

Alex_Williams_A1

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2.

a)

I chose to add each datapoint one at a time to hopefully reduce errors when inputting values

```
plants<-data.frame(Growth = c(14.6),
                    Plot    = c(1),
                    Pot     = c(1),
                    Treatment = c(1))

# plot 1, treatment 1
plants<-rbind(plants, list(15.2, 1, 1, 1))
plants<-rbind(plants, list(13.2, 1, 2, 1))
plants<-rbind(plants, list(12.9, 1, 2, 1))
plants<-rbind(plants, list(16.4, 1, 3, 1))
plants<-rbind(plants, list(12.2, 1, 3, 1))

# plot 2, treatment 1
plants<-rbind(plants, list(18.5, 2, 1, 1))
plants<-rbind(plants, list(16.7, 2, 1, 1))
plants<-rbind(plants, list(22.2, 2, 2, 1))
plants<-rbind(plants, list(18.8, 2, 2, 1))
plants<-rbind(plants, list(24.7, 2, 3, 1))
plants<-rbind(plants, list(20.3, 2, 3, 1))

# plot 1, treatment 2
plants<-rbind(plants, list(7.1, 1, 1, 2))
plants<-rbind(plants, list(7.7, 1, 1, 2))
plants<-rbind(plants, list(6.8, 1, 2, 2))
plants<-rbind(plants, list(6.0, 1, 2, 2))
plants<-rbind(plants, list(10.0, 1, 3, 2))
plants<-rbind(plants, list(8.3, 1, 3, 2))

# plot 2, treatment 2
plants<-rbind(plants, list(9.7, 2, 1, 2))
plants<-rbind(plants, list(8.8, 2, 1, 2))
plants<-rbind(plants, list(6.8, 2, 2, 2))
plants<-rbind(plants, list(9.0, 2, 2, 2))
plants<-rbind(plants, list(10.4, 2, 3, 2))
plants<-rbind(plants, list(11.3, 2, 3, 2))

plants
```

```
##      Growth Plot Pot Treatment
```

## 1	14.6	1	1	1
## 2	15.2	1	1	1
## 3	13.2	1	2	1
## 4	12.9	1	2	1
## 5	16.4	1	3	1
## 6	12.2	1	3	1
## 7	18.5	2	1	1
## 8	16.7	2	1	1
## 9	22.2	2	2	1
## 10	18.8	2	2	1
## 11	24.7	2	3	1
## 12	20.3	2	3	1
## 13	7.1	1	1	2
## 14	7.7	1	1	2
## 15	6.8	1	2	2
## 16	6.0	1	2	2
## 17	10.0	1	3	2
## 18	8.3	1	3	2
## 19	9.7	2	1	2
## 20	8.8	2	1	2
## 21	6.8	2	2	2
## 22	9.0	2	2	2
## 23	10.4	2	3	2
## 24	11.3	2	3	2

b)

```
plants <- plants[order(plants$Growth),]
plants
```

##	Growth	Plot	Pot	Treatment
## 16	6.0	1	2	2
## 15	6.8	1	2	2
## 21	6.8	2	2	2
## 13	7.1	1	1	2
## 14	7.7	1	1	2
## 18	8.3	1	3	2
## 20	8.8	2	1	2
## 22	9.0	2	2	2
## 19	9.7	2	1	2
## 17	10.0	1	3	2
## 23	10.4	2	3	2
## 24	11.3	2	3	2
## 6	12.2	1	3	1
## 4	12.9	1	2	1
## 3	13.2	1	2	1
## 1	14.6	1	1	1
## 2	15.2	1	1	1
## 5	16.4	1	3	1
## 8	16.7	2	1	1
## 7	18.5	2	1	1
## 10	18.8	2	2	1
## 12	20.3	2	3	1
## 9	22.2	2	2	1

```
## 11    24.7    2    3          1
```

c)

```
attach(plants)
mean <- sum(Growth) / length(Growth)
mean
```

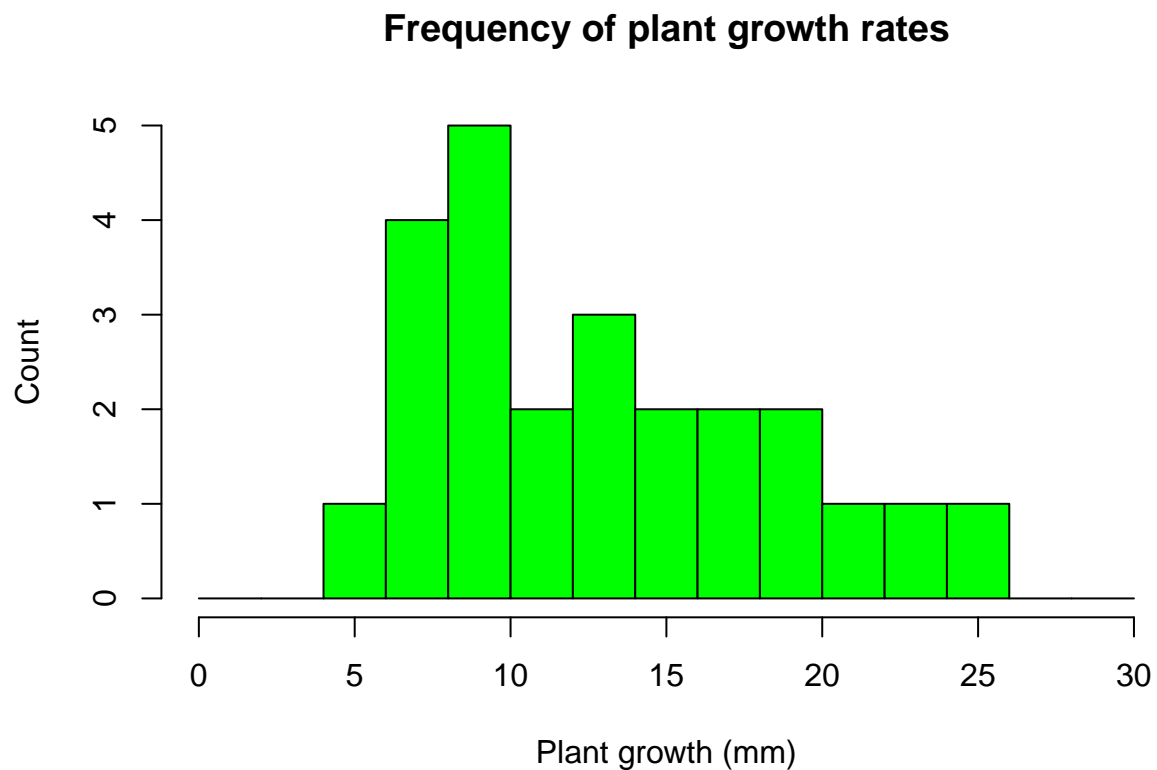
```
## [1] 12.81667
```

```
sd<- sd(Growth)
sd
```

```
## [1] 5.296813
```

d)

```
hist(Growth,
     breaks = seq(from=0, to=30, by=2),
     main = "Frequency of plant growth rates",
     xlab = "Plant growth (mm)",
     ylab = "Count",
     col = 'green')
```



```
detach(plants)
```

3.

```
get.variance<-function(y)
{
  mean = sum(y) / length(y)
  sample.var<- (sum(y^2) - (length(y) * mean^2)) / (length(y) - 1)
  sample.var
}
y<-c(11,11,10,8,11,3,15,11,7,6)
get.variance(y)
```

```
## [1] 11.34444
```

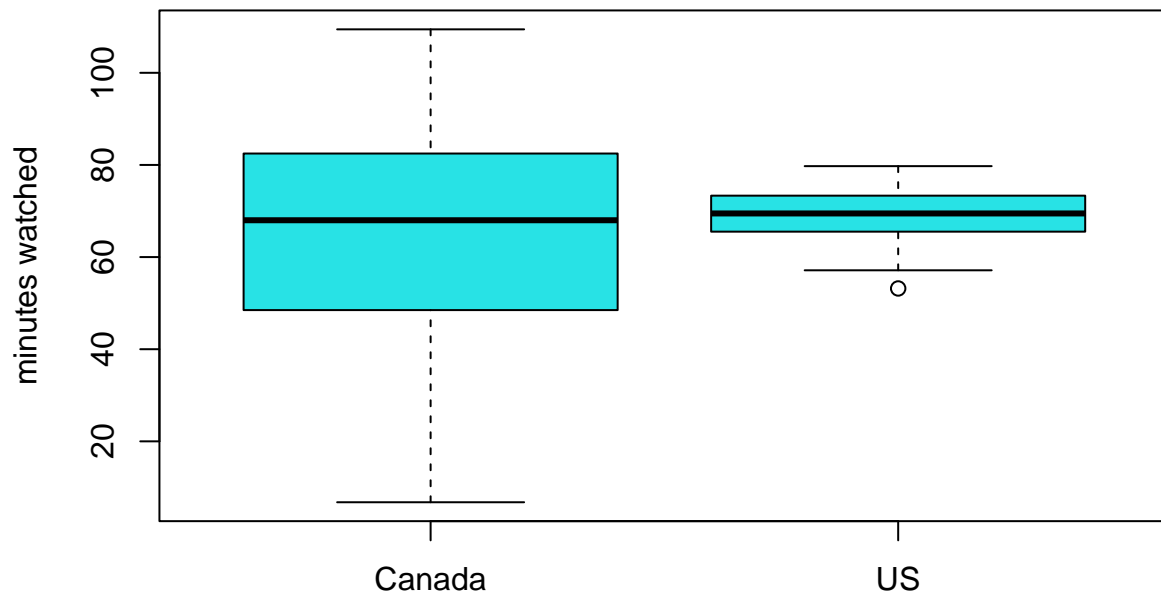
4.

a)

```
tv<-read.table(file="~/Documents/uni/STAT359/data/tv.txt",
               sep=" ",
               header=TRUE)
attach(tv)
Canada<-Canada[!is.na(Canada)]
US<-US[!is.na(US)]

boxplot(Canada, US,
        names=c("Canada", "US"),
        ylab="minutes watched",
        main="TV Watching Time",
        col=5)
```

TV Watching Time



```
summary(tv)
```

```
##      Canada      US
## Min.   : 6.781  Min.   :53.19
## 1st Qu.: 48.667 1st Qu.:65.58
## Median : 67.995 Median :69.47
## Mean   : 64.313 Mean   :69.33
## 3rd Qu.: 82.340 3rd Qu.:73.21
## Max.   :109.433 Max.   :79.74
## NA's   :10
```

The mean values for Canada and US watch times are similar, though Canada's is slightly lower. Canada's watching time also appears to have a significantly larger sample variance than the US

c)

```
z.test<-function(y1, y2, H1)
{
  est<- mean(y1) - mean(y2)
  param <- 0 # since H0: mu1 - mu2 = 0
  t.obs <- (est - param) / (sqrt((var(y1) / length(y1)) + (var(y2) / length(y2))))
  if(H1=='less')
  {
    return.val <- pnorm(t.obs)
  }
  else if(H1 == 'greater')
  {
    return.val <- 1 - pnorm(t.obs)
  }
}
```

```

    return.val <- 1-pnorm(t.obs)
  }
  else if (H1 == 'two.sided')
  {
    return.val <- 2 * (1 - pnorm(abs(t.obs)))
  }
  return.val
}

```

c)

```

pval.less <- z.test(Canada, US, 'less')
pval.less

## [1] 0.02208637

pval.greater <- z.test(Canada, US, 'greater')
pval.greater

## [1] 0.9779136

pval.ts <- z.test(Canada, US, 'two.sided')
pval.ts

## [1] 0.04417275

```

d)

Since the goal of the study was to see if Canadian teenagers watched less TV than American teenagers, we use the alternative hypothesis $H_1 : \mu_{Canada} - \mu_{US} < 0$, calculated with `z.test(Canada, US, 'less')`. This returns a p-value of ~0.0221. This means that 2.21% of the time, if we were to run the experiment again, the result would be at least as extreme as this one, or the means would be at least this far apart.

We did not declare an alpha value before doing the experiment, so let us choose a standard value of $\alpha = 0.05$. since the p-value is less than alpha, we have evidence to reject the null hypothesis that Canadian and American teenagers watch the same amount of TV. Or, in other words, we have reason to believe that Canadian teenagers watch less TV than American teens.