1
30	10	9	30	5	1	10	1000	1000	5
31	0	1	70	5	1	10	1000	1000	-5
32	4	1	70	5	1	10	784	812	-1
33	5	1	70	5	1	10	55	54	0
34	6	1	70	5	1	10	776	842	1
35	10	1	70	5	1	10	1000	1000	5
36	0	4	70	5	1	10	1000	1000	-5
37	4	4	70	5	1	10	648	242	-1
38	5	4	70	5	1	10	70	4	0
39	6	4	70	5	1	10	668	244	1
40	10	4	70	5	1	10	1000	1000	5
41	0	9	70	5	1	10	1000	1000	-5
42	4	9	70	5	1	10	526	29	-1
43	5	9	70	5	1	10	44	1	0
44	6	9	70	5	1	10	530	31	1
45	10	9	70	5	1	10	1000	1000	5
46	0	1	10	5	1	30	1000	1000	-5
47	4	1	10	5	1	30	728	734	-1
48	5	1	10	5	1	30	47	53	0
49	6	1	10	5	1	30	729	753	1
50	10	1	10	5	1	30	1000	1000	5
51	0	4	10	5	1	30	1000	1000	-5
52	4	4	10	5	1	30	301	534	-1
53	5	4	10	5	1	30	50	161	0

Test Case	μ_1	σ_1^2	n_1	μ_2	σ_2^2	n_2	Test Results Unpooled	Test Results Pooled	Difference in Mean
54	6	4	10	5	1	30	273	523	1
55	10	4	10	5	1	30	1000	1000	5
56	0	9	10	5	1	30	996	1000	-5
57	4	9	10	5	1	30	165	417	-1
58	5	9	10	5	1	30	53	203	0
59	6	9	10	5	1	30	158	404	1
60	10	9	10	5	1	30	995	1000	5
61	0	1	30	5	1	30	1000	1000	-5
62	4	1	30	5	1	30	967	968	-1
63	5	1	30	5	1	30	62	46	0
64	6	1	30	5	1	30	967	963	1
65	10	1	30	5	1	30	1000	1000	5
66	0	4	30	5	1	30	1000	1000	-5
67	4	4	30	5	1	30	655	696	-1
68	5	4	30	5	1	30	62	65	0
69	6	4	30	5	1	30	680	665	1
70	10	4	30	5	1	30	1000	1000	5
71	0	9	30	5	1	30	1000	1000	-5
72	4	9	30	5	1	30	391	383	-1
73	5	9	30	5	1	30	54	56	0
74	6	9	30	5	1	30	374	397	1
75	10	9	30	5	1	30	1000	1000	5
76	0	1	70	5	1	30	1000	1000	-5
77	4	1	70	5	1	30	997	997	-1
78	5	1	70	5	1	30	45	42	0
79	6	1	70	5	1	30	997	994	1
80	10	1	70	5	1	30	1000	1000	5
81	0	4	70	5	1	30	1000	1000	-5
82	4	4	70	5	1	30	902	763	-1
83	5	4	70	5	1	30	48	8	0
84	6	4	70	5	1	30	910	764	1
85	10	4	70	5	1	30	1000	1000	5
86	0	9	70	5	1	30	1000	1000	-5
87	4	9	70	5	1	30	700	396	-1
88	5	9	70	5	1	30	46	7	0
89	6	9	70	5	1	30	681	422	1
90	10	9	70	5	1	30	1000	1000	5
91	0	1	10	5	1	70	1000	1000	-5
92	4	1	10	5	1	70	788	825	-1
93	5	1	10	5	1	70	52	47	0
94	6	1	10	5	1	70	756	838	1
95	10	1	10	5	1	70	1000	1000	5
96	0	4	10	5	1	70	1000	1000	-5
97	4	4	10	5	1	70	285	628	-1
98	5	4	10	5	1	70	57	242	0
99	6	4	10	5	1	70	297	623	1
100	10	4	10	5	1	70	1000	1000	5
101	0	9	10	5	1	70	996	1000	-5
102	4	9	10	5	1	70	163	544	-1
103	5	9	10	5	1	70	60	323	0
104	6	9	10	5	1	70	160	544	1
105	10	9	10	5	1	70	992	1000	5
106	0	1	30	5	1	70	1000	1000	-5
107	4	1	30	5	1	70	992	993	-1
108	5	1	30	5	1	70	40	47	0
109	6	1	30	5	1	70	995	991	1

Test Case	μ_1	σ_1^2	n_1	μ_2	σ_2^2	n_2	Test Results Unpooled	Test Results Pooled	Difference in Mean
110	10	1	30	5	1	70	1000	1000	5
111	0	4	30	5	1	70	1000	1000	-5
112	4	4	30	5	1	70	728	872	-1
113	5	4	30	5	1	70	45	121	0
114	6	4	30	5	1	70	714	872	1
115	10	4	30	5	1	70	1000	1000	5
116	0	9	30	5	1	70	1000	1000	-5
117	4	9	30	5	1	70	391	655	-1
118	5	9	30	5	1	70	60	186	0
119	6	9	30	5	1	70	423	639	1
120	10	9	30	5	1	70	1000	1000	5
121	0	1	70	5	1	70	1000	1000	-5
122	4	1	70	5	1	70	1000	1000	-1
123	5	1	70	5	1	70	58	45	0
124	6	1	70	5	1	70	999	1000	1
125	10	1	70	5	1	70	1000	1000	5
126	0	4	70	5	1	70	1000	1000	-5
127	4	4	70	5	1	70	958	969	-1
128	5	4	70	5	1	70	45	53	0
129	6	4	70	5	1	70	951	948	1
130	10	4	70	5	1	70	1000	1000	5
131	0	9	70	5	1	70	1000	1000	-5
132	4	9	70	5	1	70	742	738	-1
133	5	9	70	5	1	70	50	57	0
134	6	9	70	5	1	70	760	732	1
135	10	9	70	5	1	70	1000	1000	5

Appendix IV: Code

```
knitr::opts_chunk$set(echo = TRUE)

#Use required packages
library(tidyverse) #for plots and data manipulation
library(cowplot) #aligning plots
library(gridExtra)
library(scales)

df_data <- read_csv("framingham_data.csv") # Read in data
df_data$index <- seq(nrow(df_data)) # Add an index column

#df_data %>% summary # Summarize Data

# Split data into smoker and nonsmoker
df_smoker <- df_data %>% filter(currentSmoker == 1)
df_nonsmoker <- df_data %>% filter(currentSmoker == 0)

#Create a sample variance function to ensure proper calculation
sample_variance <- function(x, sampling = TRUE){
    if (sampling == TRUE){
        sum((x - mean(x))^2) / (length(x) - 1)
    } else if(sampling == FALSE) {
        sum((x - mean(x))^2) / (length(x))
    }
}
#Create pooled sample variance function
f_pooled_variance <- function(x, y){
    ((length(x) - 1) * sample_variance(x) +
     (length(y) - 1) * sample_variance(y)) /
    (length(x) + length(y) - 2)
}

# Skewness function
skew_function <- function(x){
    mean((x - mean(x))^3) / sqrt(sample_variance(x))^3
}

# kurtosis function
kurt_function <- function(x){
    mean((x - mean(x))^4) / sqrt(sample_variance(x))^4
}

# Create a Satterthawaite Approximation Function

satterth <- function(s1, s2, n1, n2){
    term1 <- s1/n1
    term2 <- s2/n2
    nu <- (term1 + term2)^2 / ((term1^2/(n1 - 1)) + (term2^2/(n2 - 1)))
    return(floor(nu))
}


#Plot and compare split data

#options(repr.plot.width = 6, repr.plot.height = 4, repr.plot.res = 150)
```

```r
plot_colors <- c("#001427","#708d81","#f4d58d","#bf0603","#8d0801")
y_limits <- c(0, 0.0225)

total_data <- ggplot(df_data) + geom_density(aes(sysBP),
                                             fill = plot_colors[1],
                                             alpha = 0.6) +
                        ylim(y_limits) + ylab("Density") + xlab("")

sep_data <- ggplot() + geom_density(data = df_smoker, aes(sysBP),
                                    fill = plot_colors[3], alpha = 0.6) +
                       geom_density(data = df_nonsmoker, aes(sysBP),
                                    fill = plot_colors[5], alpha = 0.6) +
                       ylim(y_limits) + ylab("") + xlab("Systolic Blood Pressure")

plot_3 <- ggplot() + geom_density(data = df_smoker, aes(sysBP,
                                    fill = plot_colors[3]), alpha = 0.5) +
                       geom_density(data = df_data, aes(sysBP,
                                    fill = plot_colors[1]), alpha = 0.5) +
                       geom_density(data = df_nonsmoker, aes(sysBP,
                                    fill = plot_colors[5]), alpha = 0.5) +
                       ylim(y_limits) + ylab("") + xlab("") +
                       scale_fill_manual("",
                                         values = plot_colors[c(1, 5, 3)],
                                         labels = c("Total", "Non Smoker", "Smoker")) +
                       theme(legend.position = c(0.8, 0.9),
                             legend.text = element_text(size = 6),
                             legend.key.height = unit(0.25, 'cm'),
                             legend.key.width = unit(0.25, 'cm'))

#plot_grid(total_data, sep_data, plot_3, align = 'vh',
          #hjust = -1,nrow = 2, ncol = 2)

data_kurtosis <- kurt_function(df_data$sysBP)
data_skew <- skew_function(df_data$sysBP)
data_IQR <- as.numeric(quantile(df_data$sysBP, probs = 0.75)) -
       as.numeric(quantile(df_data$sysBP, probs = 0.25))
data_MAD <- median(abs(df_data$sysBP - median(df_data$sysBP)))
data_samVar <- sample_variance(df_data$sysBP)

eIQR <- data_IQR / 1.35
eMAD <- data_MAD / 0.675

# Q-Q Plot

data_qqplot <-
ggplot(df_data, aes(sample = sysBP)) +
stat_qq(shape = 1) + stat_qq_line() +
ggtitle("Normal Q-Q Plot for Blood Pressure Data") +
xlab("Theoretical Quantiles") +
ylab("Sample Quantiles")

# Common values for analysis

alpha <- 0.05

mu_smoker <- mean(df_smoker$sysBP)
var_smoker <- sample_variance(df_smoker$sysBP)
```

```r
n_smoker <- length(df_smoker$sysBP)

mu_nonsmoker <- mean(df_nonsmoker$sysBP)
var_nonsmoker <- sample_variance(df_nonsmoker$sysBP)
n_nonsmoker <- length(df_nonsmoker$sysBP)

# Two Sample T-test - Pooled Sample Variance - P-value

dof_1 <- (n_smoker + n_nonsmoker - 2)

p_sample_var_1 <- f_pooled_variance(df_smoker$sysBP,
                                    df_nonsmoker$sysBP)
p_sample_var_w <- sqrt(p_sample_var_1/n_smoker + p_sample_var_1/n_nonsmoker)

t_obs_1 <- (mu_smoker - mu_nonsmoker) / (p_sample_var_w )

t_stat_1 <- qt(alpha / 2, dof_1)

p_value_obs_1 <- dt(t_obs_1, dof_1)

#Two Sample T-test - Difference Variance Sample Variance - P-value

dof_2 <- satterth(var_smoker, var_nonsmoker, n_smoker, n_nonsmoker)

np_sample_var_2 <- (var_nonsmoker/n_smoker + var_nonsmoker/n_nonsmoker)

t_obs_2 <- (mu_smoker - mu_nonsmoker) / (sqrt(var_nonsmoker/n_smoker + var_nonsmoker/n_nonsmoker))

t_stat_2 <- qt(alpha / 2, dof_2)

p_value_obs_2 <- dt(t_obs_2, dof_2)

# Confidence Limits

diff_mu <- mu_smoker - mu_nonsmoker

#Pooled Sample variance

CL_pooled <- t_stat_1 * p_sample_var_w

#Non pooled Sample variance

CL_nonpooled <- t_stat_2 * (sqrt(var_nonsmoker/n_smoker + var_nonsmoker/n_nonsmoker))

CI_pooled <- round(c(diff_mu + CL_pooled, diff_mu - CL_pooled), 2)

CI_nonpooled <-round(c(diff_mu + CL_nonpooled, diff_mu - CL_nonpooled), 2)

#Power Calculation assuming delta means is the true delta

cv_lo_p <- qnorm(alpha / 2, 0, sqrt(p_sample_var_1/n_smoker +
                                      p_sample_var_1/n_nonsmoker))
cv_hi_p <- qnorm(1 - alpha / 2, 0, sqrt(p_sample_var_1/n_smoker +
                                        p_sample_var_1/n_nonsmoker))

power1 <- pnorm(cv_lo_p, (mu_smoker - mu_nonsmoker),
                sqrt(p_sample_var_1/n_smoker + p_sample_var_1/n_nonsmoker))
power2 <- 1 - pnorm(cv_hi_p, (mu_smoker - mu_nonsmoker),
```

```
                    sqrt(p_sample_var_1/n_smoker + p_sample_var_1/n_nonsmoker))

power_pooled <- sum(power1, power2)

cv_lo_non <- qnorm(alpha / 2, 0,
                (sqrt(var_nonsmoker/n_smoker + var_nonsmoker/n_nonsmoker)))
cv_hi_non <- qnorm(1 - alpha / 2, 0,
                (sqrt(var_nonsmoker/n_smoker + var_nonsmoker/n_nonsmoker)))

power1 <- pnorm(cv_lo_non, (mu_smoker - mu_nonsmoker),
                 (sqrt(var_nonsmoker/n_smoker + var_nonsmoker/n_nonsmoker)))
power2 <- 1 - pnorm(cv_hi_non, (mu_smoker - mu_nonsmoker),
                    (sqrt(var_nonsmoker/n_smoker + var_nonsmoker/n_nonsmoker)))

power_nonpooled <- sum(power1, power2)


#Part II
#Introduction

#options(repr.plot.width = 12, repr.plot.height = 3, repr.plot.res = 150)
set.seed(100)

null_mean <- 3
alt_means <- c(0, 3, 5)
plot_list <- list()

#plot_colors <- c("#072ac8","#1e96fc","#a2d6f9","#fcf300","#ffc600")

for(i in 1:length(alt_means)){

    sim1 <- rnorm(5000, null_mean, sqrt(1))
    sim2 <- rnorm(5000, alt_means[i], sqrt(1))

    alpha1 <- qnorm(0.025, null_mean, sqrt(1))
    alpha2 <- qnorm(0.975, null_mean, sqrt(1))

    df_set <- tibble("H0" = sim1, "HA" = sim2)

    title_string <- sprintf("Difference in Means %i", (alt_means[i] - null_mean))

    plot_list[[i]]  <-
    ggplot(data = df_set) + geom_density(aes(H0), alpha = 0.5, fill = plot_colors[5]) +
                            geom_area(
                                aes(x = stage(H0, after_scale = oob_censor(x, c(-Inf, alpha1)
                                                                           )
                                              )
                                   ),
                                stat = "density", fill = plot_colors[1]
                                 ) +
                            geom_area(
                                aes(x = stage(H0, after_scale = oob_censor(x, c(alpha2, Inf)
                                                                           )
                                              )
                                   ),
                                stat = "density", fill = plot_colors[1]
                                     ) +
                            geom_density(aes(HA), alpha = 0.5) +
```

```
                            geom_area(
                                aes(x = stage(HA, after_scale = oob_censor(x, c(alpha1, alpha2)
                                                                           )
                                              )
                                   ),
                                stat = "density", fill = plot_colors[2], alpha = 0.5
                                    ) +
                            xlim(-2, 8) + xlab("") + ylab("") + ggtitle(title_string) +
                            theme(text = element_text(size = 8))

                                }

do.call(grid.arrange, c(plot_list, ncol = 3, heights = 0.5))
#Part II
set.seed(1)

alpha <- 0.05

test_function <- function (x, y, pooled = FALSE){

    mu_1 <- mean(x)
    var_1 <- sample_variance(x, sampling = TRUE)

    mu_2 <- mean(y)
    var_2 <- sample_variance(y, sampling = TRUE)

    #Calculate the pooled sample variance
    pooled_sample <- ((length(x) - 1) * var_1 +
                          (length(y) - 1) * var_2) / (length(x) + length(y) - 2)

    #calculate the observed t statistic
    if (pooled == TRUE){

        cal_sigma <- (sqrt(pooled_sample/length(x) + pooled_sample/length(y)))

        ttest <- (mu_1 - mu_2) / cal_sigma
        dof <- length(x) + length(y) - 2 #Determine degrees of freedom

        } else {

        cal_sigma <- (sqrt(var_1/length(x) + var_2/length(y)))

        ttest <- (mu_1 - mu_2) / cal_sigma
        dof <- satterth(var_1, var_2, length(x), length(y))
    }

    # Determine whether or not the null hypothesis
    # can be rejected (1 = rejected, 0 = not rejected)
    verdict <- !between(ttest, qt(alpha / 2, dof), qt(1 - alpha / 2, dof))

    #Power calculation assuming calculated difference in means is Ha
    cv_lo <- qnorm(alpha / 2, 0, cal_sigma)
    cv_hi <- qnorm(1 - alpha / 2, 0, cal_sigma)

    power1 <- pnorm(cv_lo, (mu_1 - mu_2), cal_sigma)
    power2 <- 1 - pnorm(cv_hi, (mu_1 - mu_2), cal_sigma)

    power <- sum(power1, power2)
```

```
    #Return calculated values
    return(c(mu_1, var_1, mu_2, var_2, ttest, cal_sigma, dof, verdict, power))
}



mu1 <- c(0, 4, 5, 6, 10)
var1 <- c(1, 4, 9)
n1 <- c(10, 30, 70)

mu2 <- 5
var2 <- 1
n2 <- c(10, 30, 70)

sim_test <- function(x_mu, x_var, x_n, y_mu, y_var, y_n, pooled){

    sim_data_results <- matrix(rep(0, 9), ncol = 9)

    for (i in 1:1000){

        sim_set1 <- rnorm(x_n, x_mu, sqrt(x_var))
        sim_set2 <- rnorm(y_n, y_mu, sqrt(y_var))

        sim_data_results <- rbind(sim_data_results,
                                  test_function(sim_set1, sim_set2, pooled))

        #print(sim_data_results)
    }

    df_sim_data <- data.frame(sim_data_results[2 : nrow(sim_data_results),])
    colnames(df_sim_data) = c("Null Mean", "Null Variance", "Alternate Mean",
                              "Alternate Variance", "T statistic",
                              "Calculated Variance", "DoF", "Null Reject",
                              "Power")
    return(df_sim_data)
}

# HA: mean = 5, var = 1
df_combo <- expand.grid(mu1, var1, n1, mu2, var2, n2)
df_combo2 <- tibble(cbind(1:nrow(df_combo), df_combo,
                          matrix(rep(0, 2 * nrow(df_combo)), ncol = 2)))
colnames(df_combo2) <- c("Test_Case", "mu1", "var1", "n1", "mu2", "var2",
                         "n2", "Test_Results_up", "Test_Results_po")

test_results <- list()
test_results2 <- list()

for (i in 1:nrow(df_combo)){
    test_results[[i]] <- do.call(sim_test,
                                 as.list(as.numeric(c(df_combo[i,],
                                                      pooled = FALSE))))
    test_results2[[i]] <- do.call(sim_test,
                                  as.list(as.numeric(c(df_combo[i,],
                                                       pooled = TRUE))))
    df_combo2[i, 8] <- sum(as.data.frame(test_results[i])[,8])
    df_combo2[i, 9] <- sum(as.data.frame(test_results2[i])[,8])
    }
```

```
df_combo2 <- df_combo2 %>% mutate(diff = mu1 - mu2)
#df_combo2 %>%  head()

pow_tab_9 <- test_results[[9]] %>% pull(Power) %>% summary() %>% unname() %>% matrix(ncol = 1)
pow_tab_129 <- test_results[[129]] %>% pull(Power) %>% summary() %>% unname() %>% matrix(ncol = 1)

d <- cbind(pow_tab_9, pow_tab_129)

colnames(d) = c("Test Case #9","Test Case #129")
rownames(d) = c("Min", "1st Quantile", "Median", "Mean", "3rd Quantile", "Max")

knitr::kable(d)

# Plotting
options(repr.plot.width = 6, repr.plot.height = 4, repr.plot.res = 150)

plot_grid(total_data, sep_data, plot_3, align = 'vh',
          hjust = -1,nrow = 1, ncol = 3, labels = c("A", "B", "C"))
data_qqplot + theme_bw()
d1 <- matrix(c(mean(df_data$sysBP), sample_variance(df_data$sysBP),
               mu_smoker, var_smoker,
               mu_nonsmoker, var_nonsmoker,
               diff_mu, p_sample_var_1, p_sample_var_w,
               np_sample_var_2, CI_pooled, CI_nonpooled), ncol = 1)


rownames(d1) <- c("Data Mean", "Data Sample Variance", "Smoker Mean",
                  "Smoker Variance",
                  "Nonsmoker Mean", "Nonsmoker Variance",
                  "Difference in Mean", "Pooled Sample Varance",
                  "Weighted Pooled Sample Root Variance",
                  "Weighted Nonpooled Sample Root Variance",
                  "CI Pooled Lower", "CI Pooled Upper",
                  "CI Nonpooled Lower", "CI Nonpooled Upper")

d1 %>% knitr::kable(col.names = c("Attribute Value"))
knitr::kable(df_combo2, col.names = c("Test Case",
                                      "$\\mu_1$",
                                      "$\\sigma_1^2$",
                                      "$n_1$",
                                      "$\\mu_2$",
                                      "$\\sigma_2^2$",
                                      "$n_2$",
                                      "Test Results Unpooled",
                                      "Test Results Pooled",
                                      "Difference in Mean"),
             escape = FALSE)
```