

Project

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```
library(NHANES)
library(dplyr)
library(corrplot)
library(doBy)
library(table1)
library(knitr)
library(papeR)
library(stats)
library(tidyverse)
library(ggplot2)
library(corrplot)
SD_pop<-function(x,n){sqrt(sum( (x - mean(x) )^2)/(n))}
```

```
data(NHANES)
ls(NHANES)
```

```
## [1] "Age" "Age1stBaby" "AgeDecade" "AgeFirstMarij"
## [5] "AgeMonths" "AgeRegMarij" "Alcohol12PlusYr" "AlcoholDay"
## [9] "AlcoholYear" "BMI" "BMI_WHO" "BMICatUnder20yrs"
## [13] "BPDia1" "BPDia2" "BPDia3" "BPDiaAve"
## [17] "BPSys1" "BPSys2" "BPSys3" "BPSysAve"
## [21] "CompHrsDay" "CompHrsDayChild" "DaysMentHlthBad" "DaysPhysHlthBad"
## [25] "Depressed" "Diabetes" "DiabetesAge" "DirectChol"
## [29] "Education" "Gender" "HardDrugs" "HeadCirc"
## [33] "HealthGen" "Height" "HHIncome" "HHIncomeMid"
## [37] "HomeOwn" "HomeRooms" "ID" "Length"
## [41] "LittleInterest" "Marijuana" "MaritalStatus" "nBabies"
## [45] "nPregnancies" "PhysActive" "PhysActiveDays" "Poverty"
## [49] "PregnantNow" "Pulse" "Race1" "Race3"
## [53] "RegularMarij" "SameSex" "SexAge" "SexEver"
## [57] "SexNumPartnLife" "SexNumPartYear" "SexOrientation" "SleepHrsNight"
## [61] "SleepTrouble" "Smoke100" "Smoke100n" "SmokeAge"
## [65] "SmokeNow" "SurveyYr" "Testosterone" "TotChol"
## [69] "TVHrsDay" "TVHrsDayChild" "UrineFlow1" "UrineFlow2"
## [73] "UrineVol1" "UrineVol2" "Weight" "Work"
```

```
NHANES<-NHANES[!duplicated(NHANES$ID),]

df<-select(NHANES, ID, Gender, Age, BMI, HHIncomeMid, UrineFlow1)
df<-df[complete.cases(df),]
df<-df %>% filter(Age > 18)
```

```

for (i in 1:length(df$BMI))
{
  if (df$BMI[i]<18.5) {
    df$BMI_Factor[i]<-"Under Weight"
  }
  else if(df$BMI[i]>=18.5 & df$BMI[i]<25){
    df$BMI_Factor[i]<-"Normal"
  }
  else if(df$BMI[i]>=25 & df$BMI[i]<30){
    df$BMI_Factor[i]<-"Over Weight"
  }
  else if(df$BMI[i]>=30){
    df$BMI_Factor[i]<-"Obese"
  }
}

```

Warning: Unknown or uninitialised column: 'BMI_Factor'.

```

df$BMI_Factor<-factor(df$BMI_Factor,order=TRUE,
                      levels = c("Under Weight","Normal","Over Weight","Obese"))
df$Income_Factor <- cut(df$HHIncomeMid,breaks = c(min(df$HHIncomeMid)-1,22500,87500,max(df$HHIncomeMid)),
df$Income_Factor <-factor(df$Income_Factor,order=TRUE,levels=c("Low","Medium","High"))
summary(df$Income_Factor)

```

```

##      Low Medium   High
##    1039    2109    845

```

```

set.seed(25)
selection<-sample(df$ID[df$Age > 18],500)
df1<-data.frame("ID"=df$ID[df$ID %in% selection],
               "age"=df$Age[df$ID %in% selection],
               "Gender"=df$Gender[df$ID %in% selection],
               "BMI"=df$BMI[df$ID %in% selection],
               "BMI_Factor"=df$BMI_Factor[df$ID %in% selection],
               "Urine_Flow"=df$UrineFlow1[df$ID %in% selection],
               "Income"=df$HHIncomeMid[df$ID %in% selection],
               "Income_Factor"=df$Income_Factor[df$ID %in% selection])

```

The Summary Statistics of the Population:

```
kable(summarize(df))
```

	N	Mean	SD	Min	Q1	Median	Q3	Max
ID	3993	61678.99	5874.41	51630.00	56664.00	61575.00	66822.00	71915.00
Age	3993	46.79	17.53	19.00	32.00	45.00	60.00	80.00
BMI	3993	28.82	6.72	15.02	24.10	27.70	32.20	81.25
HHIncomeMid	3993	54256.82	32903.22	2500.00	22500.00	50000.00	87500.00	100000.00
UrineFlow1	3993	1.01	0.94	0.00	0.43	0.74	1.26	12.35

```
kable(summarize(df, type = "factor", cumulative=TRUE))
```

	Level	N	%	\sum %
Gender	female	2041	51.1	51.1
	male	1952	48.9	100.0
BMI_Factor	Under Weight	69	1.7	1.7
	Normal	1146	28.7	30.4
	Over Weight	1341	33.6	64.0
	Obese	1437	36.0	100.0
Income_Factor	Low	1039	26.0	26.0
	Medium	2109	52.8	78.8
	High	845	21.2	100.0

The Summary Statistics of the Sample:

```
kable(summarize(df1))
```

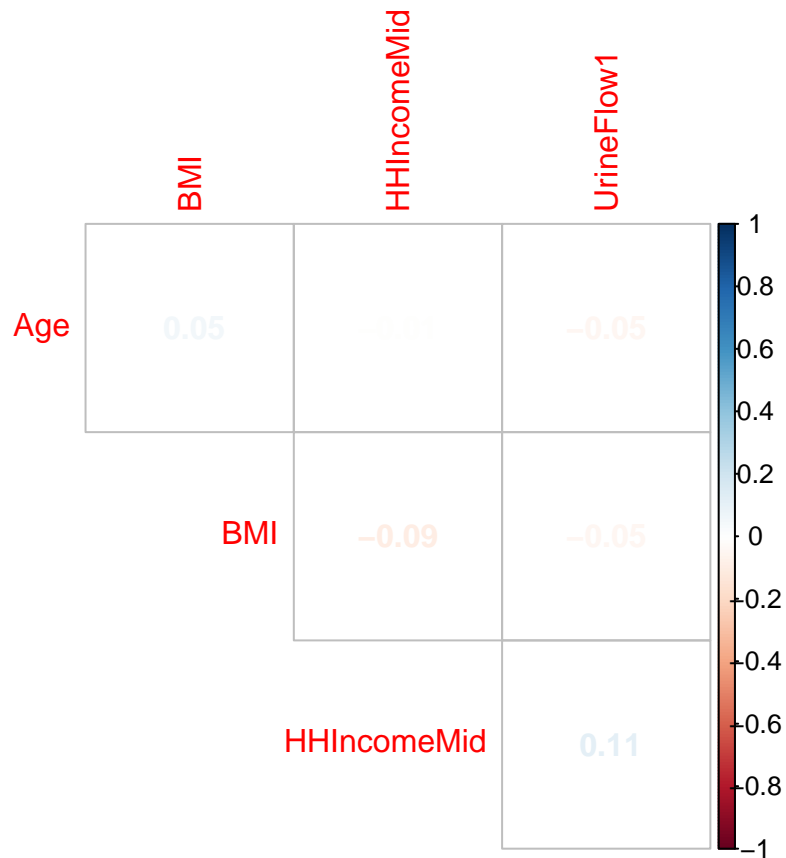
	N	Mean	SD	Min	Q1	Median	Q3	Max
ID	500	61760.50	5825.41	51654.00	56973.50	61526.50	66925.50	71875.00
age	500	46.98	17.36	19.00	33.00	46.00	61.00	80.00
BMI	500	29.20	7.12	15.97	24.27	28.44	32.80	81.25
Urine_Flow	500	1.04	1.10	0.00	0.45	0.72	1.23	12.35
Income	500	57515.00	33449.59	2500.00	30000.00	50000.00	100000.00	100000.00

```
kable(summarize(df1, type = "factor", cumulative=TRUE))
```

	Level	N	%	\sum %
Gender	female	253	50.6	50.6
	male	247	49.4	100.0
BMI_Factor	Under Weight	6	1.2	1.2
	Normal	146	29.2	30.4
	Over Weight	151	30.2	60.6
	Obese	197	39.4	100.0
Income_Factor	Low	116	23.2	23.2
	Medium	257	51.4	74.6
	High	127	25.4	100.0

```
## [1] -0.04621187
```

```
## [1] -0.09219838
```



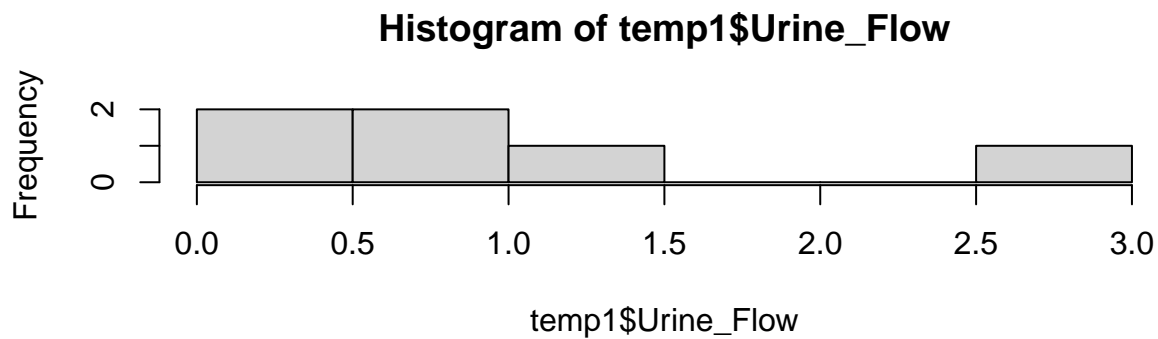
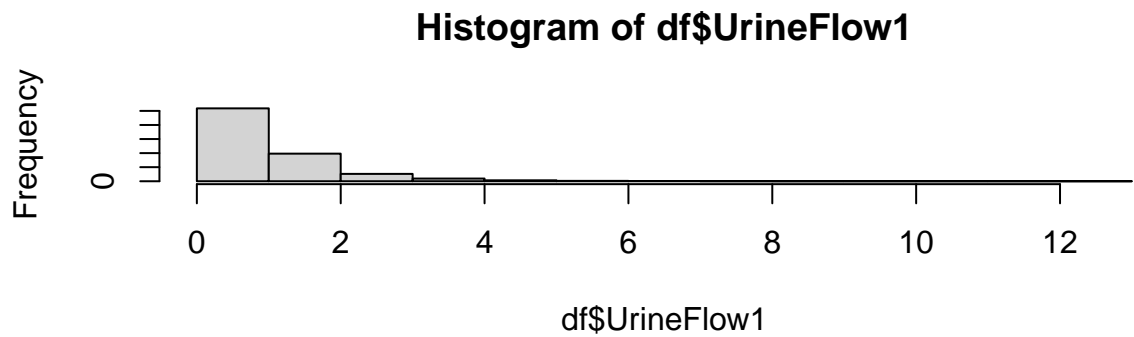
```
# z-test
temp1<-df1[df1$BMI_Factor=='Under Weight',]
summary(temp1$Urine_Flow)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## 0.0910  0.4150  0.7205  0.9295  0.9600  2.6920
```

```
summary(df$UrineFlow1)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## 0.000   0.430   0.739   1.006   1.261   12.346
```

```
par(mfrow=c(2,1))
hist(df$UrineFlow1)
hist(temp1$Urine_Flow)
```



```
mew<-mean(df$UrineFlow1[(df$Age>18)])
sigma<-SD_pop(df$UrineFlow1[(df$Age>18)],
              n=length(df$UrineFlow1[(df$Age>18)]))
sigma_estimated<-sd(temp1$Urine_Flow)
xbar<-mean(temp1$Urine_Flow)
n<-length(temp1$Urine_Flow)
SEM<-(sigma/sqrt(n))

z<-(xbar-mew)/SEM
z
```

```
## [1] -0.2002546
```

```
#2-tailed
p_2tailed<-2 * pnorm( - abs(z))
p_2tailed
```

```
## [1] 0.8412814
```

```
#not rejecting the null
```

```
#1-tailed
#Null hypothesis sample is greater/equal than the mew
#Research hypothesis sample is smaller than the mew
```

```
p_1tailed_smaller <- pnorm(z)
p_1tailed_smaller
```

```
## [1] 0.4206407
```

```
#not rejecting the null
```

```
#1-tailed
#Null hypothesis sample is smaller/equal than the mew
#Research hypothesis sample is greater than the mew
p_1tailed_greater <- 1 - pnorm(z)
p_1tailed_greater
```

```
## [1] 0.5793593
```

```
#not rejecting the null
```

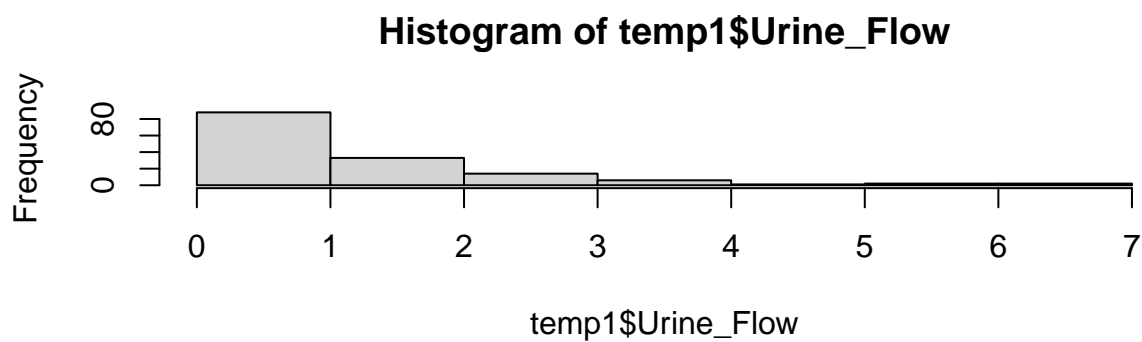
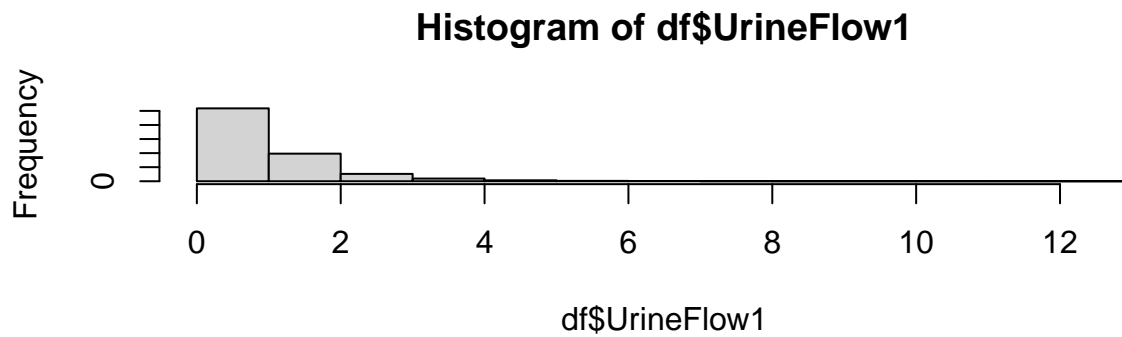
```
# z-test
temp1<-df1[df1$BMI_Factor=='Normal',]
summary(temp1$Urine_Flow)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  0.0970  0.4248  0.7980  1.1925  1.5835  6.9000
```

```
summary(df$UrineFlow1)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   0.000   0.430   0.739   1.006   1.261  12.346
```

```
par(mfrow=c(2,1))
hist(df$UrineFlow1)
hist(temp1$Urine_Flow)
```



```
mew<-mean(df$UrineFlow1[(df$Age>18)])
sigma<-SD_pop(df$UrineFlow1[(df$Age>18)],
              n=length(df$UrineFlow1[(df$Age>18)]))
sigma_estimated<-sd(temp1$Urine_Flow)
xbar<-mean(temp1$Urine_Flow)
n<-length(temp1$Urine_Flow)
SEM<-(sigma/sqrt(n))

z<-(xbar-mew)/SEM
z
```

```
## [1] 2.390759
```

```
#2-tailed
p_2tailed<-2 * pnorm( - abs(z))
p_2tailed
```

```
## [1] 0.01681359
```

```
#not rejecting the null
```

```
#1-tailed
#Null hypothesis sample is greater/equal than the mew
#Research hypothesis sample is smaller than the mew
```

```
p_1tailed_smaller <- pnorm(z)
p_1tailed_smaller
```

```
## [1] 0.9915932
```

```
#not rejecting the null
```

```
#1-tailed
#Null hypothesis sample is smaller/equal than the mew
#Research hypothesis sample is greater than the mew
p_1tailed_greater <- 1 - pnorm(z)
p_1tailed_greater
```

```
## [1] 0.008406796
```

```
#not rejecting the null
```

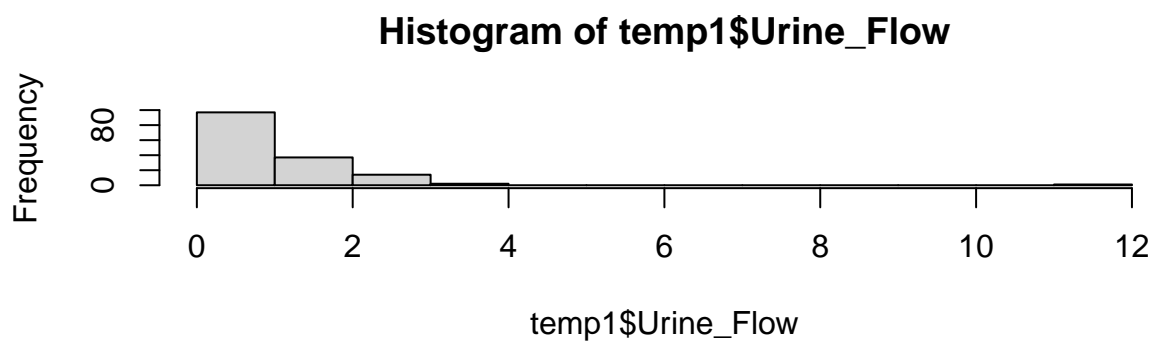
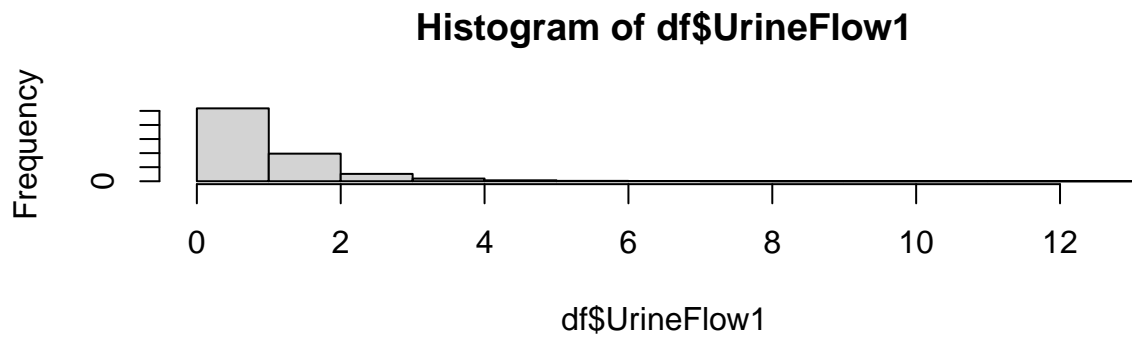
```
# z-test
temp1<-df1[df1$BMI_Factor=='Over Weight',]
summary(temp1$Urine_Flow)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    0.051   0.464   0.731   1.007   1.224   11.069
```

```
summary(df$UrineFlow1)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    0.000   0.430   0.739   1.006   1.261   12.346
```

```
par(mfrow=c(2,1))
hist(df$UrineFlow1)
hist(temp1$Urine_Flow)
```

```
mew<-mean(df$UrineFlow1[(df$Age>18)])
sigma<-SD_pop(df$UrineFlow1[(df$Age>18)],
              n=length(df$UrineFlow1[(df$Age>18)]))
sigma_estimated<-sd(temp1$Urine_Flow)
xbar<-mean(temp1$Urine_Flow)
n<-length(temp1$Urine_Flow)
SEM<-(sigma/sqrt(n))

z<-(xbar-mew)/SEM
z
```

```
## [1] 0.001591493
```

```
#2-tailed
p_2tailed<-2 * pnorm( - abs(z))
p_2tailed
```

```
## [1] 0.9987302
```

```
#not rejecting the null
```

```
#1-tailed
#Null hypothesis sample is greater/equal than the mew
#Research hypothesis sample is smaller than the mew
```

```
p_1tailed_smaller <- pnorm(z)
p_1tailed_smaller
```

```
## [1] 0.5006349
```

```
#not rejecting the null
```

```
#1-tailed
#Null hypothesis sample is smaller/equal than the mew
#Research hypothesis sample is greater than the mew
p_1tailed_greater <- 1 - pnorm(z)
p_1tailed_greater
```

```
## [1] 0.4993651
```

```
#not rejecting the null
```

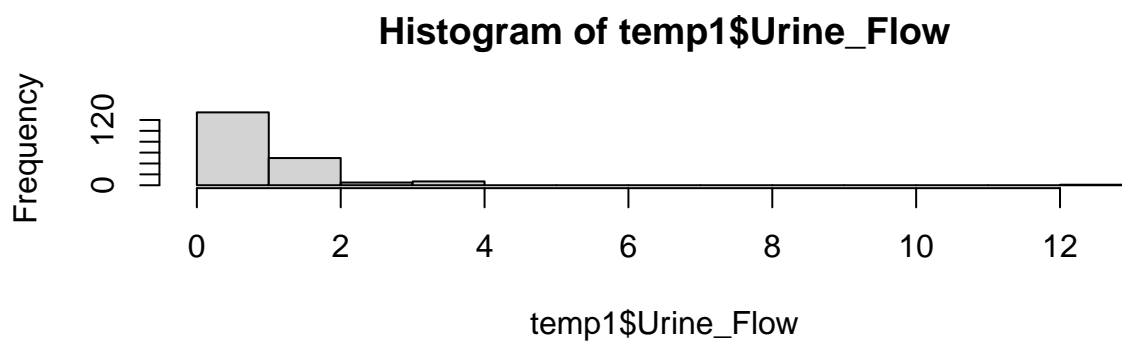
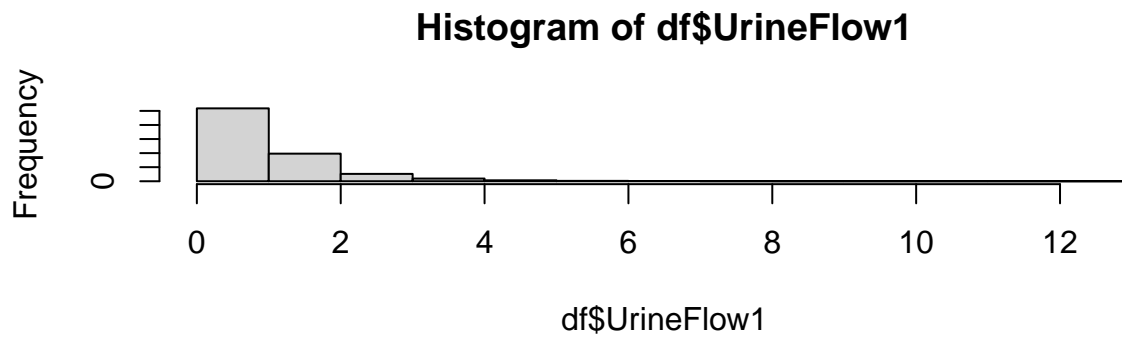
```
# z-test
temp1<-df1[df1$BMI_Factor=='Obese',]
summary(temp1$Urine_Flow)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  0.0000  0.4600  0.6860  0.9588  1.1690 12.3460
```

```
summary(df$UrineFlow1)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   0.000   0.430   0.739   1.006   1.261  12.346
```

```
par(mfrow=c(2,1))
hist(df$UrineFlow1)
hist(temp1$Urine_Flow)
```



```
mew<-mean(df$UrineFlow1[(df$Age>18)])
sigma<-SD_pop(df$UrineFlow1[(df$Age>18)],
              n=length(df$UrineFlow1[(df$Age>18)]))
sigma_estimated<-sd(temp1$Urine_Flow)
xbar<-mean(temp1$Urine_Flow)
n<-length(temp1$Urine_Flow)
SEM<-(sigma/sqrt(n))

z<-(xbar-mew)/SEM
z
```

```
## [1] -0.710129
```

```
#2-tailed
p_2tailed<-2 * pnorm( - abs(z))
p_2tailed
```

```
## [1] 0.4776242
```

```
#not rejecting the null
```

```
#1-tailed
#Null hypothesis sample is greater/equal than the mew
#Research hypothesis sample is smaller than the mew
```

```
p_1tailed_smaller <- pnorm(z)
p_1tailed_smaller
```

```
## [1] 0.2388121
```

```
#not rejecting the null
```

```
#1-tailed
#Null hypothesis sample is smaller/equal than the mew
#Research hypothesis sample is greater than the mew
p_1tailed_greater <- 1 - pnorm(z)
p_1tailed_greater
```

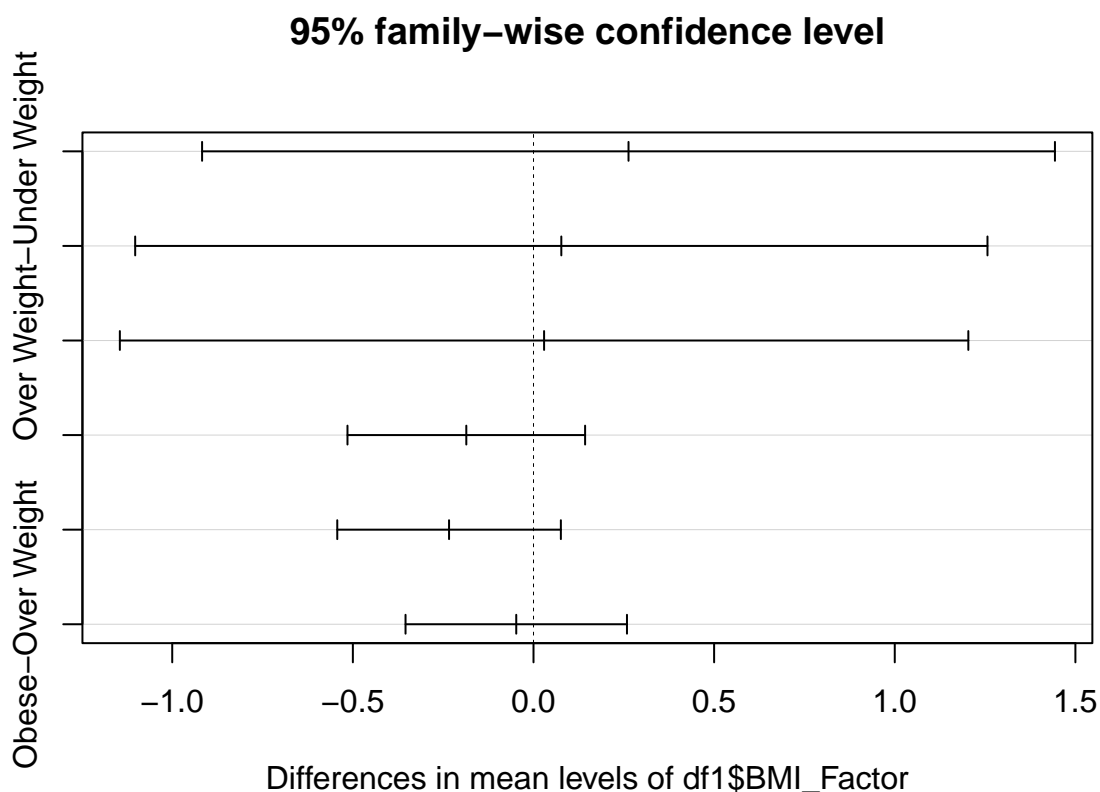
```
## [1] 0.7611879
```

```
#not rejecting the null
```

```
anova_test<-aov(df1$Urine_Flow~df1$BMI_Factor)
summary(anova_test)
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## df1$BMI_Factor    3     4.9   1.646   1.362  0.254
## Residuals       496   599.4   1.208
```

```
Tukey<-TukeyHSD(anova_test)
plot(Tukey)
```



Tukey

```
## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = df1$Urine_Flow ~ df1$BMI_Factor)
##
## $'df1$BMI_Factor'
##
```

	diff	lwr	upr	p adj
## Normal-Under Weight	0.26304110	-0.9173331	1.44341529	0.9396922
## Over Weight-Under Weight	0.07702980	-1.1025727	1.25663233	0.9983025
## Obese-Under Weight	0.02931218	-1.1450154	1.20363973	0.9999043
## Over Weight-Normal	-0.18601129	-0.5149109	0.14288826	0.4639303
## Obese-Normal	-0.23372891	-0.5431768	0.07571895	0.2098848
## Obese-Over Weight	-0.04771762	-0.3542088	0.25877358	0.9781094

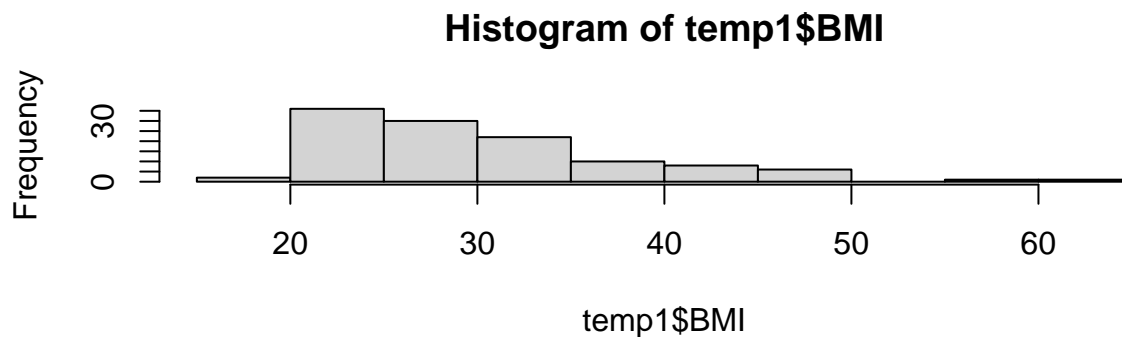
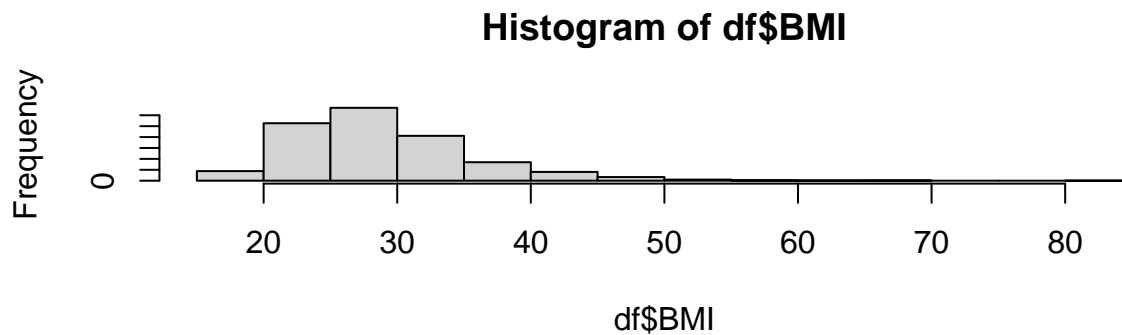
```
# z-test
templ<-df1[df1$Income_Factor=='Low',]
summary(templ$BMI)
```

```
## Min. 1st Qu. Median Mean 3rd Qu. Max.
## 16.70 24.29 27.82 30.09 33.64 61.01
```

```
summary(df$BMI)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  15.02   24.10   27.70   28.82   32.20   81.25
```

```
par(mfrow=c(2,1))
hist(df$BMI)
hist(temp1$BMI)
```



```
mew<-mean(df$BMI[(df$Age>18)])
sigma<-SD_pop(df$BMI[(df$Age>18)],
              n=length(df$BMI[(df$Age>18)]))
sigma_estimated<-sd(temp1$BMI)
xbar<-mean(temp1$BMI)
n<-length(temp1$BMI)
SEM<-(sigma/sqrt(n))

z<-(xbar-mew)/SEM
z
```

```
## [1] 2.035792
```

```
#2-tailed
p_2tailed<-2 * pnorm( - abs(z))
p_2tailed
```

```
## [1] 0.0417712
```

```
#not rejecting the null
```

```
#1-tailed
#Null hypothesis sample is greater/equal than the mew
#Research hypothesis sample is smaller than the mew
p_1tailed_smaller <- pnorm(z)
p_1tailed_smaller
```

```
## [1] 0.9791144
```

```
#not rejecting the null
```

```
#1-tailed
#Null hypothesis sample is smaller/equal than the mew
#Research hypothesis sample is greater than the mew
p_1tailed_greater <- 1 - pnorm(z)
p_1tailed_greater
```

```
## [1] 0.0208856
```

```
#rejecting the null
```

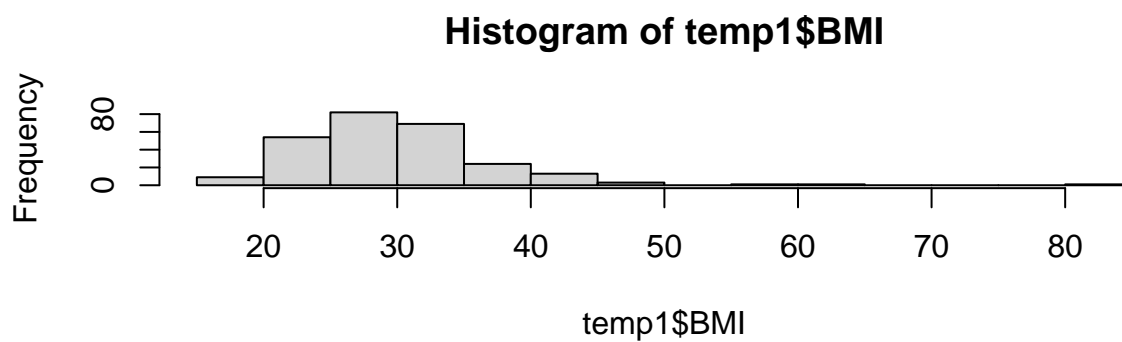
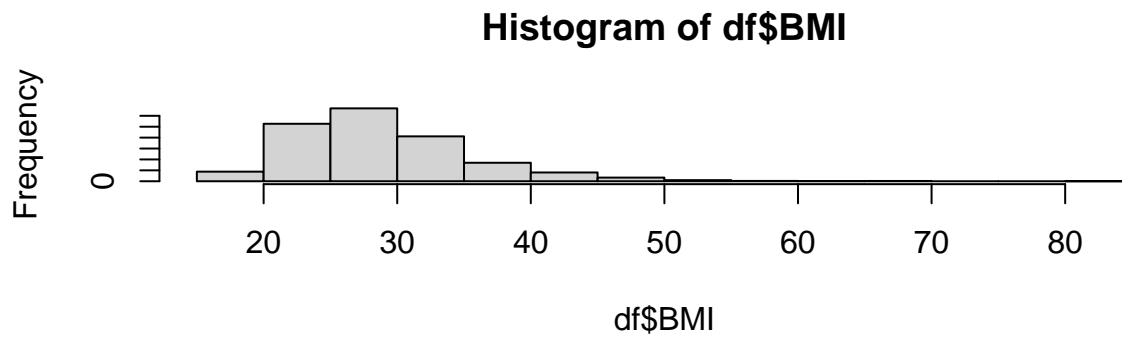
```
# z-test
temp1<-df1[df1$Income_Factor=='Medium',]
summary(temp1$BMI)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##      17.60   25.10   29.10   29.87   33.50   81.25
```

```
summary(df$BMI)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##      15.02   24.10   27.70   28.82   32.20   81.25
```

```
par(mfrow=c(2,1))
hist(df$BMI)
hist(temp1$BMI)
```



```
mew<-mean(df$BMI[(df$Age>18)])
sigma<-SD_pop(df$BMI[(df$Age>18)],
              n=length(df$BMI[(df$Age>18)]))
sigma_estimated<-sd(temp1$BMI)
xbar<-mean(temp1$BMI)
n<-length(temp1$BMI)
SEM<-(sigma/sqrt(n))

z<-(xbar-mew)/SEM
z
```

```
## [1] 2.493383
```

```
#2-tailed
p_2tailed<-2 * pnorm( - abs(z))
p_2tailed
```

```
## [1] 0.01265323
```

```
#not rejecting the null
```

```
#1-tailed
#Null hypothesis sample is greater/equal than the mew
#Research hypothesis sample is smaller than the mew
```



```
p_1tailed_smaller <- pnorm(z)
p_1tailed_smaller
```

```
## [1] 0.9936734
```

```
#not rejecting the null
```

```
#1-tailed
#Null hypothesis sample is smaller/equal than the mew
#Research hypothesis sample is greater than the mew
p_1tailed_greater <- 1 - pnorm(z)
p_1tailed_greater
```

```
## [1] 0.006326614
```

```
#rejecting the null
```

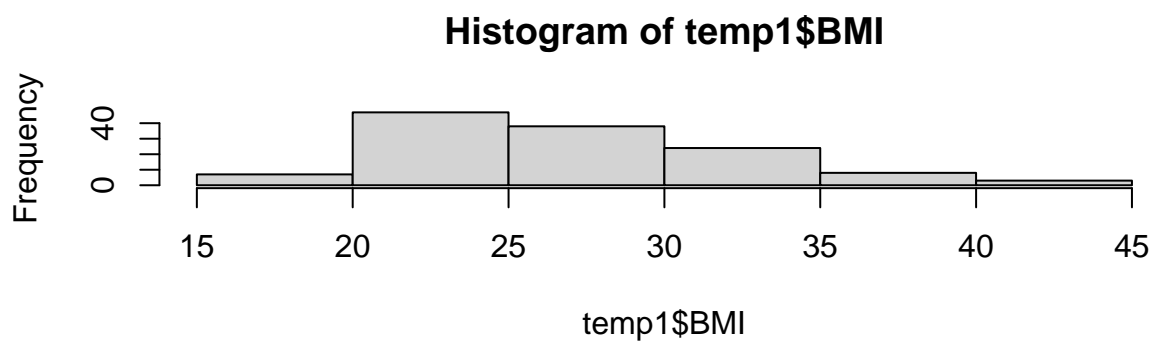
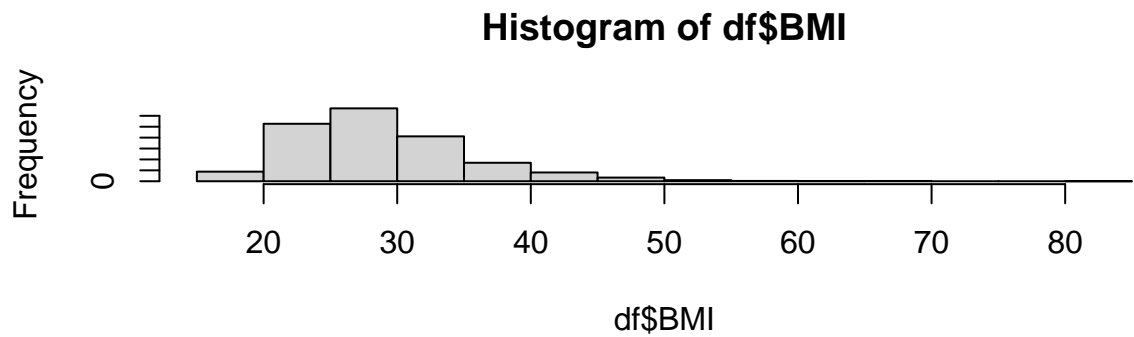
```
# z-test
temp1<-df1[df1$Income_Factor=='High',]
summary(temp1$BMI)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##      15.97   23.09   26.70   27.04   30.23   43.50
```

```
summary(df$BMI)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##      15.02   24.10   27.70   28.82   32.20   81.25
```

```
par(mfrow=c(2,1))
hist(df$BMI)
hist(temp1$BMI)
```



```
mew<-mean(df$BMI[(df$Age>18)])
sigma<-SD_pop(df$BMI[(df$Age>18)],
              n=length(df$BMI[(df$Age>18)]))
sigma_estimated<-sd(temp1$BMI)
xbar<-mean(temp1$BMI)
n<-length(temp1$BMI)
SEM<-(sigma/sqrt(n))

z<-(xbar-mew)/SEM
z
```

```
## [1] -2.987004
```

```
#2-tailed
p_2tailed<-2 * pnorm( - abs(z))
p_2tailed
```

```
## [1] 0.002817256
```

```
#not rejecting the null
```

```
#1-tailed
#Null hypothesis sample is greater/equal than the mew
#Research hypothesis sample is smaller than the mew
```

```
p_1tailed_smaller <- pnorm(z)
p_1tailed_smaller
```

```
## [1] 0.001408628
```

```
#not rejecting the null
```

```
#1-tailed
#Null hypothesis sample is smaller/equal than the mew
#Research hypothesis sample is greater than the mew
p_1tailed_greater <- 1 - pnorm(z)
p_1tailed_greater
```

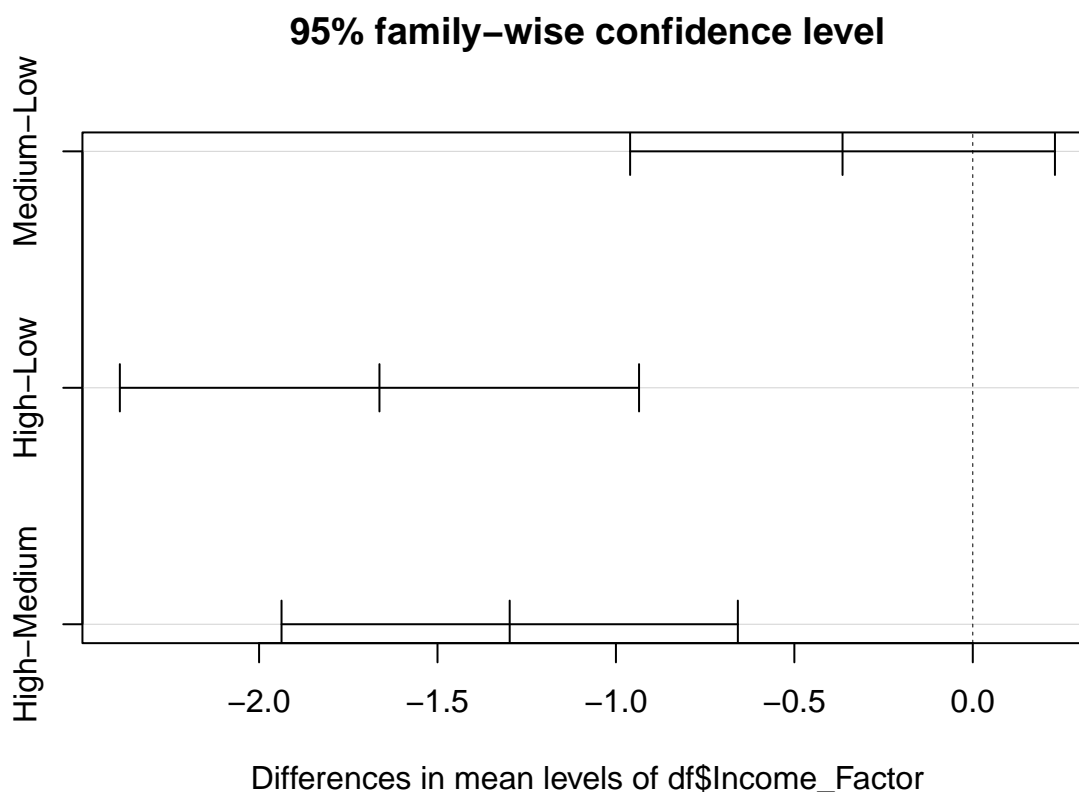
```
## [1] 0.9985914
```

```
#rejecting the null
```

```
anova_test1<-aov(df$BMI~df$Income_Factor)
summary(anova_test1)
```

```
##               Df Sum Sq Mean Sq F value    Pr(>F)
## df$Income_Factor    2   1433    716.3   15.96 1.24e-07 ***
## Residuals          3990 179019     44.9
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Tukey1<-TukeyHSD(anova_test1)
plot(Tukey1)
```



Tukey1

```
## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = df$BMI ~ df$Income_Factor)
##
## $'df$Income_Factor'
##          diff          lwr          upr          p adj
## Medium-Low -0.3649835 -0.9602329  0.2302659 0.3216591
## High-Low    -1.6626948 -2.3901931 -0.9351966 0.0000003
## High-Medium -1.2977113 -1.9371019 -0.6583207 0.0000061
```

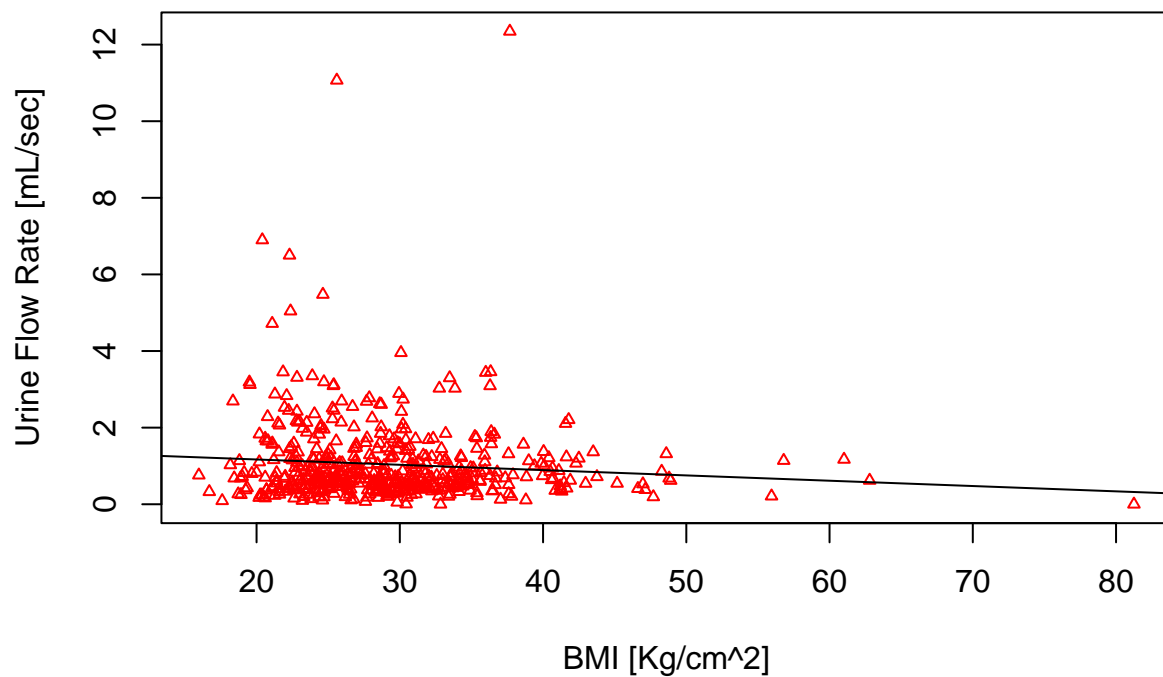
```
fit_all<-lm(Urine_Flow ~ BMI, data=df1)
fit_all
```

```
##
## Call:
## lm(formula = Urine_Flow ~ BMI, data = df1)
##
## Coefficients:
## (Intercept)          BMI
##      1.44599      -0.01386
```

```
summary(fit_all)
```

```
##
## Call:
## lm(formula = Urine_Flow ~ BMI, data = df1)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.1110 -0.5789 -0.3061  0.2275 11.4224
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.445989   0.207435   6.971   1e-11 ***
## BMI          -0.013865   0.006902  -2.009   0.0451 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.097 on 498 degrees of freedom
## Multiple R-squared:  0.008038,    Adjusted R-squared:  0.006046
## F-statistic: 4.035 on 1 and 498 DF,  p-value: 0.0451
```

```
plot(c(min(df1$BMI,na.rm = TRUE),max(df1$BMI,na.rm = TRUE)),c(min(df1$Urine_Flow,na.rm = TRUE),max(df1$Urine_Flow,na.rm = TRUE)),
      xlab="BMI [Kg/cm^2]",ylab="Urine Flow Rate [mL/sec]")
#ggplot(df1,aes(x=age,y=SBP,color=BMI_Factor)) +
#geom_smooth(method='lm',mapping =aes(x=age,y=SBP),se=FALSE)+
# geom_jitter(width = .2)
points(df1$BMI,df1$Urine_Flow,pch=2,cex=0.6,col="red")
abline(fit_all,col="black")
```



```
fit_all<-lm(BMI ~ Income, data=df1)
fit_all
```

```
##
## Call:
## lm(formula = BMI ~ Income, data = df1)
##
## Coefficients:
## (Intercept)      Income
##  3.138e+01    -3.796e-05
```

```
summary(fit_all)
```

```
##
## Call:
## lm(formula = BMI ~ Income, data = df1)
##
## Residuals:
```

	Min	1Q	Median	3Q	Max
	-14.210	-4.939	-0.827	3.414	51.763

```
##
## Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	3.138e+01	6.239e-01	50.301	<2e-16 ***
Income	-3.796e-05	9.380e-06	-4.047	6e-05 ***

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.009 on 498 degrees of freedom
## Multiple R-squared:  0.03185,    Adjusted R-squared:  0.0299
## F-statistic: 16.38 on 1 and 498 DF,  p-value: 6.004e-05

plot(c(min(df1$Income,na.rm = TRUE),max(df1$Income,na.rm = TRUE)),c(min(df1$BMI,na.rm = TRUE),max(df1$BMI,na.rm = TRUE)),
      xlab="Income [$ /yr]",ylab="Body Mass Index [Kg/cm^2]")
#ggplot(df1,aes(x=age,y=SBP,color=BMI_Factor)) +
#geom_smooth(method='lm',mapping =aes(x=age,y=SBP),se=FALSE)+
# geom_jitter(width = .2)
points(df1$Income,df1$BMI,pch=2,cex=0.6,col="red")
abline(fit_all,col="black")
```

