Exploratory Data Analysis

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This is an R Markdown Notebook. When you execute code within the notebook, the results appear beneath the code.

Try executing this chunk by clicking the *Run* button within the chunk or by placing your cursor inside it and pressing *Ctrl+Shift+Enter*.

```
library(pacman)
```

Add a new chunk by clicking the *Insert Chunk* button on the toolbar or by pressing *Ctrl+Alt+I*.

When you save the notebook, an HTML file containing the code and output will be saved alongside it (click the *Preview* button or press *Ctrl+Shift+K* to preview the HTML file).

The preview shows you a rendered HTML copy of the contents of the editor. Consequently, unlike *Knit*, *Preview* does not run any R code chunks. Instead, the output of the chunk when it was last run in the editor is displayed.

```
p_load(dplyr, GGally, ggplot2, ggthemes, ggvis, httr, lubridate, plotly, rio, rmarkdown, shiny, stringr
```

```
stroke_data<-import("./../data/healthcare-dataset-stroke-data.csv")
```

```
str(stroke_data)
```

```
## 'data.frame':    5110 obs. of  12 variables:
##  $ id               : int  9046 51676 31112 60182 1665 56669 53882 10434 27419 60491 ...
##  $ gender           : chr  "Male" "Female" "Male" "Female" ...
##  $ age              : num  67 61 80 49 79 81 74 69 59 78 ...
##  $ hypertension     : int  0 0 0 0 1 0 1 0 0 0 ...
##  $ heart_disease    : int  1 0 1 0 0 0 1 0 0 0 ...
##  $ ever_married     : chr  "Yes" "Yes" "Yes" "Yes" ...
##  $ work_type        : chr  "Private" "Self-employed" "Private" "Private" ...
##  $ Residence_type   : chr  "Urban" "Rural" "Rural" "Urban" ...
##  $ avg_glucose_level: num  229 202 106 171 174 ...
##  $ bmi              : chr  "36.6" "N/A" "32.5" "34.4" ...
##  $ smoking_status   : chr  "formerly smoked" "never smoked" "never smoked" "smokes" ...
##  $ stroke           : int  1 1 1 1 1 1 1 1 1 1 ...
```

```
install.packages("binom", repos = "https://cloud.r-project.org/")
```

```
## Installing package into '/geode2/home/u060/mdprin/Carbonate/R/x86_64-pc-linux-gnu-library/4.2'
## (as 'lib' is unspecified)
```

```
library(binom)
```

```
head(stroke_data,15)
```

```
##       id gender age hypertension heart_disease ever_married     work_type
## 1   9046   Male  67            0             1          Yes       Private
## 2  51676 Female  61            0             0          Yes Self-employed
```

```
## 3  31112   Male  80            0             1          Yes       Private
## 4  60182 Female  49            0             0          Yes       Private
## 5   1665 Female  79            1             0          Yes Self-employed
## 6  56669   Male  81            0             0          Yes       Private
## 7  53882   Male  74            1             1          Yes       Private
## 8  10434 Female  69            0             0           No       Private
## 9  27419 Female  59            0             0          Yes       Private
## 10 60491 Female  78            0             0          Yes       Private
## 11 12109 Female  81            1             0          Yes       Private
## 12 12095 Female  61            0             1          Yes      Govt_job
## 13 12175 Female  54            0             0          Yes       Private
## 14  8213   Male  78            0             1          Yes       Private
## 15  5317 Female  79            0             1          Yes       Private
##    Residence_type avg_glucose_level  bmi  smoking_status stroke
## 1           Urban            228.69 36.6 formerly smoked      1
## 2           Rural            202.21  N/A    never smoked      1
## 3           Rural            105.92 32.5    never smoked      1
## 4           Urban            171.23 34.4          smokes      1
## 5           Rural            174.12   24    never smoked      1
## 6           Urban            186.21   29 formerly smoked      1
## 7           Rural             70.09 27.4    never smoked      1
## 8           Urban             94.39 22.8    never smoked      1
## 9           Rural             76.15  N/A         Unknown      1
## 10          Urban             58.57 24.2         Unknown      1
## 11          Rural             80.43 29.7    never smoked      1
## 12          Rural            120.46 36.8          smokes      1
## 13          Urban            104.51 27.3          smokes      1
## 14          Urban            219.84  N/A         Unknown      1
## 15          Urban            214.09 28.2    never smoked      1
```

data cleaning

```r
#removing all the rows having NA values

stroke_data<-na.omit(stroke_data)
```

```r
#removing all rows having "N/A" values
clean_stroke_data<-stroke_data[!apply(stroke_data=="N/A",1,any),]
```

```r
head(clean_stroke_data,n=15)
```

```
##       id gender age hypertension heart_disease ever_married     work_type
## 1   9046   Male  67            0             1          Yes       Private
## 3  31112   Male  80            0             1          Yes       Private
## 4  60182 Female  49            0             0          Yes       Private
## 5   1665 Female  79            1             0          Yes Self-employed
## 6  56669   Male  81            0             0          Yes       Private
## 7  53882   Male  74            1             1          Yes       Private
## 8  10434 Female  69            0             0           No       Private
## 10 60491 Female  78            0             0          Yes       Private
## 11 12109 Female  81            1             0          Yes       Private
## 12 12095 Female  61            0             1          Yes      Govt_job
## 13 12175 Female  54            0             0          Yes       Private
## 15  5317 Female  79            0             1          Yes       Private
## 16 58202 Female  50            1             0          Yes Self-employed
## 17 56112   Male  64            0             1          Yes       Private
```

```
## 18 34120   Male  75            1             0          Yes       Private
##    Residence_type avg_glucose_level  bmi  smoking_status stroke
## 1           Urban            228.69 36.6 formerly smoked      1
## 3           Rural            105.92 32.5    never smoked      1
## 4           Urban            171.23 34.4          smokes      1
## 5           Rural            174.12   24    never smoked      1
## 6           Urban            186.21   29 formerly smoked      1
## 7           Rural             70.09 27.4    never smoked      1
## 8           Urban             94.39 22.8    never smoked      1
## 10          Urban             58.57 24.2         Unknown      1
## 11          Rural             80.43 29.7    never smoked      1
## 12          Rural            120.46 36.8          smokes      1
## 13          Urban            104.51 27.3          smokes      1
## 15          Urban            214.09 28.2    never smoked      1
## 16          Rural            167.41 30.9    never smoked      1
## 17          Urban            191.61 37.5          smokes      1
## 18          Urban            221.29 25.8          smokes      1
```

```
#keeping only male and females
clean_g_stroke_data<-clean_stroke_data %>%
  filter(gender!="Other")
```

```
#converting bmi column to numeric
clean_g_stroke_data$bmi<-as.numeric(clean_g_stroke_data$bmi)
str(clean_g_stroke_data)
```

```
## 'data.frame':    4908 obs. of  12 variables:
##  $ id               : int  9046 31112 60182 1665 56669 53882 10434 60491 12109 12095 ...
##  $ gender           : chr  "Male" "Male" "Female" "Female" ...
##  $ age              : num  67 80 49 79 81 74 69 78 81 61 ...
##  $ hypertension     : int  0 0 0 1 0 1 0 0 1 0 ...
##  $ heart_disease    : int  1 1 0 0 0 1 0 0 0 1 ...
##  $ ever_married     : chr  "Yes" "Yes" "Yes" "Yes" ...
##  $ work_type        : chr  "Private" "Private" "Private" "Self-employed" ...
##  $ Residence_type   : chr  "Urban" "Rural" "Urban" "Rural" ...
##  $ avg_glucose_level: num  229 106 171 174 186 ...
##  $ bmi              : num  36.6 32.5 34.4 24 29 27.4 22.8 24.2 29.7 36.8 ...
##  $ smoking_status   : chr  "formerly smoked" "never smoked" "smokes" "never smoked" ...
##  $ stroke           : int  1 1 1 1 1 1 1 1 1 1 ...
```

```
bmi_gen<-clean_g_stroke_data %>% select(gender, bmi)
str(bmi_gen)
```

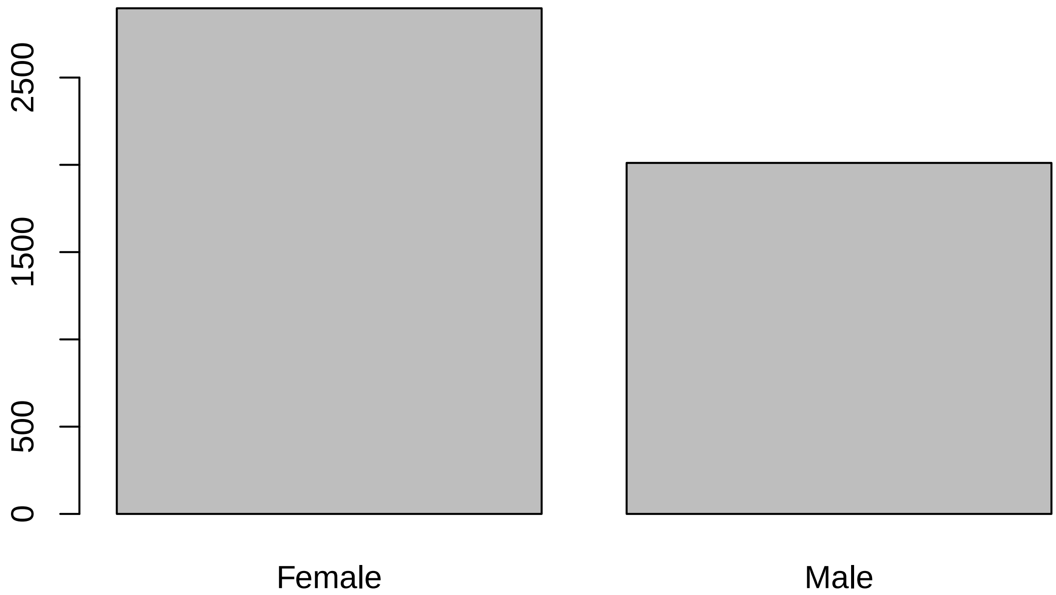
```
## 'data.frame':    4908 obs. of  2 variables:
##  $ gender: chr  "Male" "Male" "Female" "Female" ...
##  $ bmi   : num  36.6 32.5 34.4 24 29 27.4 22.8 24.2 29.7 36.8 ...
```

```
bmi_gen$gender<-as.factor(bmi_gen$gender)
```

```
str(bmi_gen)
```

```
## 'data.frame':    4908 obs. of  2 variables:
##  $ gender: Factor w/ 2 levels "Female","Male": 2 2 1 1 2 2 1 1 1 1 ...
##  $ bmi   : num  36.6 32.5 34.4 24 29 27.4 22.8 24.2 29.7 36.8 ...
```

```
plot(bmi_gen$gender)
```




```r
bmi_mar<- clean_g_stroke_data %>% select(ever_married, bmi)
```

```r
bmi_mar$ever_married<-as.factor(bmi_mar$ever_married)
bmi_mar$bmi<-as.numeric(bmi_mar$bmi)
```

```r
#calculating the mean and the median

# I have to ensure that the ever_married column is of factor or character type.

mar_mean<-mean(bmi_mar$bmi[bmi_mar$ever_married=="Yes"], na.rm=TRUE)
mar_median<-median(bmi_mar$bmi[bmi_mar$ever_married=="Yes"], na.rm=TRUE)
unmar_mean<-mean(bmi_mar$bmi[bmi_mar$ever_married!="Yes"], na.rm=TRUE)
unmar_median<-median(bmi_mar$bmi[bmi_mar$ever_married!="Yes"], na.rm=TRUE)



p <- ggplot(bmi_mar, aes(x=bmi, fill=ever_married)) +
  geom_histogram(alpha=0.5, position="identity", bins=40) +
  scale_fill_manual(values=c("red", "green4"))+
  geom_vline(aes(xintercept=mar_mean), color="green4", linetype="dashed", size=1, show.legend=TRUE, labe
  geom_vline(aes(xintercept=mar_median), color="green4", linetype="solid", size=1, show.legend=TRUE, la
  geom_vline(aes(xintercept=unmar_mean), color="red", linetype="dashed", size=1, show.legend=TRUE, label
  geom_vline(aes(xintercept=unmar_median), color="red", linetype="solid", size=1, show.legend=TRUE, labe
  theme_minimal() +
  labs(title = "Histograms by Marital Status with Mean and Median", x = "BMI Value", y = "Count")
```

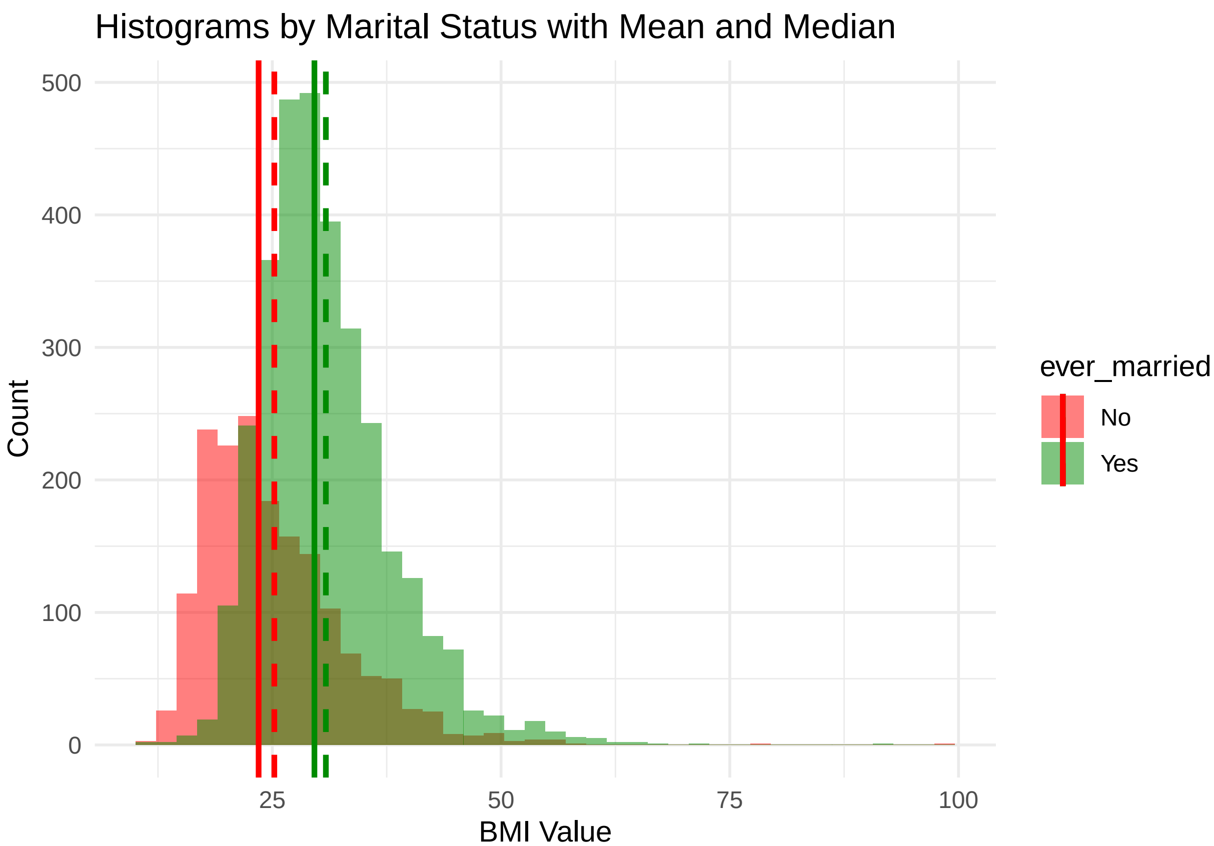
```
## Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
## i Please use `linewidth` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

```
## Warning in geom_vline(aes(xintercept = mar_mean), color = "green4", linetype =
## "dashed", : Ignoring unknown parameters: `label`
```

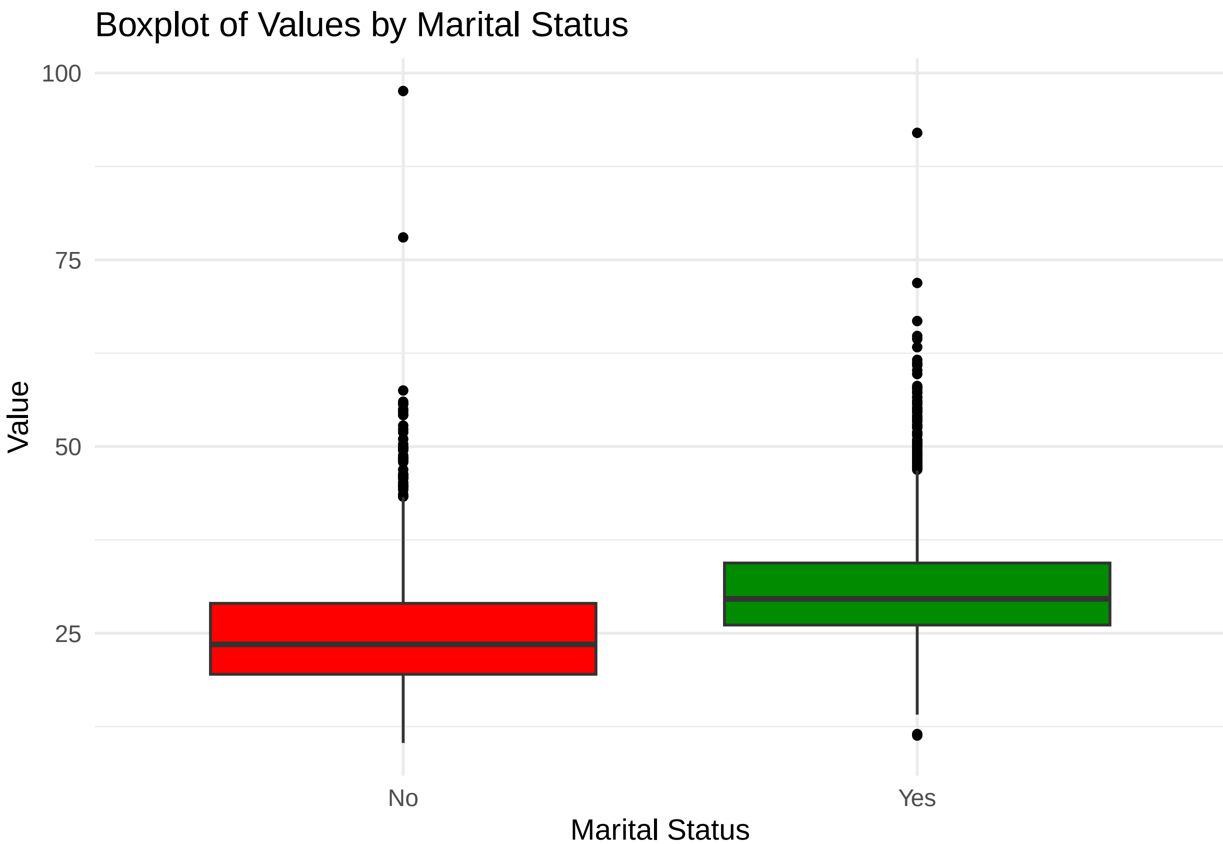
```
## Warning in geom_vline(aes(xintercept = mar_median), color = "green4", linetype
## = "solid", : Ignoring unknown parameters: `label`
```

```
## Warning in geom_vline(aes(xintercept = unmar_mean), color = "red", linetype =
## "dashed", : Ignoring unknown parameters: `label`

## Warning in geom_vline(aes(xintercept = unmar_median), color = "red", linetype =
## "solid", : Ignoring unknown parameters: `label`
```

```r
print(p)
```




```r
q <- ggplot(bmi_mar, aes(x=ever_married, y=bmi)) +
  geom_boxplot(aes(fill=ever_married), outlier.color="black", outlier.shape=16) +
  labs(title="Boxplot of Values by Marital Status", x="Marital Status", y="Value") +
  theme_minimal() +
  scale_fill_manual(values=c("Yes"="green4", "No"="red")) +  # Manual coloring
  theme(legend.position="none")  # Removing legend since fill color indicates category

print(q)
```




```
summary(filter(bmi_mar, bmi_mar$ever_married=="Yes"))
```

```
##  ever_married      bmi
##  No  :   0      Min.   :11.30
##  Yes:3204       1st Qu.:26.10
##                 Median :29.60
##                 Mean   :30.85
##                 3rd Qu.:34.40
##                 Max.   :92.00
```

```
summary(filter(bmi_mar, bmi_mar$ever_married=="No"))
```

```
##  ever_married      bmi
##  No :1704       Min.   :10.30
##  Yes:   0       1st Qu.:19.50
##                 Median :23.50
##                 Mean   :25.22
##                 3rd Qu.:29.00
##                 Max.   :97.60
```

Here, we can see that Mean and Median BMI of married people are 30.85 and 29.60 respectively whereas, Mean and Median BMI of unmarried people are 25.21 and 23.50. In histogram also, it is skewed to the right(greater BMI) which belongs to married population. In Boxplot also, the 3rd quantile of Unmarried people is in between 1st quartile and mean BMI of married people. That means, the proposition is true, people trends to get weight after marriage.

```
summary(clean_g_stroke_data)
```

```
##        id            gender               age          hypertension
```

```
##  Min.   :   77   Length:4908        Min.   : 0.08   Min.   :0.00000
##  1st Qu.:18602   Class :character   1st Qu.:25.00   1st Qu.:0.00000
##  Median :37580   Mode  :character   Median :44.00   Median :0.00000
##  Mean   :37060                      Mean   :42.87   Mean   :0.09189
##  3rd Qu.:55182                      3rd Qu.:60.00   3rd Qu.:0.00000
##  Max.   :72940                      Max.   :82.00   Max.   :1.00000
##  heart_disease     ever_married        work_type         Residence_type
##  Min.   :0.00000   Length:4908        Length:4908        Length:4908
##  1st Qu.:0.00000   Class :character   Class :character   Class :character
##  Median :0.00000   Mode  :character   Mode  :character   Mode  :character
##  Mean   :0.04951
##  3rd Qu.:0.00000
##  Max.   :1.00000
##  avg_glucose_level      bmi        smoking_status         stroke
##  Min.   : 55.12    Min.   :10.30   Length:4908        Min.   :0.00000
##  1st Qu.: 77.07    1st Qu.:23.50   Class :character   1st Qu.:0.00000
##  Median : 91.68    Median :28.10   Mode  :character   Median :0.00000
##  Mean   :105.30    Mean   :28.89                      Mean   :0.04258
##  3rd Qu.:113.50    3rd Qu.:33.10                      3rd Qu.:0.00000
##  Max.   :271.74    Max.   :97.60                      Max.   :1.00000
```

```r
clean_g_stroke_data$hypertension<-as.factor(clean_g_stroke_data$hypertension)
clean_g_stroke_data$heart_disease<-as.factor(clean_g_stroke_data$heart_disease)
clean_g_stroke_data$stroke<-as.factor(clean_g_stroke_data$stroke)
```

```r
install.packages("cowplot",repos="https://cloud.r-project.org/")
```

```
## Installing package into '/geode2/home/u060/mdprin/Carbonate/R/x86_64-pc-linux-gnu-library/4.2'
## (as 'lib' is unspecified)
```

```r
library(cowplot)
```

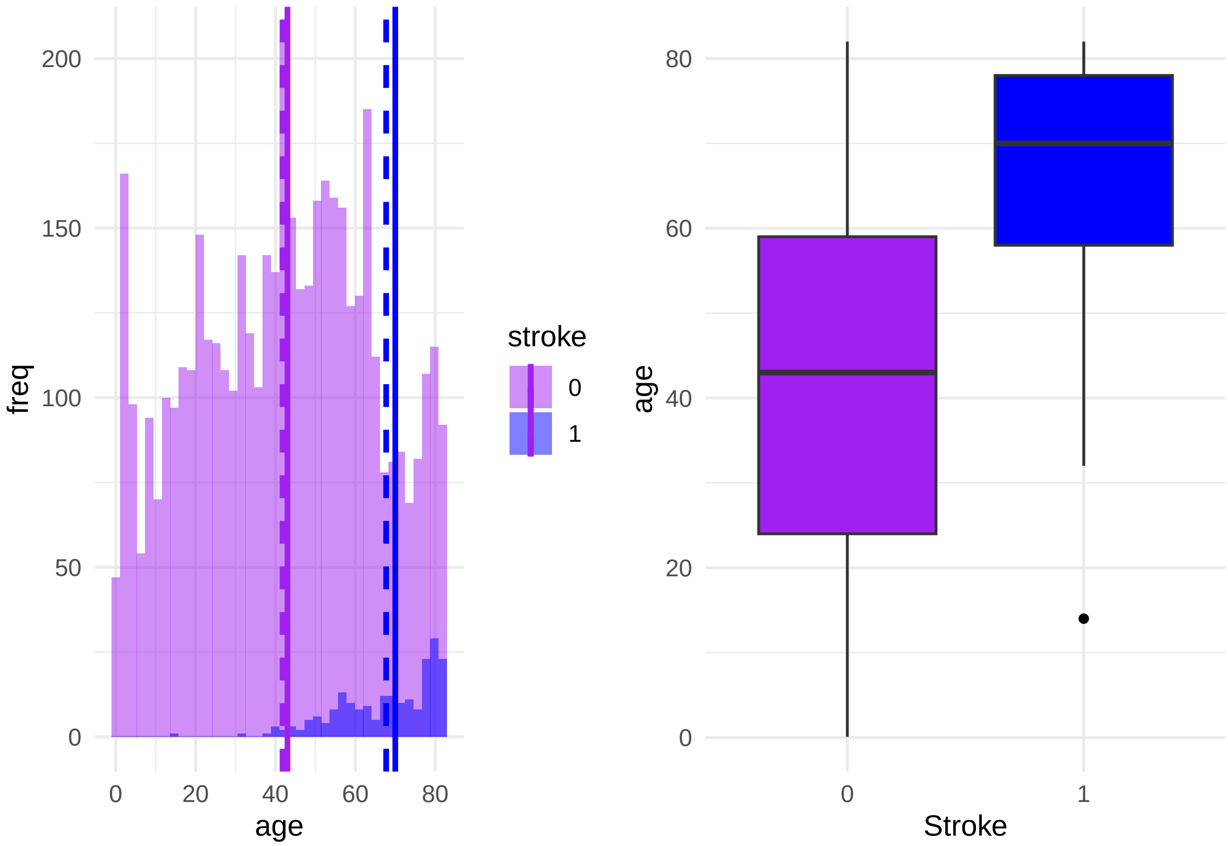
```
##
## Attaching package: 'cowplot'

## The following object is masked from 'package:lubridate':
##
##     stamp

## The following object is masked from 'package:ggthemes':
##
##     theme_map
```

```r
data<-clean_g_stroke_data

# a generic function to plot any column variable with respect of stroke
dist_plot<-function(param){
  #calculating the mean and the median
  #people who had a stroke
  mar_mean<-mean(data[[param]][data$stroke==1], na.rm=TRUE)
  mar_median<-median(data[[param]][data$stroke==1], na.rm=TRUE)
  #people who did not have a stroke
  unmar_mean<-mean(data[[param]][data$stroke==0], na.rm=TRUE)
  unmar_median<-median(data[[param]][data$stroke==0], na.rm=TRUE)


  #histogram by stroke status(e.g. age distribution by stroke)
```

```r
  hist <- ggplot(data, aes(x=eval(parse(text=param)), fill=stroke)) +
    geom_histogram(alpha=0.5, position="identity", bins=40) +
    scale_fill_manual(values=c("purple", "blue"))+
    geom_vline(aes(xintercept=mar_mean), color="blue", linetype="dashed", size=1, show.legend=TRUE, labe
    geom_vline(aes(xintercept=mar_median), color="blue", linetype="solid", size=1, show.legend=TRUE, lal
    geom_vline(aes(xintercept=unmar_mean), color="purple", linetype="dashed", size=1, show.legend=TRUE,
    geom_vline(aes(xintercept=unmar_median), color="purple", linetype="solid", size=1, show.legend=TRUE
    theme_minimal() +
    labs( x = param, y = "freq")


  box <- ggplot(data, aes(x=stroke, y=eval(parse(text=param)))) + #kind of opposite of histogram
  geom_boxplot(aes(fill=stroke), outlier.color="black", outlier.shape=16) +
  labs( x="Stroke", y=param) +
  theme_minimal() +
  scale_fill_manual(values=c("1"="blue", "0"="purple")) +  # Manual coloring
  theme(legend.position="none")  # Removing legend since fill color indicates category

  return(plot_grid(hist,box))
}
```

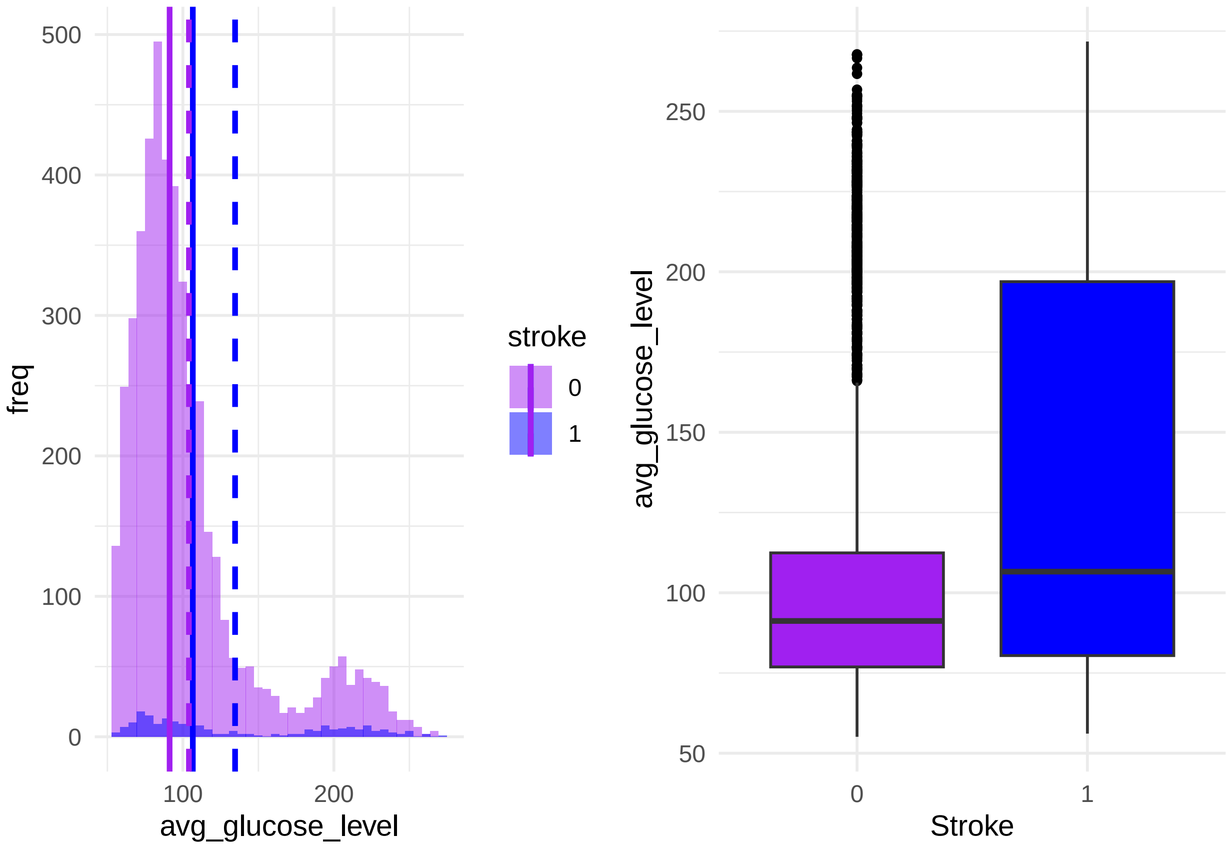
```r
dist_plot("age")
```

```
## Warning in geom_vline(aes(xintercept = mar_mean), color = "blue", linetype =
## "dashed", : Ignoring unknown parameters: `label`

## Warning in geom_vline(aes(xintercept = mar_median), color = "blue", linetype =
## "solid", : Ignoring unknown parameters: `label`

## Warning in geom_vline(aes(xintercept = unmar_mean), color = "purple", linetype
## = "dashed", : Ignoring unknown parameters: `label`

## Warning in geom_vline(aes(xintercept = unmar_median), color = "purple", :
## Ignoring unknown parameters: `label`
```




```r
dist_plot("avg_glucose_level")
```

```
## Warning in geom_vline(aes(xintercept = mar_mean), color = "blue", linetype =
## "dashed", : Ignoring unknown parameters: `label`

## Warning in geom_vline(aes(xintercept = mar_median), color = "blue", linetype =
## "solid", : Ignoring unknown parameters: `label`

## Warning in geom_vline(aes(xintercept = unmar_mean), color = "purple", linetype
## = "dashed", : Ignoring unknown parameters: `label`

## Warning in geom_vline(aes(xintercept = unmar_median), color = "purple", :
## Ignoring unknown parameters: `label`
```



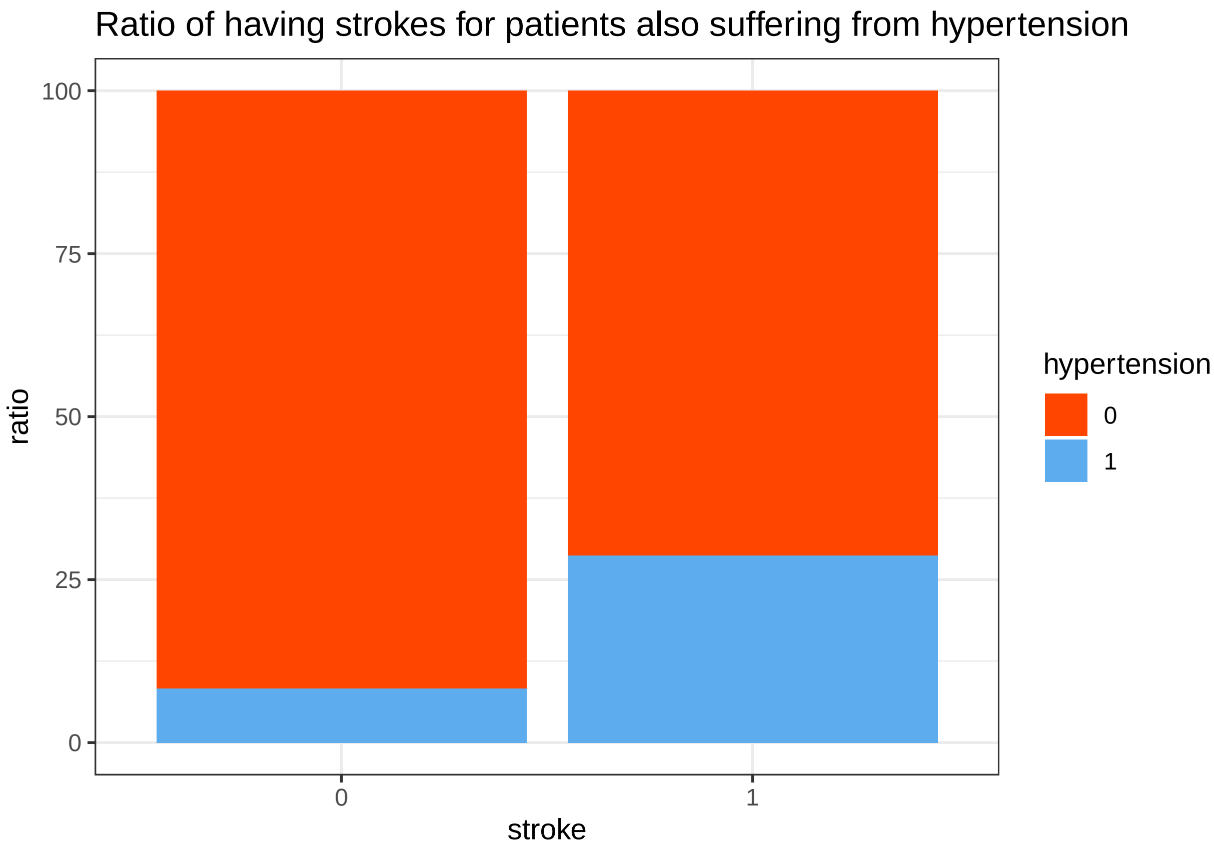

```
ratio_barpplot<-function(x){
  # here at first x will be in character format.
  barplt<-data %>% select(stroke, x, gender) %>%
            group_by(stroke,param=eval(parse(text=x))) %>% #parsing x from text to act as a column name
            summarise(count = length(gender)) %>%
            group_by(stroke) %>%
            mutate(ratio=round((count*100)/sum(count),1)) %>%
            ggplot(aes(x=stroke, y=ratio, fill=param)) +
            geom_bar(stat="identity") +
            scale_fill_manual(values=c("orangered", "steelblue2"))+

            labs(title = paste("Ratio of having strokes for patients also suffering from",x), fill=x)+
            theme_bw()
  return(barplt)
}
```

```
ratio_barpplot("hypertension")
```

```
## Warning: Using an external vector in selections was deprecated in tidyselect 1.1.0.
## i Please use `all_of()` or `any_of()` instead.
##   # Was:
##   data %>% select(x)
##
##   # Now:
##   data %>% select(all_of(x))
##
## See <https://tidyselect.r-lib.org/reference/faq-external-vector.html>.
## This warning is displayed once every 8 hours.
```

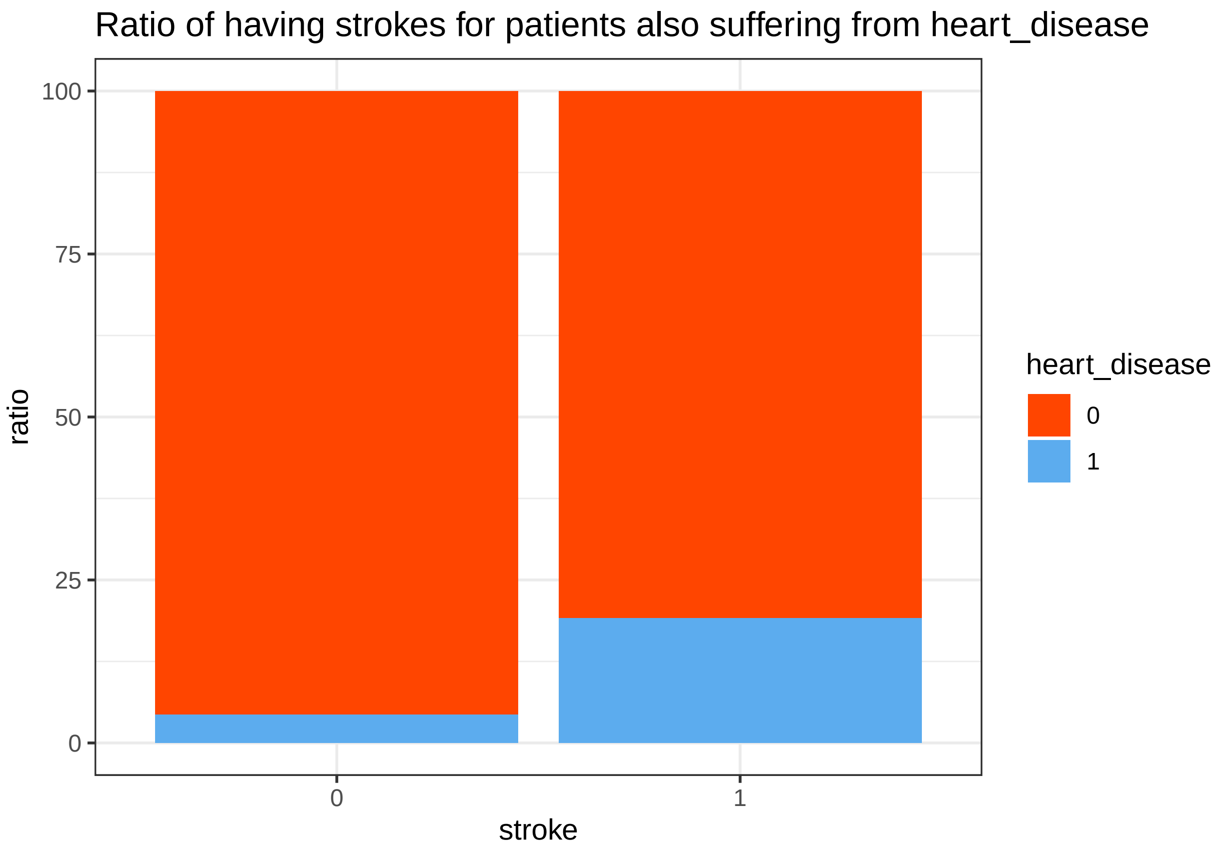
```
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

```
## `summarise()` has grouped output by 'stroke'. You can override using the
## `.groups` argument.
```



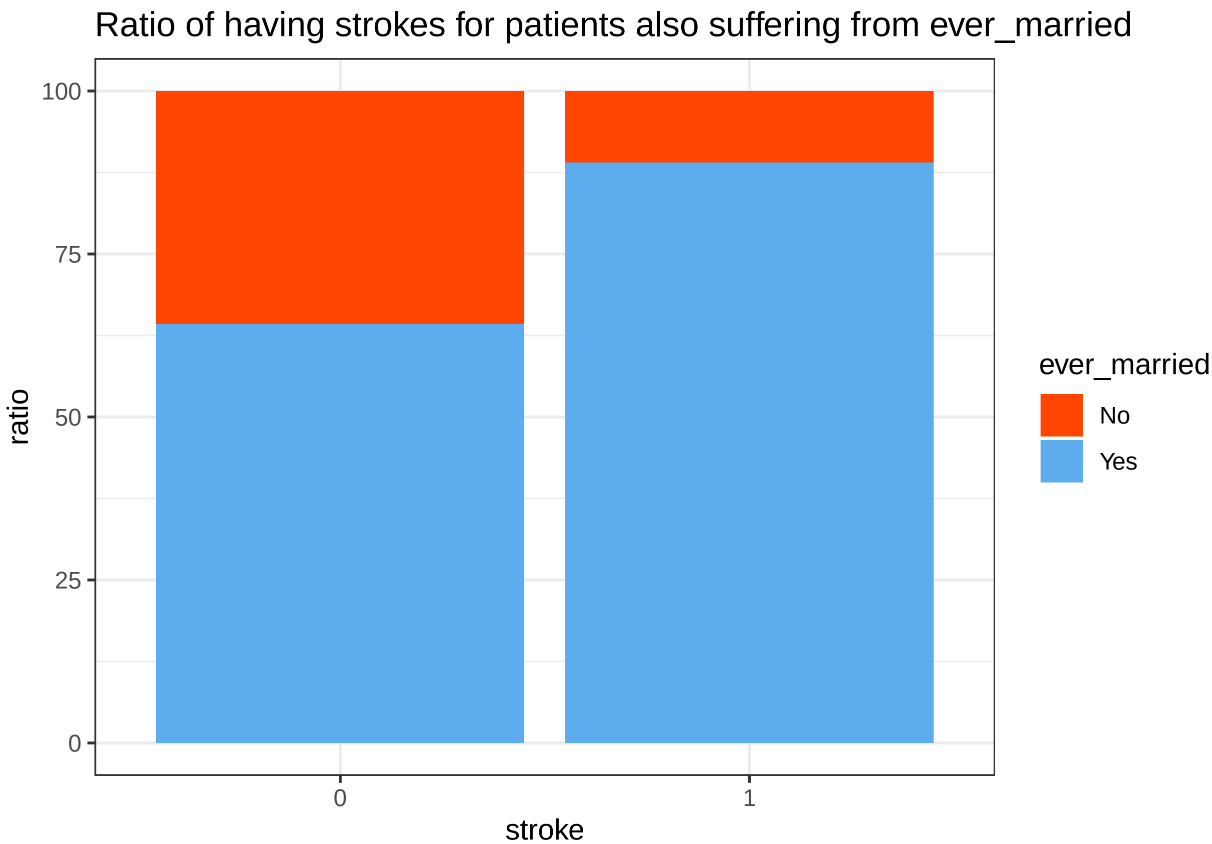

```r
ratio_barpplot("heart_disease")
```

```
## `summarise()` has grouped output by 'stroke'. You can override using the
## `.groups` argument.
```




```
ratio_barpplot("ever_married")
```

```
## `summarise()` has grouped output by 'stroke'. You can override using the
## `.groups` argument.
```



Predicting Stroke outcome

```r
install.packages("randomForest", repos = "https://cloud.r-project.org/")
```

```
## Installing package into '/geode2/home/u060/mdprin/Carbonate/R/x86_64-pc-linux-gnu-library/4.2'
## (as 'lib' is unspecified)
```

```r
library(randomForest)
```

```
## randomForest 4.7-1.1
```

```
## Type rfNews() to see new features/changes/bug fixes.
```

```
##
## Attaching package: 'randomForest'
```

```
## The following object is masked from 'package:ggplot2':
##
##     margin
```

```
## The following object is masked from 'package:dplyr':
##
##     combine
```

```r
install.packages("caret", repos = "https://cloud.r-project.org/")
```

```
## Installing package into '/geode2/home/u060/mdprin/Carbonate/R/x86_64-pc-linux-gnu-library/4.2'
## (as 'lib' is unspecified)
```

```r
library(caret)
```

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

```
##
## Attaching package: 'caret'

## The following object is masked from 'package:httr':
##
##     progress
```

```
formula<-(stroke~gender+age+hypertension+heart_disease+ever_married+work_type+Residence_type+avg_glucose
rf_clf<-randomForest(formula=formula,data=data)
pred<-predict(object=rf_clf, newdata=select(data, -stroke), type="class")
confusionMatrix(data=pred, reference=data$stroke)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction    0    1
##          0 4699   31
##          1    0  178
##
##                Accuracy : 0.9937
##                  95% CI : (0.991, 0.9957)
##     No Information Rate : 0.9574
##     P-Value [Acc > NIR] : < 2.2e-16
##
##                   Kappa : 0.9166
##
##  Mcnemar's Test P-Value : 7.118e-08
##
##             Sensitivity : 1.0000
##             Specificity : 0.8517
##          Pos Pred Value : 0.9934
##          Neg Pred Value : 1.0000
##              Prevalence : 0.9574
##          Detection Rate : 0.9574
##    Detection Prevalence : 0.9637
##       Balanced Accuracy : 0.9258
##
##        'Positive' Class : 0
##
```

```
# Central Limit Theorem
bmi<-data$bmi[data$stroke==0]
#hist(bmi, col="lightblue",breaks=40)
print(paste("Mean BMI of the total population is", round(mean(bmi),1)))
```

```
## [1] "Mean BMI of the total population is 28.8"
```

```
s<-2000
bmi_set1<-rep(0,20)
bmi_set2<-rep(0,200)
bmi_set3<-rep(0,2000)
for (i in 1:s){
  bmi_sample<-sample(bmi,size=20,replace=F)
  if (i<=2000){
    bmi_set3[i]<-mean(bmi_sample)
  }
```

```r
  if(i<=200){
    bmi_set2[i]<-mean(bmi_sample)
  }
  if(i<=20){
    bmi_set1[i]<-mean(bmi_sample)
  }
}
```

```r
library(reshape2)
```

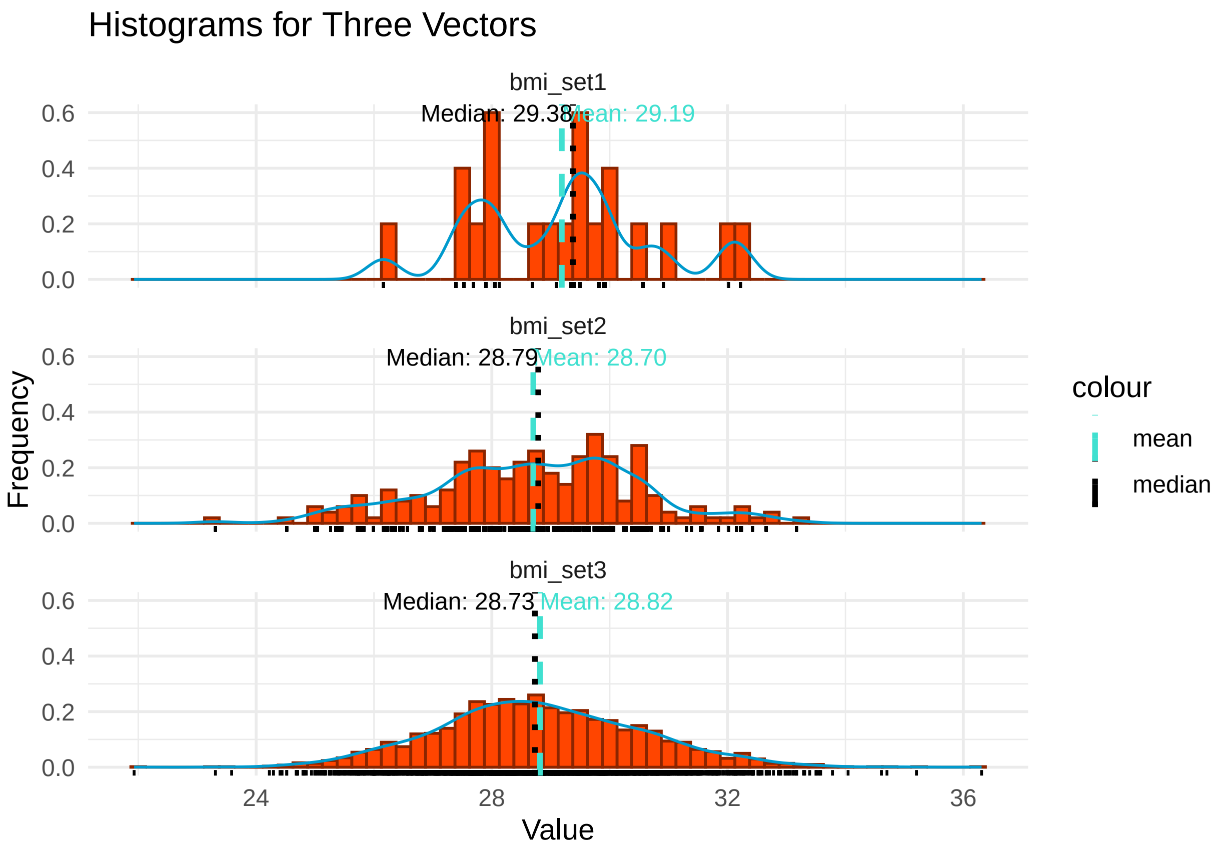
```
##
## Attaching package: 'reshape2'

## The following object is masked from 'package:tidyr':
##
##     smiths
```

```r
# Combine into a single data frame
df <- data.frame(bmi_set1, bmi_set2, bmi_set3)
mean_vals <- sapply(df, mean)
median_vals <- sapply(df, median)

# Create data frames for mean and median
mean_df <- data.frame(variable = names(mean_vals), value = mean_vals)
median_df <- data.frame(variable = names(median_vals), value = median_vals)
# Melt the data
melted_df <- melt(df)
```

```
## No id variables; using all as measure variables
```

```r
# Plot using ggplot2
ggplot(melted_df, aes(x=value)) +
  geom_histogram(aes(y=..density..), binwidth=0.25, bins=100, fill="orangered", color="orangered4", alph
  geom_density(color="deepskyblue3") +
  geom_rug() +
  geom_vline(data=mean_df, aes(xintercept=value, color="mean"), linetype="dashed", size=1) +
  geom_vline(data=median_df, aes(xintercept=value, color="median"), linetype="dotted", size=1) +
  geom_text(data=mean_df, aes(x=value, label=sprintf("Mean: %.2f", value), y=Inf, hjust=0), vjust=1, si
  geom_text(data=median_df, aes(x=value, label=sprintf("Median: %.2f", value), y=Inf, hjust=1), vjust=1
  facet_wrap(~variable, ncol=1) +
  scale_color_manual(values=c("mean"="turquoise", "median"="black")) +
  theme_minimal() +
  labs(title="Histograms for Three Vectors", x="Value", y="Frequency")
```

```
## Warning: The dot-dot notation (`..density..`) was deprecated in ggplot2 3.4.0.
## i Please use `after_stat(density)` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```



So, we can observe as the sample set is becoming larger and larger, the sampling distribution of the sample mean is having a normal or central tendency. And according to the Central Limit Theorem, mean of the sampling distribution of the sample mean is becoming equal to that of the actual population mean. 28.95 –> 28.97 –> 28.82 (whre, original population mean= 28.8)

```
#Law of Large Numbers (LLN)
#converting [1,2] to [0,1] using levels
hyper<-as.numeric(levels(data$hypertension))[data$hypertension]
str(hyper)
```

```
##  num [1:4908] 0 0 0 1 0 1 0 0 1 0 ...
```

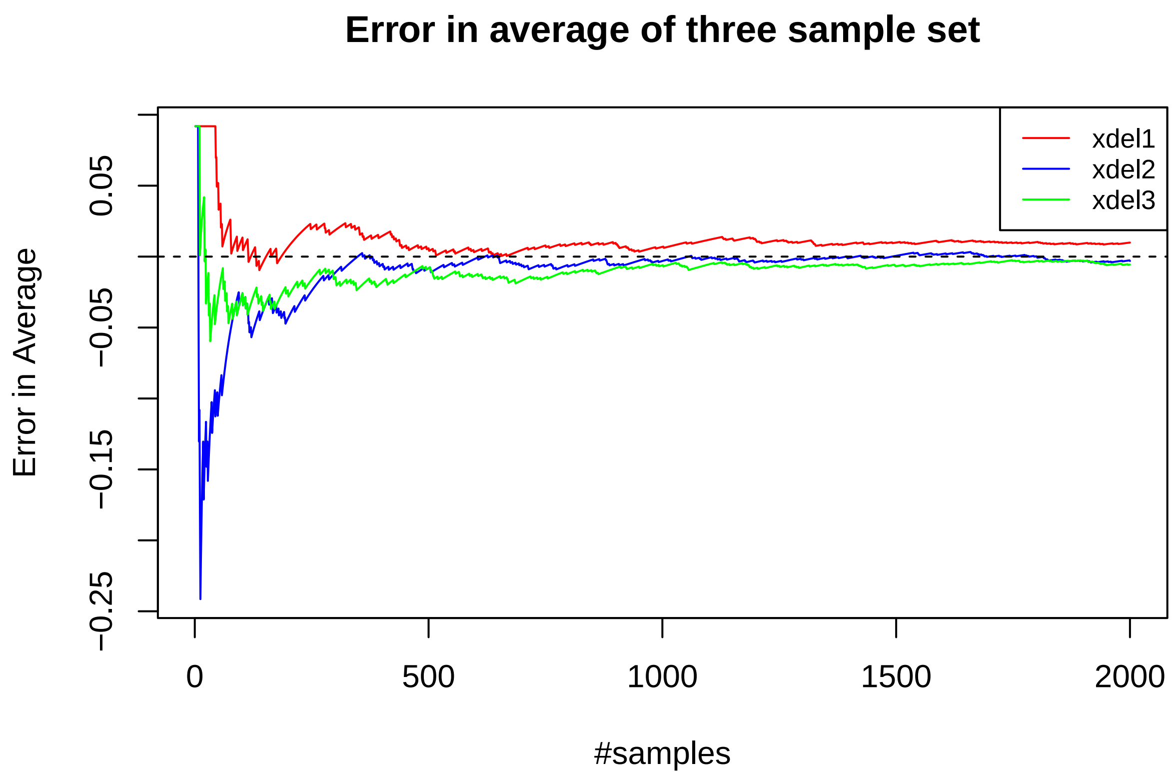
```
avg<-mean(hyper==1)
```

```
samples<- 2000
set1<-sample(hyper, samples, replace=FALSE)
set2<-sample(hyper, samples, replace=FALSE)
set3<-sample(hyper, samples, replace=FALSE)
```

```
xdel1<-rep(0,samples)
xdel2<-rep(0,samples)
xdel3<-rep(0,samples)
for (i in 1:samples){
  xdel1[i]<-mean(set1[1:i])
  xdel2[i]<-mean(set2[1:i])
  xdel3[i]<-mean(set3[1:i])
}
```

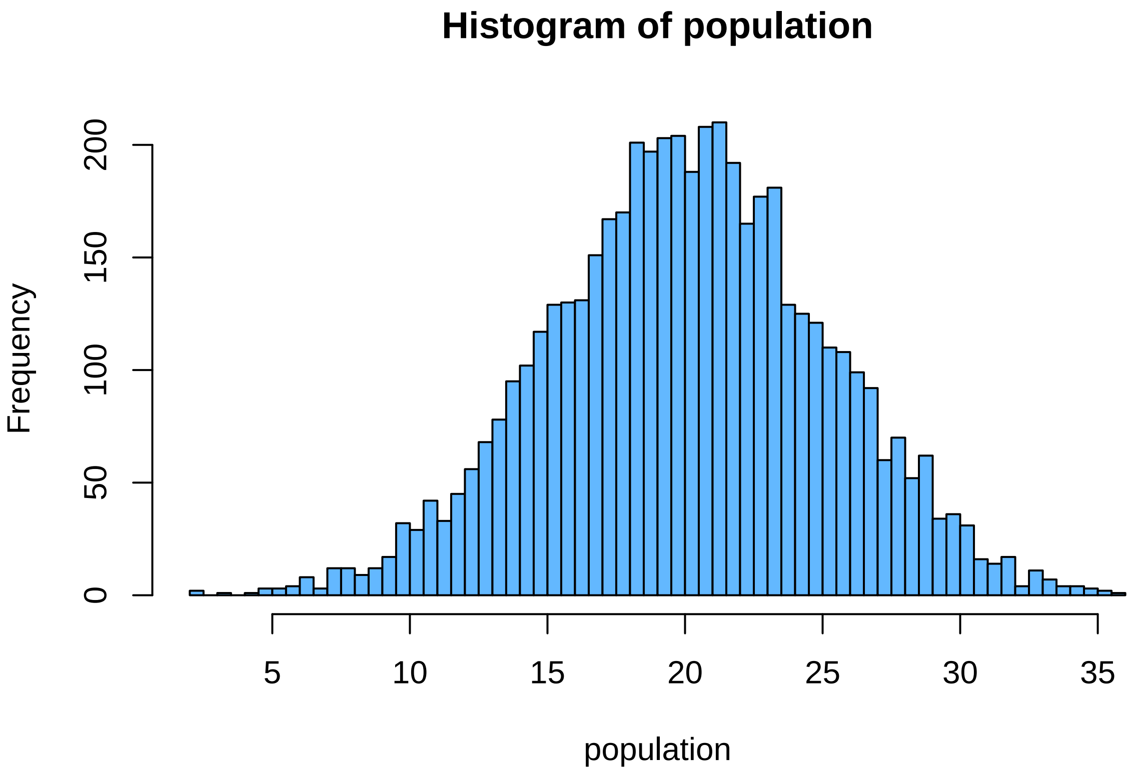
```
# Create a sequence of indices for x-axis
x <- seq(1, samples, by=1)
```

```r
# Plot the first vector
plot(x, avg-xdel1, type="l", col="red", ylim=c(min(avg-xdel1, avg-xdel2, avg-xdel3), max(avg-xdel1, avg-

# Add the second vector
lines(x, avg-xdel2, col="blue")

# Add the third vector
lines(x, avg-xdel3, col="green")

# Add the horizontal line at y=0
abline(h=0, col="black", lty=2)  # lty=2 makes the line dashed

# Add a legend
legend("topright", legend=c("xdel1", "xdel2", "xdel3"), col=c("red", "blue", "green"), lty=1, cex=0.8)
```



Hence, as the sample size become larger and larger the error in calculating ratio of people having hypertension trends to zero (a pure demonstration of Law of Large Numbers(LLN))

```r
#Confidence Intervals
# first using a random population
population<-rnorm(5000, 20, 5)
hist(population, breaks=50, col="steelblue1")
```




```
pop_mean=round(mean(population),3)
pop_sd=round(sd(population),3)
print(paste0("Population Mean ", pop_mean))
```

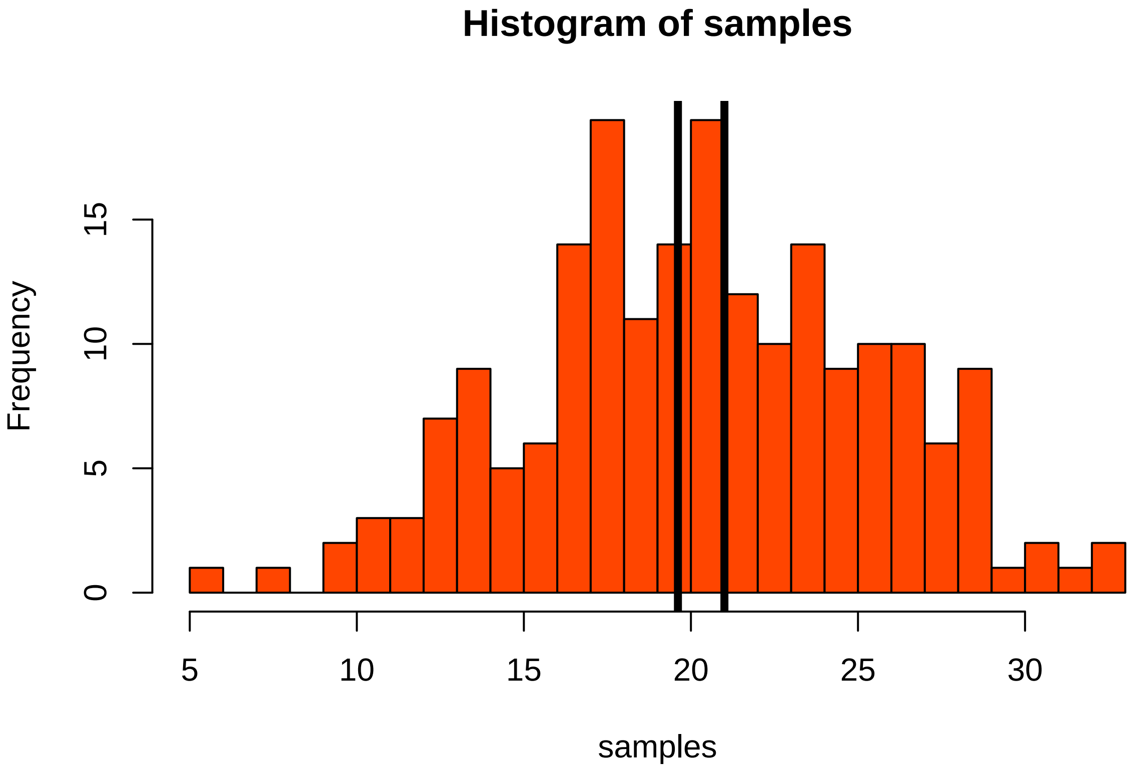
```
## [1] "Population Mean 20.085"
```

```
print(paste0("Population Std Err ", pop_sd))
```

```
## [1] "Population Std Err 5.019"
```

```
# constructing confidence interval:

# taking n=200 samples and trying to estimate the true population mean
n=200
samples<-sample(population, n, replace=FALSE)
samp_mean<-mean(samples)
# say, our claim is mean has changed.
# So, Null Hypothesis H_o=> mu = 19.977
# and, alternative Hypothesis H_a=> mu != 19.977

# for 95% CI:
alpha<- 0.05
quant<- 1-alpha/2
z<-qnorm(quant,lower.tail=TRUE) # calculating z-score from z-table
# using Z-statistic needs to know the true population std dev.
# assuming we know the true population std. dev (from previous step)
se<-pop_sd/sqrt(n)

upper_bound<-samp_mean + z*se
lower_bound<-samp_mean - z*se
```

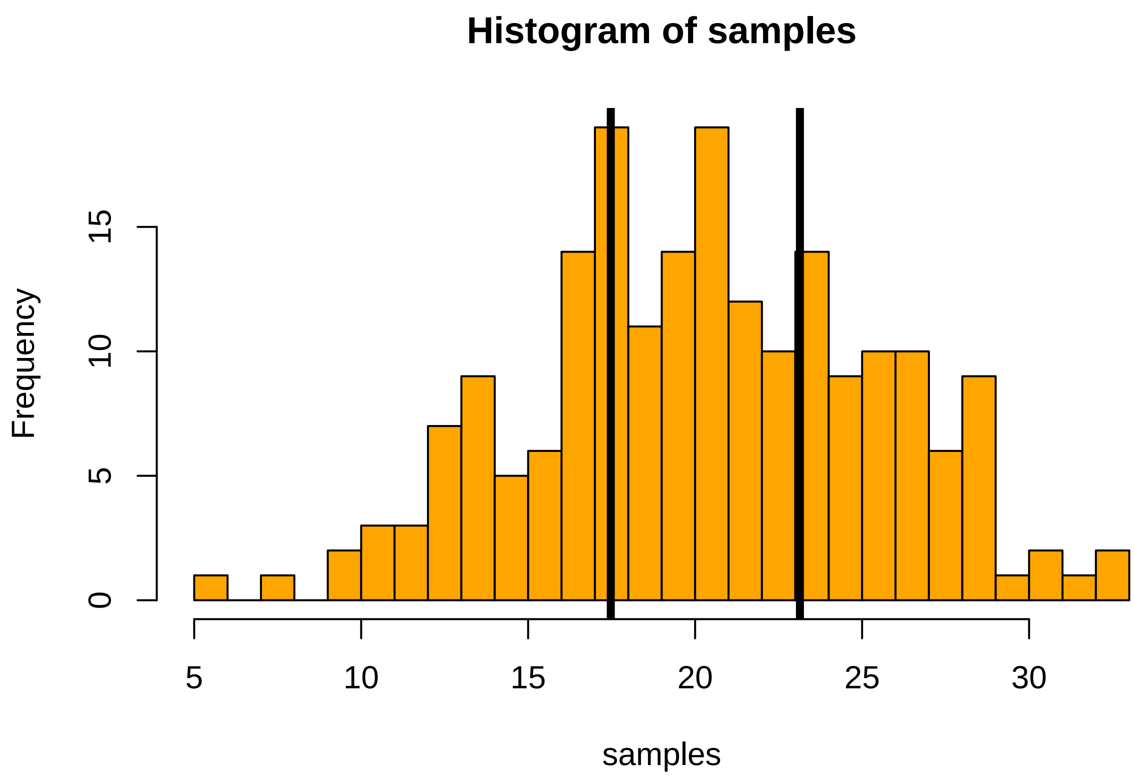
```r
hist(samples,breaks=20, col="orangered")
abline(v=upper_bound,lwd=4)
abline(v=lower_bound, lwd=4)
```




```r
print(paste0("With 95% confidence we can say that population mean is in interval [", round(lower_bound,
```

```
## [1] "With 95% confidence we can say that population mean is in interval [19.6; 21]"
```

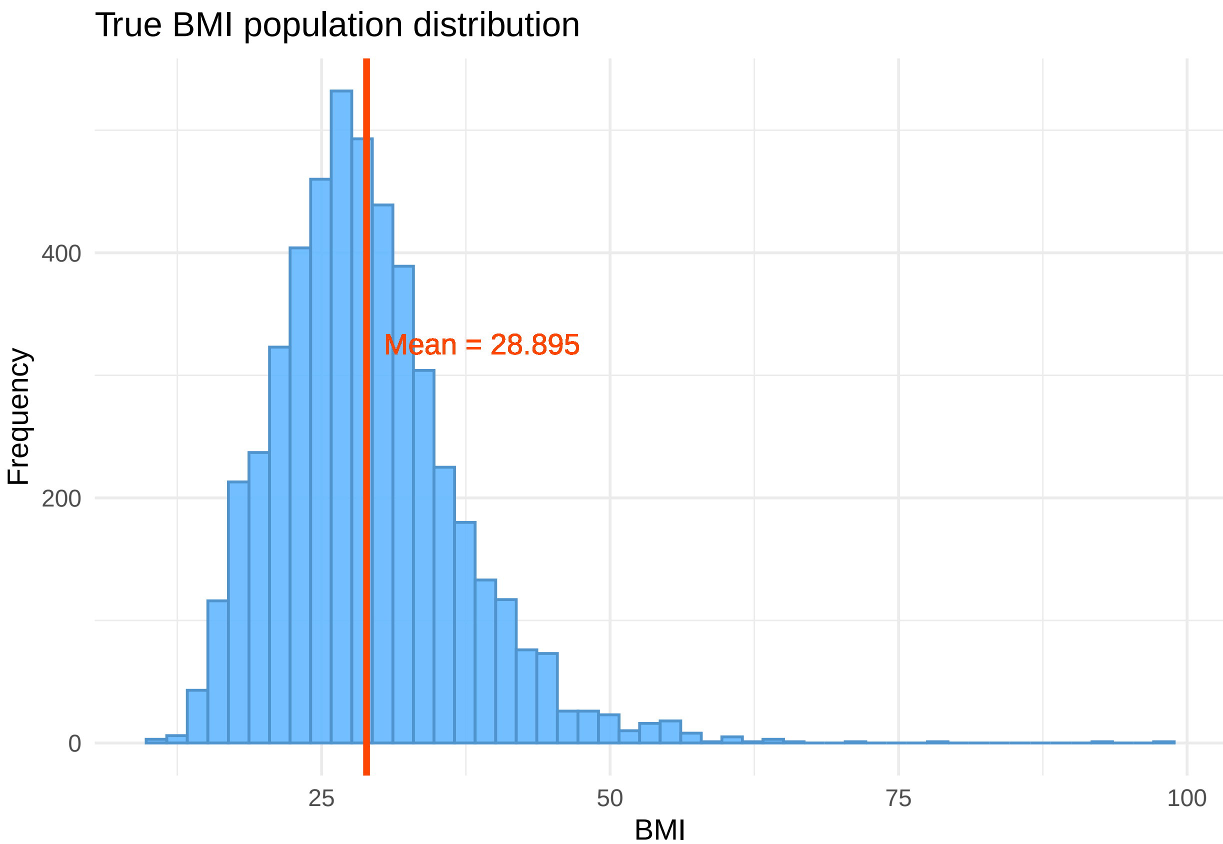
```r
# using t-statistic
# for t-statistic we do not have to have any prior knowledge(mean,sd) of the original population mean
dff<- n-1
t<-qt(quant,dff)
se<-mean(samples)/sqrt(n)
upper_bound<-samp_mean + t*se
lower_bound<-samp_mean - t*se

hist(samples,breaks=20, col="orange")
abline(v=upper_bound,lwd=4)
abline(v=lower_bound, lwd=4)
```




```
print(paste0("With 95% confidence we can say that population mean is in interval [", round(lower_bound,
```

```
## [1] "With 95% confidence we can say that population mean is in interval [17.5; 23.1]"
```

```
all_bmi<- data$bmi
bmi_pop_mean<-round(mean(all_bmi),3)
p <- ggplot(data.frame(all_bmi), aes(x = all_bmi)) +
  geom_histogram(bins = 50, fill = "steelblue1",col="steelblue3", alpha = 0.9) +
  geom_vline(aes(xintercept = bmi_pop_mean), color = "orangered1", linetype = "solid", size = 1.2) +
  geom_text(aes(x = bmi_pop_mean+10,y=300, label = paste("Mean =", bmi_pop_mean)), vjust = -1, hjust = 
  xlab("BMI") +
  ylab("Frequency") +
  theme_minimal()+
  labs(title="True BMI population distribution")

# Show the plot
print(p)
```

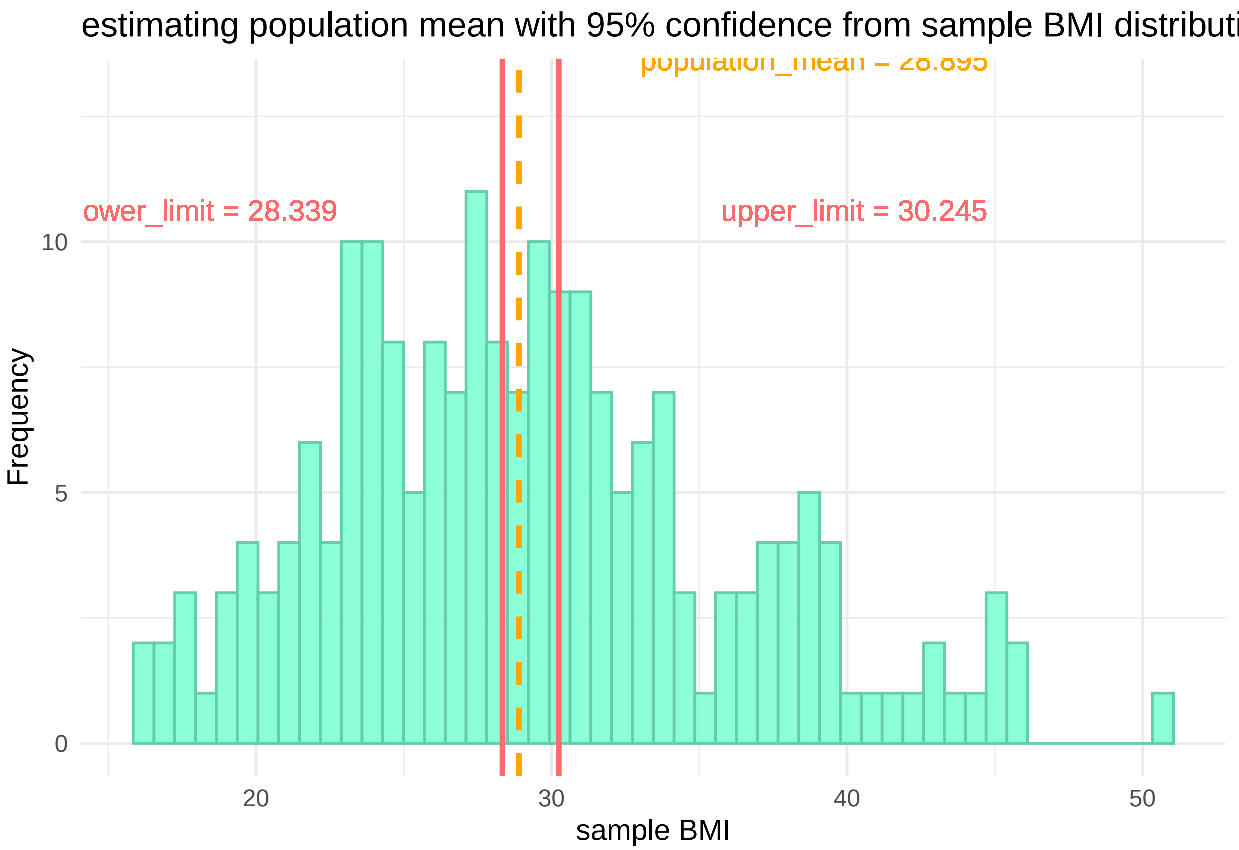



```
print(paste0("True population mean= ", bmi_pop_mean))
```

```
## [1] "True population mean= 28.895"
```

```
# 95% CI on bmi
# for t-statistic we do not have to have any prior knowledge(mean,sd) of the original population mean
sample_size<-200
samp_bmi<-sample(all_bmi, sample_size)
samp_bmi_mean<-round(mean(samp_bmi),3)
samp_bmi_sd<-sd(samp_bmi)
alpha<-0.05# as Confidence level= 95%
quant<-(1-alpha/2)
df_bmi<-sample_size-1
t_score<-qt(quant,df_bmi)
bmi_conf_upper<-samp_bmi_mean + t_score*(samp_bmi_sd/sqrt(sample_size))
bmi_conf_lower<-samp_bmi_mean - t_score*(samp_bmi_sd/sqrt(sample_size))


q <- ggplot(data.frame(samp_bmi), aes(x = samp_bmi)) +
  geom_histogram(bins = 50, fill = "aquamarine1",col="aquamarine3", alpha = 0.9) +
  geom_vline(aes(xintercept = bmi_conf_upper), color = "indianred1", linetype = "solid", size = 1) +
  geom_text(aes(x = bmi_conf_upper+10,y=10, label = paste("upper_limit =", round(bmi_conf_upper,3))), v
  geom_vline(aes(xintercept = bmi_conf_lower), color = "indianred1", linetype = "solid", size = 1) +
  geom_text(aes(x = bmi_conf_lower-10,y=10, label = paste("lower_limit =", round(bmi_conf_lower,3))), v
  geom_vline(aes(xintercept = bmi_pop_mean), color = "orange", linetype = "dashed", size = 1) +
  geom_text(aes(x = bmi_pop_mean+10,y=13, label = paste("population_mean =", bmi_pop_mean)), vjust = -1
  xlab("sample BMI") +
  ylab("Frequency") +
```

```r
  theme_minimal()+
  labs(title="estimating population mean with 95% confidence from sample BMI distribution ")

# Show the plot
print(q)
```




```r
print(paste0("sample population mean= ", samp_bmi_mean))
```

```
## [1] "sample population mean= 29.292"
```

```r
print(paste0("With 95% confidence we can say that population mean is in interval [", round(bmi_conf_lowe
```

```
## [1] "With 95% confidence we can say that population mean is in interval [28.3; 30.2]"
```

```r
sample_n(data,10)
```

```
##       id gender age hypertension heart_disease ever_married     work_type
## 1  28559   Male   2            0             0           No      children
## 2  47330   Male   9            0             0           No      children
## 3  58037   Male  21            0             0           No       Private
## 4  56976 Female  42            0             0          Yes       Private
## 5  49976 Female  54            0             1          Yes       Private
## 6  20364 Female   4            0             0           No      children
## 7  56233 Female  44            0             0           No       Private
## 8  54347   Male  61            0             0          Yes Self-employed
## 9  55680   Male  13            0             0           No      children
## 10 12807 Female  63            1             0          Yes       Private
##    Residence_type avg_glucose_level  bmi  smoking_status stroke
```

```
## 1           Urban             88.54 17.5         Unknown      0
## 2           Rural             60.39 16.4         Unknown      0
## 3           Rural             78.52 27.2    never smoked      0
## 4           Urban             96.01 38.7         Unknown      0
## 5           Urban            140.28 37.1 formerly smoked      0
## 6           Urban            107.25 12.0         Unknown      0
## 7           Rural            116.95 26.1    never smoked      0
## 8           Rural            155.32 26.6 formerly smoked      0
## 9           Urban            114.84 18.3         Unknown      0
## 10          Urban             81.54 24.2    never smoked      0
```

```r
# t- test
str<-data$age[data$stroke==1]
no_str<-data$age[data$stroke==0]
str_df <- data.frame(str)

# Create a data frame for individuals without stroke
no_str_df <- data.frame(no_str)

# Summarise the data frame for individuals with stroke
summary_str <- summarise(str_df,
                         mean_age = mean(str, na.rm = TRUE),
                         median_age = median(str, na.rm = TRUE),
                         sd_age = sd(str, na.rm = TRUE),
                         min_age = min(str, na.rm = TRUE),
                         max_age = max(str, na.rm = TRUE),
                         count = nrow(str_df))

# Summarise the data frame for individuals without stroke
summary_no_str <- summarise(no_str_df,
                            mean_age = mean(no_str, na.rm = TRUE),
                            median_age = median(no_str, na.rm = TRUE),
                            sd_age = sd(no_str, na.rm = TRUE),
                            min_age = min(no_str, na.rm = TRUE),
                            max_age = max(no_str, na.rm = TRUE),
                            count = nrow(no_str_df))
```

```r
# Print summaries
print(summary_str)
```

```
##   mean_age median_age   sd_age min_age max_age count
## 1 67.71292         70 12.40285      14      82   209
```

```r
print(summary_no_str)
```

```
##   mean_age median_age   sd_age min_age max_age count
## 1 41.76381         43 22.26931    0.08      82  4699
```

```r
#difference in average age for people having and not having a stroke:
mean(str)-mean(no_str)
```

```
## [1] 25.94911
```

So, we see here the average age difference = 25.949 our hypothesis: H_o : there is no age difference, mu= 0 H_a : there is a difference, mu != 0

```r
len_str<- length(str)
var_str<-var(str)


len_no_str<- length(no_str)
var_no_str<-var(no_str)

diff_mean<- mean(no_str)-mean(str)

se<-sqrt(var_str/len_str + var_no_str/len_no_str)


alpha<-0.05
quant<-(1-alpha/2)
df_age<-len_str+len_no_str-2

t_age<-qt(quant,df_age)

upper_limit<- diff_mean+t_age*se
lower_limit<- diff_mean-t_age*se

print(paste0("With 95% confidence we can say that population mean is in interval [", round(upper_limit,
```

```
## [1] "With 95% confidence we can say that population mean is in interval [-24.2; -27.7]"
```

As, the confidence interval doesn't include 0 rather is way below 0. So, with 95% confidence we can say that the age difference in between people having stroke and not having stroke is significant. So, we reject our Null Hypothesis (H_o) and accept alternative hypothesis (H_a)

```r
# alternative way:
t_age<- (diff_mean - 0)/se
print(paste("t score",t_age))
```

```
## [1] "t score -28.2863881984247"
```

```r
p_value <- pt(-abs(t_age), df_age, lower.tail = TRUE)
print(paste("Probability of having a t_score of that is:", p_value))
```

```
## [1] "Probability of having a t_score of that is: 1.70630768710462e-163"
```

Here, P_value « alpha : reject H_o accept H_a Hence, the age difference is significant.

```r
#using R library

t.test(age~stroke, data=data, var.equal=FALSE, paired=FALSE,conf.level=0.95)
```

```
##
##  Welch Two Sample t-test
##
## data:  age by stroke
## t = -28.286, df = 271.68, p-value < 2.2e-16
## alternative hypothesis: true difference in means between group 0 and group 1 is not equal to 0
## 95 percent confidence interval:
##  -27.75517 -24.14305
## sample estimates:
## mean in group 0 mean in group 1
##        41.76381        67.71292
```

```r
# using F statistic
var.test(age~stroke, data= data)
```

```
##
##  F test to compare two variances
##
## data:  age by stroke
## F = 3.2238, num df = 4698, denom df = 208, p-value < 2.2e-16
## alternative hypothesis: true ratio of variances is not equal to 1
## 95 percent confidence interval:
##  2.624126 3.890156
## sample estimates:
## ratio of variances
##           3.223819
```

```r
install.packages("bootstrap", repos = "https://cloud.r-project.org/")
```

```
## Installing package into '/geode2/home/u060/mdprin/Carbonate/R/x86_64-pc-linux-gnu-library/4.2'
## (as 'lib' is unspecified)
```

```r
library(bootstrap)
```

```r
#Resampling
bmi_len<- length(bmi)
bias_var=function(x){
  n=length(x)
  (n-1)*var(x)/n
}
jackknife(bmi, bias_var)
```

```
## $jack.se
## [1] 2.120335
##
## $jack.bias
## [1] -0.01331039
##
## $jack.values
##    [1] 62.52059 62.52261 62.51871 62.53487 62.52540 62.44916 62.51919 62.54482
##    [9] 62.54296 62.40409 62.53741 62.53562 62.52172 62.54395 62.50630 62.54182
##   [17] 62.52781 62.53702 62.54173 62.54274 62.50969 62.32649 62.54401 62.54504
##   [25] 62.53994 62.54155 62.54549 62.54474 62.54457 62.54433 62.54242 62.54304
##   [33] 62.54516 62.51052 62.54482 62.54389 62.54258 62.54462 62.54209 62.53927
##   [41] 62.54546 62.52195 62.52895 62.52702 62.53457 62.54526 62.54516 62.54551
##   [49] 62.54466 62.54068 62.54552 62.54551 62.53767 62.54258 62.53661 62.54428
##   [57] 62.54401 62.51847 62.50215 62.53233 62.54549 62.53316 62.54433 62.53380
##   [65] 62.54535 62.53915 62.54453 62.54526 62.53457 62.52477 62.54521 62.54258
##   [73] 62.51320 62.53781 62.53633 62.54118 62.53915 62.51847 62.54345 62.53533
##   [81] 62.52601 62.54395 62.54494 62.54371 62.40299 62.54529 62.52328 62.54490
##   [89] 62.54225 62.54274 62.52662 62.54553 62.46561 62.53843 62.54173 62.54359
##   [97] 62.54395 62.54553 62.54497 62.53148 62.54524 62.53024 62.53961 62.53972
##  [105] 62.54274 62.52127 62.53950 62.53904 62.26999 62.54542 62.54137 62.54533
##  [113] 62.54225 62.53715 62.54296 62.49905 62.53250 62.47286 62.51372 62.52951
##  [121] 62.54098 62.54389 62.53442 62.54453 62.54443 62.50773 62.54504 62.53078
##  [129] 62.53576 62.51424 62.50969 62.50913 62.51267 62.51627 62.54550 62.54490
##  [137] 62.52800 62.49255 62.53781 62.54146 62.53647 62.54428 62.52081 62.54542
```

```
## [145] 62.52261 62.53457 62.52838 62.51750 62.51133 62.51919 62.53316 62.51078
## [153] 62.54016 62.53994 62.54209 62.52349 62.52800 62.54443 62.53880 62.52456
## [161] 62.53426 62.53364 62.51651 62.54304 62.47902 62.51475 62.47826 62.54428
## [169] 62.54407 62.53688 62.53216 62.53199 62.53891 62.53619 62.49747 62.51750
## [177] 62.54549 62.54377 62.53938 62.40299 62.54173 62.53165 62.54443 62.54352
## [185] 62.54365 62.52059 62.54551 62.54544 62.53562 62.54546 62.54553 62.54407
## [193] 62.54474 62.53880 62.54535 62.53199 62.54553 62.54453 62.54546 62.50659
## [201] 62.53095 62.54494 62.52682 62.53880 62.54513 62.48844 62.53503 62.54137
## [209] 62.51577 62.52702 62.45186 62.54531 62.54258 62.54466 62.33595 62.54516
## [217] 62.54542 62.54504 62.54510 62.53619 62.53806 62.54448 62.53831 62.54250
## [225] 62.53591 62.53702 62.54318 62.54412 62.54383 62.52895 62.54389 62.54433
## [233] 62.53473 62.54098 62.54242 62.53233 62.54553 62.54537 62.49454 62.44084
## [241] 62.52035 62.53818 62.53741 62.53348 62.54552 62.54037 62.53457 62.51293
## [249] 62.54490 62.54146 62.54304 62.54478 62.53793 62.52581 62.54377 62.53547
## [257] 62.52838 62.54537 62.53517 62.53972 62.52035 62.51651 62.53380 62.51500
## [265] 62.54191 62.53250 62.48983 62.54407 62.54547 62.51078 62.52498 62.54281
## [273] 62.53983 62.52172 62.54553 62.54365 62.54433 62.53216 62.54325 62.54453
## [281] 62.53856 62.54457 62.54535 62.54504 62.43606 62.53042 62.54541 62.54486
## [289] 62.54068 62.15049 62.54098 62.51919 62.53728 62.54542 62.54438 62.54553
## [297] 62.52127 62.53715 62.54535 62.52622 62.54549 62.54457 62.51449 62.51676
## [305] 62.54547 62.51106 62.54521 62.51320 62.53517 62.51160 62.54173 62.54339
## [313] 62.53661 62.52581 62.51701 62.54478 62.54118 62.54428 62.53818 62.54377
## [321] 62.53576 62.53781 62.54539 62.53576 62.51601 62.54549 62.53250 62.52895
## [329] 62.54457 62.52240 62.53868 62.54526 62.53283 62.54137 62.52662 62.50687
## [337] 62.54311 62.54466 62.54304 62.53950 62.44826 62.54395 62.51823 62.54098
## [345] 62.54470 62.53927 62.54462 62.53972 62.52371 62.54526 62.51424 62.54433
## [353] 62.51577 62.54533 62.52781 62.54552 62.54497 62.53647 62.54482 62.50801
## [361] 62.53938 62.51449 62.54546 62.54217 62.53533 62.52081 62.54547 62.46887
## [369] 62.52217 62.54539 62.54490 62.54433 62.53856 62.53182 62.53961 62.54519
## [377] 62.53517 62.53843 62.54533 62.54457 62.54513 62.54537 62.40409 62.53904
## [385] 62.53576 62.54482 62.53442 62.54546 62.53781 62.51726 62.54533 62.53332
## [393] 62.53818 62.54553 62.54457 62.53591 62.54526 62.51651 62.53831 62.54289
## [401] 62.53591 62.54539 62.48527 62.54549 62.54541 62.53395 62.53781 62.39176
## [409] 62.54118 62.54474 62.54289 62.53661 62.52195 62.54383 62.53250 62.39176
## [417] 62.54521 62.53078 62.54513 62.53533 62.54553 62.53395 62.54371 62.53380
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## [4689] 62.51500 62.51823 62.54547 62.54155 62.53473 62.47597 62.52328 62.51894
## [4697] 62.54486 62.54332 62.54407
##
## $call
## jackknife(x = bmi, theta = bias_var)
```

B O 0 T S T R A P P I N G

Statistical Rigor: Estimation of Sampling Distribution: It allows for the empirical estimation of the sampling distribution of almost any statistic, providing a way to estimate standard errors, confidence intervals, and other distributional characteristics. Bias and Variance Estimation: Bootstrapping can help in estimating the bias and variance of a statistic, providing more information than just a point estimate.

Flexibility: Model Validation: It can be used for model validation and for diagnosing the fit of a model. Hypothesis Testing: Bootstrapping can be adapted for hypothesis testing, especially for tests where the analytic form is complex or not available. Small Sample Performance Small Sample Size: Bootstrapping can be particularly useful when your sample size is small, making it difficult to make reliable parametric assumptions.

Limitations and Caveats: It's important to note that while bootstrapping is powerful, it is not without its limitations. For example:

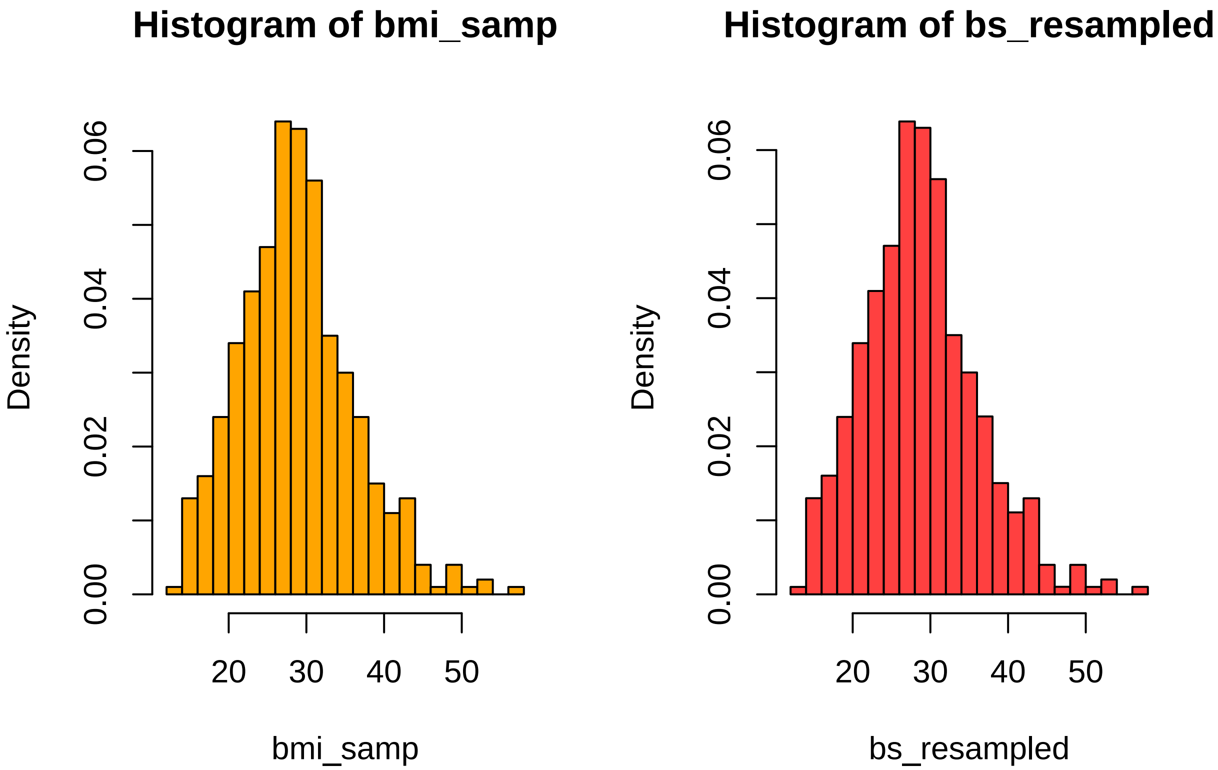
It may not perform well for data that has a complex dependence structure (e.g., time series data). Bootstrapping provides an approximation, and the quality of this approximation depends on the actual sample size and the underlying distribution.

```
#Bootstrapping
sample_size<- 500
samples<- 10000
```

```r
bmi_samp<- sample(bmi, sample_size, replace = FALSE)
print(paste("Mean of the sampled true population: ",mean(bmi_samp)))
```

```
## [1] "Mean of the sampled true population:  28.7948"
```

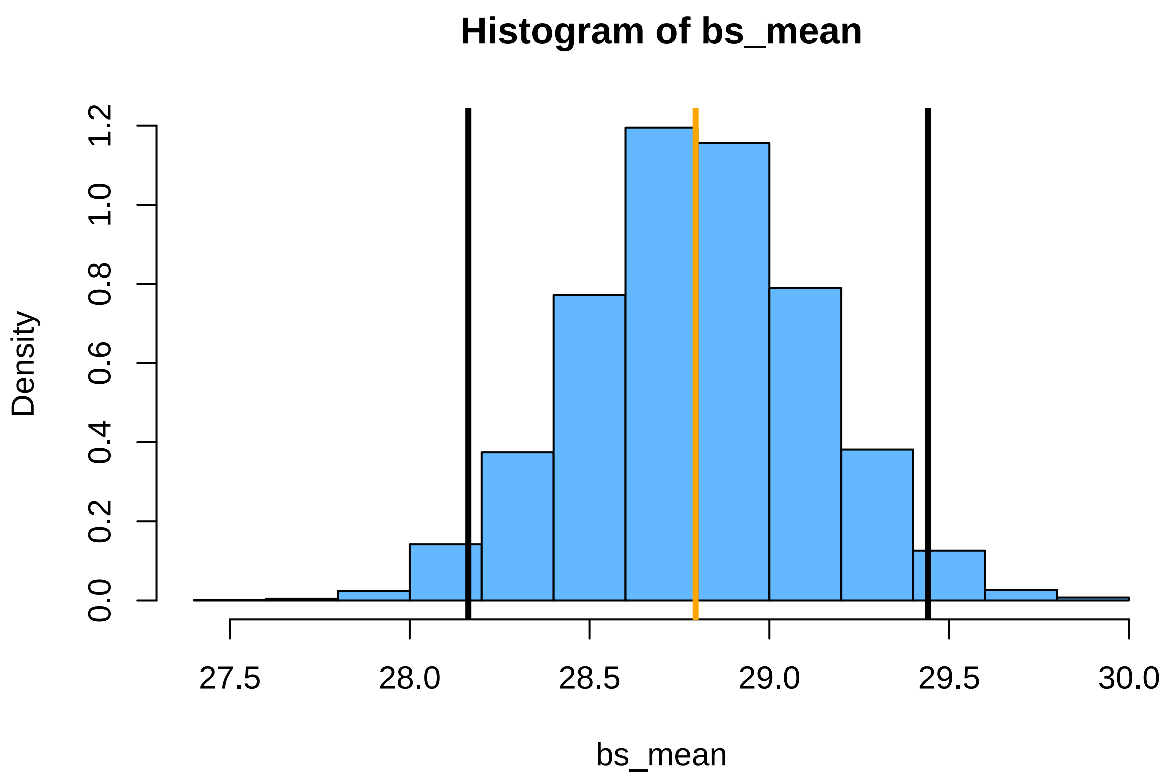
```r
bs_resampled<-matrix(sample(bmi_samp, sample_size*samples,replace = TRUE),nrow=samples, ncol=sample_siz
par(mfcol=c(1,2))
hist(bmi_samp,probability=TRUE,breaks=20, col="orange")
hist(bs_resampled,probability=TRUE, breaks=20, col="brown1")
```



Here, both distribution is looking identical. And it was expected. Cause we were trying to emulate the left one ((assumed)true distribution(though it was sampled from total population, just assume that it is the true distribution)) by sampling(bootsrapping) many times and got that on the right histogram.

```r
#calculating mean for each row
bs_mean<-rowMeans(bs_resampled)

hist(bs_mean,probability = TRUE, breaks=10, col="steelblue1")
abline(v=mean(bmi_samp),col="orange",lwd=3)
abline(v=quantile(bs_mean,c(.025,0.975)), lwd=3)# 95% confidence interval
```




```
print(paste("Std. error: ", round(sd(bs_mean),3)))
```

```
## [1] "Std. error:  0.324"
```

The standard deviation of this bootstrapped distribution gives us an idea of how much mean(statistic) would vary if we were to draw many different samples from the population, thereby acting as an estimate of the standard error.

```
# getting confidence interval in every possible way:
# say, we want to see the prevalence of hypertension in our population
n=200
hyper<-sample(data$hypertension,n)
hyper_prop<-length(hyper[hyper==1])
print(binom.confint(hyper_prop, n=n, conf.level = 0.95, methods = "all"))
```

```
##           method  x   n       mean      lower      upper
## 1  agresti-coull 13 200 0.06500000 0.03744211 0.10895332
## 2     asymptotic 13 200 0.06500000 0.03083389 0.09916611
## 3          bayes 13 200 0.06716418 0.03457082 0.10225126
## 4        cloglog 13 200 0.06500000 0.03640889 0.10485405
## 5          exact 13 200 0.06500000 0.03506071 0.10858724
## 6          logit 13 200 0.06500000 0.03811331 0.10871006
## 7         probit 13 200 0.06500000 0.03724733 0.10663196
## 8        profile 13 200 0.06500000 0.03629941 0.10475423
## 9            lrt 13 200 0.06500000 0.03629393 0.10475306
## 10     prop.test 13 200 0.06500000 0.03650749 0.11104309
## 11        wilson 13 200 0.06500000 0.03837635 0.10801908
```

That means, with 95% confidence we can say, roughly [4% to 12%] of the population have hypertension.