Name: Parth Pareek
UNI: PP2547
Date: 2/17/2016
Assignment: HW3

1. A single sample t test is run on the ratio of post-treatment over pre-treatment data
   p-value: 0.0001
   95% CI: 5.5984 to 12.8476
   Estimated value: 9.2230

   A single sample t-test is run on the ratio of post-treatment over pre-treatment data after a logarithmic transformation
   p-value: 3.8e-07
   95% CI: 4.76075 11.42625
   Estimated value: 7.3755

   Lastly, a Wilcoxon signed rank test was also run on the data
   p-value: 0.0002
   CI is computed by running a sequence from 3 to 14 (approximated from previous CIs)
   95% CI: 4.67 to 12.56

   There is no information on how the subjects were allotted to groups, so there is a high probability of confounding variables creeping in.

2. A single sample Wilcoxon sign test is run on the difference of vomiting incidence in Placebo vs. Marijuana data sets.
   P-value = 0.001
   CI is calculated by approximating the additive factor by trial and error method
   95% CI: 9.01 to 54.5
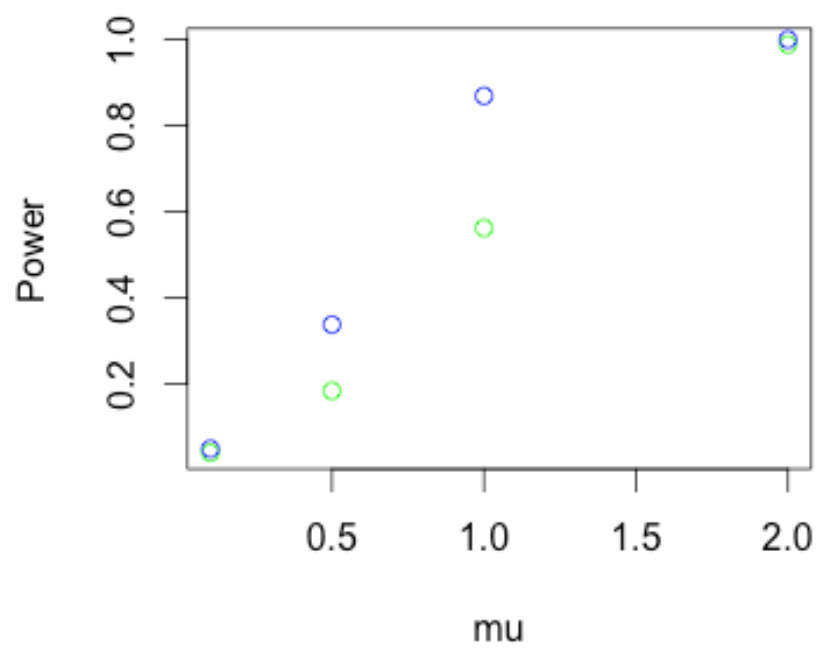
3. On paper

4. Power = 0.4105232

5. On paper

6.

   n = 10

mu	0.1	0.5	1	2
power	0.04023588	0.18383753	0.56198462	0.98817899

   n = 20

mu	0.1	0.5	1	2
power	0.04930484	0.33770837	0.86895280	0.99998657

7.

Histogram of p-values
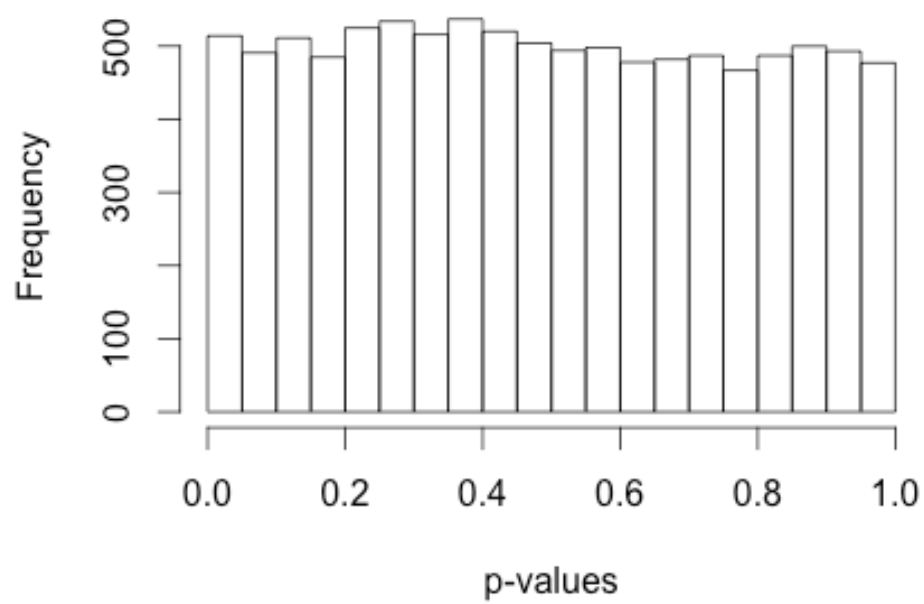
CODES

```
#Question1
library(Sleuth3)
attach(ex0430)
data <- ex0430
multiplier <- data$Sunscreen/data$PreTreatment
t.test(multiplier)

exp(t.test(log(data$Sunscreen)-log(data$PreTreatment))$conf.int)
exp(t.test(log(data$Sunscreen)-log(data$PreTreatment))$estimate)

wilcox.test(log(data$Sunscreen),log(data$PreTreatment),paired = TRUE,
conf.int = TRUE)
wilcox.test(log(data$Sunscreen)-log(data$PreTreatment))$p.value
CI <- vector(mode = "numeric", length = 0)
for (i in seq(3,14,length.out=100)){
  if (wilcox.test(log(data$Sunscreen/i),log(data$PreTreatment),paired =
TRUE)$p.value > 0.05){
    CI <- c(i,CI)
  }
}

min(CI)
max(CI)


#Question2
library(Sleuth3)
attach(ex0432)
data <- ex0432

wilcox.test(data$Placebo - data$Marijuana, conf.int = TRUE)

CI <- vector(mode = "numeric", length = 0)
for (i in seq(1,100,length.out = 10000)){
  if((wilcox.test(data$Placebo - data$Marijuana - i)$p.value) > 0.05){
    CI <- c(i,CI)
  }
}

min(CI)
max(CI)


#Question4
library(pwr)
pwr.t2n.test(n1=35, n2=24, d=0.01/0.0214, sig.level = 0.05)


#Question6
mu = c(0.1, 0.5, 1, 2)
power10 <- power.t.test(n=10, delta = mu, sd = 1, sig.level = 0.05, type =
"two.sample", alternative = "two.sided")
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```
power10
power20 <- power.t.test(n=20, delta = mu, sd = 1, sig.level = 0.05, type =
"two.sample", alternative = "two.sided")
power20
plot(mu,power10$power,col="green", ylab = "Power")
points(mu,power20$power, col="blue")


#Question7
pval <- vector(mode = "numeric", length = 0)

for(i in 1:10000){
  a <- rnorm(100, mean = 0, sd = 1)
  pval[i] <- t.test(a)$p.value
}
hist(pval, xlab = "p-values", main = "Histogram of p-values")
```