Untitled

```
install.packages("UsingR",repos='http://cran.us.r-project.org')
```

```
##
## The downloaded binary packages are in
##  /var/folders/7s/hkmf91n17r16m10b11sp3_5c0000gn/T//RtmpSGfb5e/downloaded_packages
```

```
library(UsingR)
```

```
## Warning: package 'UsingR' was built under R version 4.1.2
```

```
## Loading required package: MASS
```

```
## Loading required package: HistData
```

```
## Loading required package: Hmisc
```

```
## Warning: package 'Hmisc' was built under R version 4.1.2
```

```
## Loading required package: lattice
```

```
## Loading required package: survival
```

```
## Loading required package: Formula
```

```
## Loading required package: ggplot2
```

```
##
## Attaching package: 'Hmisc'
```

```
## The following objects are masked from 'package:base':
##
##     format.pval, units
```

```
##
## Attaching package: 'UsingR'
```

```
## The following object is masked from 'package:survival':
##
##     cancer
```

```
mandms
```

```
##                    blue   brown   green  orange      red  yellow
## milk chocolate 10.0000 30.0000 10.0000 10.0000 20.0000 20.0000
## Peanut         20.0000 20.0000 10.0000 10.0000 20.0000 20.0000
## Peanut Butter  20.0000 20.0000 20.0000  0.0000 20.0000 20.0000
## Almond         16.6667 16.6667 16.6667 16.6667 16.6667 16.6667
## kid minis      16.6667 16.6667 16.6667 16.6667 16.6667 16.6667
```

A. Assumptions are cells are freequencies, data is independent, levels are mu7tually exclusive, And 2+ varaibles measured in categories. H0: Values for all colors are the same, HA: Values fo9rat least one color is different

```
Observed <- c(15,34,7,19,29,24)
expected = c(20,20,10,10,20,20)
Ch.square <- sum((Observed - expected)^2/expected)
Ch.square
```

```
## [1] 24.9
```

P = 24.9, so plugged into the applet with v = 12, x = 24.9, value is 0.00015<0.05. Not enough evidence to reject null, all are close enough to peanut.

C - H0: package and milk chocolate are same. HA: at least one is different

```
Observed <- c(15,34,7,19,29,24)
expected = c(10,30,10,10,20,20)
Ch.square <- sum((Observed - expected)^2/expected)
Ch.square
```

```
## [1] 16.88333
```

Value - 16.884, in calculator with pf = 5 = 0.00473<0.005, so fail to reject null. not enough evidence to prove at least one color is different.

D. p- value for milk chocolate *is closer* to 0.005, so i would *suspect* C is the *true source*.

PROBLEM 2

A. Null - male and female have the same distribution of voting . Alternative - at least one voting category is different between male and female

```
table = rbind(c(48,26,24),c(17,14,18))
chisq.test(table, correct = FALSE)
```

```
##
##  Pearson's Chi-squared test
##
## data:  table
## X-squared = 3.272, df = 2, p-value = 0.1948
```

P value = 0.1948>0.04, reject null. At least one category is different.

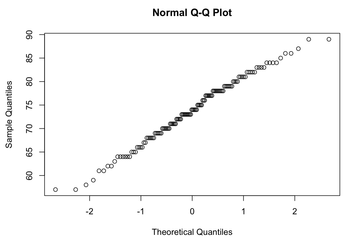
C. Assumptions are independent, at least two categorical variables. assumptions met.' ' PROBLEM 3

a. For F test needs independent and random. Is parametric test so also needs normal.

```
library(readxl)
```

```
## Warning: package 'readxl' was built under R version 4.1.2
```

```
BodyTemperature <- read_excel("/Users/ericzou/Downloads/BodyTemperature.xls")
qqnorm(BodyTemperature$`Heart Rate`)
```



yep looks good.

B. H0 - Male and female have same heart rate variance. HA: Male and female heart rate variance is different.

```
var.test(BodyTemperature$`Body Temp` ~ BodyTemperature$Gender, alternative = "two.sided")
```

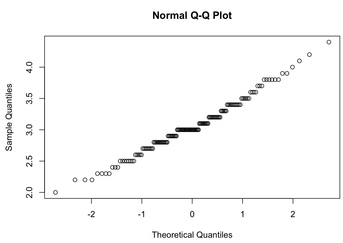
```
##
##  F test to compare two variances
##
## data:  BodyTemperature$`Body Temp` by BodyTemperature$Gender
## F = 1.1321, num df = 64, denom df = 64, p-value = 0.6211
## alternative hypothesis: true ratio of variances is not equal to 1
## 95 percent confidence interval:
##  0.6905408 1.8561126
## sample estimates:
## ratio of variances
##           1.132131
```

P = 0.6211>0.05, so reject null. not equal.

PROBLEM 4

a)Data needs to be quantitative, independent, and normally distributed.

```
iris <- read_excel("/Users/ericzou/Downloads/iris.xls")
qqnorm(iris$Sepal.Width)
```



yep looks good. pretty normal

b. Null: all species have same variance in sepial width Alternative: at least one species is not equal in variance of sepial width

```
install.packages('car',repos='http://cran.us.r-project.org')
```

```
##
## The downloaded binary packages are in
##  /var/folders/7s/hkmf91n17r16m10b11sp3_5c0000gn/T//RtmpSGfb5e/downloaded_packages
```

```
library(car)
```

```
## Warning: package 'car' was built under R version 4.1.2
```

```
## Loading required package: carData
```

```
## Warning: package 'carData' was built under R version 4.1.2
```

```
leveneTest(Sepal.Width~Species, iris)
```

```
## Warning in leveneTest.default(y = y, group = group, ...): group coerced to
## factor.
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value Pr(>F)
## group  2  0.5902 0.5555
##       147
```

P value = 0.5555>0.01, so reject null. At least one species has a variance not similar to the others.

PROBLEM 5

a. Appropriate test is use a chi square test test for association

b. Null is male and female have same distribution of mac/pc. Alternate is at least one (pc/mac) has different distributin between male and female.

```
table = rbind(c(66,40),c(30,87))
colnames(table) = c("PC","Mac")
rownames(table) = c("Male", "Female")
table
```

```
##        PC Mac
## Male   66  40
## Female 30  87
```

```
chisq.test(table, correct = FALSE)
```

```
##
##  Pearson's Chi-squared test
##
## data:  table
## X-squared = 30.425, df = 1, p-value = 3.47e-08
```

P - value very small. way smaller than 0.01. reject null, they are not equal.