Project

2022-11-17

```
library(readr)
library(imputeTS)
```

```
## Registered S3 method overwritten by 'quantmod':
##   method            from
##   as.zoo.data.frame zoo
```

```
library(ggplot2)
library(kernlab)
```

```
##
## Attaching package: 'kernlab'
```

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

```
library(caret)
```

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

```
library(tidyverse)
```

```
## -- Attaching packages --------------------------------------- tidyverse 1.3.2 --
```

```
## v tibble  3.1.8      v dplyr   1.0.10
## v tidyr   1.2.1      v stringr 1.4.1
## v purrr   0.3.4      v forcats 0.5.2
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x kernlab::alpha() masks ggplot2::alpha()
## x purrr::cross()   masks kernlab::cross()
## x dplyr::filter()  masks stats::filter()
## x dplyr::lag()     masks stats::lag()
## x purrr::lift()    masks caret::lift()
```

```
library(dplyr)
library(rio)
library(rpart)
library(rpart.plot)
library(e1071)
library(arules)
```

```
## Loading required package: Matrix
##
## Attaching package: ’Matrix’
##
## The following objects are masked from ’package:tidyr’:
##
##     expand, pack, unpack
##
##
## Attaching package: ’arules’
##
## The following object is masked from ’package:dplyr’:
##
##     recode
##
## The following object is masked from ’package:kernlab’:
##
##     size
##
## The following objects are masked from ’package:base’:
##
##     abbreviate, write
```

```
library(arulesViz)
library(rsample)
```

```
##
## Attaching package: ’rsample’
##
## The following object is masked from ’package:e1071’:
##
##     permutations
```

```
library(ggmap)
```

```
## Google’s Terms of Service: https://cloud.google.com/maps-platform/terms/.
## Please cite ggmap if you use it! See citation("ggmap") for details.
```

```
library(mapproj)
```

```
## Loading required package: maps
##
## Attaching package: ’maps’
##
## The following object is masked from ’package:purrr’:
##
##     map
```

```
data <- read_csv("https://intro-datascience.s3.us-east-2.amazonaws.com/HMO_data.csv")
```

```
## Rows: 7582 Columns: 14
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr (8): smoker, location, location_type, education_level, yearly_physical, ...
## dbl (6): X, age, bmi, children, hypertension, cost
##
## i Use ‘spec()‘ to retrieve the full column specification for this data.
## i Specify the column types or set ‘show_col_types = FALSE‘ to quiet this message.
```

```
proj_df <- data.frame(data)
str(proj_df)
```

```
## 'data.frame':    7582 obs. of  14 variables:
##  $ X              : num  1 2 3 4 5 7 9 10 11 12 ...
##  $ age            : num  18 19 27 34 32 47 36 59 24 61 ...
##  $ bmi            : num  27.9 33.8 33 22.7 28.9 ...
##  $ children       : num  0 1 3 0 0 1 2 0 0 0 ...
##  $ smoker         : chr  "yes" "no" "no" "no" ...
##  $ location       : chr  "CONNECTICUT" "RHODE ISLAND" "MASSACHUSETTS" "PENNSYLVANIA" ...
##  $ location_type  : chr  "Urban" "Urban" "Urban" "Country" ...
##  $ education_level: chr  "Bachelor" "Bachelor" "Master" "Master" ...
##  $ yearly_physical: chr  "No" "No" "No" "No" ...
##  $ exercise       : chr  "Active" "Not-Active" "Active" "Not-Active" ...
##  $ married        : chr  "Married" "Married" "Married" "Married" ...
##  $ hypertension   : num  0 0 0 1 0 0 0 1 0 0 ...
##  $ gender         : chr  "female" "male" "male" "male" ...
##  $ cost           : num  1746 602 576 5562 836 ...
```

```
summary(proj_df)
```

```
##        X                  age             bmi           children    
##  Min.   :        1   Min.   :18.00   Min.   :15.96   Min.   :0.000  
##  1st Qu.:     5635   1st Qu.:26.00   1st Qu.:26.60   1st Qu.:0.000  
##  Median :    24916   Median :39.00   Median :30.50   Median :1.000  
##  Mean   :   712602   Mean   :38.89   Mean   :30.80   Mean   :1.109  
##  3rd Qu.:   118486   3rd Qu.:51.00   3rd Qu.:34.77   3rd Qu.:2.000  
##  Max.   :131101111   Max.   :66.00   Max.   :53.13   Max.   :5.000  
##                                      NA's   :78                     
##     smoker            location         location_type      education_level   
##  Length:7582        Length:7582        Length:7582        Length:7582       
##  Class :character   Class :character   Class :character   Class :character  
##  Mode  :character   Mode  :character   Mode  :character   Mode  :character  
##                                                                             
##                                                                             
##                                                                             
##                                                                             
##  yearly_physical      exercise           married           hypertension   
##  Length:7582        Length:7582        Length:7582        Min.   :0.0000  
##  Class :character   Class :character   Class :character   1st Qu.:0.0000  
##  Mode  :character   Mode  :character   Mode  :character   Median :0.0000  
##                                                           Mean   :0.2005  
##                                                           3rd Qu.:0.0000  
##                                                           Max.   :1.0000  
##                                                           NA's   :80      
##     gender                cost      
##  Length:7582        Min.   :    2  
##  Class :character   1st Qu.:  970  
##  Mode  :character   Median : 2500  
##                     Mean   : 4043  
##                     3rd Qu.: 4775  
##                     Max.   :55715  
## 
```

```
any(is.na(proj_df$X))
```

```
## [1] FALSE
```

```
any(is.na(proj_df$age))
```

```
## [1] FALSE
```

```
any(is.na(proj_df$bmi))
```

```
## [1] TRUE
```

```
proj_df$bmi <- na.interpolation(proj_df$bmi, option = "linear")
```

```
## Warning: na.interpolation will be replaced by na_interpolation.
##             Functionality stays the same.
##             The new function name better fits modern R code style guidelines.
##             Please adjust your code accordingly.
```

```
any(is.na(proj_df$bmi))
```

```
## [1] FALSE
```

```
any(is.na(proj_df$children))
```

```
## [1] FALSE
```

```
any(is.na(proj_df$smoker))
```

```
## [1] FALSE
```

```
any(is.na(proj_df$location))
```

```
## [1] FALSE
```

```
any(is.na(proj_df$location_type))
```

```
## [1] FALSE
```

```r
any(is.na(proj_df$hypertension))
```

```
## [1] TRUE
```

```r
proj_df$hypertension <- na.interpolation(proj_df$hypertension)
```

```
## Warning: na.interpolation will be replaced by na_interpolation.
##            Functionality stays the same.
##            The new function name better fits modern R code style guidelines.
##            Please adjust your code accordingly.
```

```r
any(is.na(proj_df$hypertension))
```

```
## [1] FALSE
```

```r
any(is.na(proj_df$cost))
```

```
## [1] FALSE
```

```r
proj_df$state_name <- proj_df$location
quantile(proj_df$cost)
```

```
##    0%   25%   50%   75%  100% 
##     2   970  2500  4775 55715
```

```r
# proj_df$expensive <- with(proj_df, ifelse(cost > 4775, "TRUE", "FALSE"))
proj_df$expensive <- proj_df$cost>4775
Expensive <- proj_df %>% group_by(expensive) %>% filter(expensive==1)
InExpensive <- proj_df %>% group_by(expensive) %>% filter(expensive==0)

proj_df$expensive <- as.factor(proj_df$expensive)
#View(proj_df)
head(proj_df)
```

```
##   X age    bmi children smoker      location location_type education_level
## 1 1  18 27.900        0    yes   CONNECTICUT         Urban        Bachelor
## 2 2  19 33.770        1     no  RHODE ISLAND         Urban        Bachelor
## 3 3  27 33.000        3     no MASSACHUSETTS         Urban          Master
## 4 4  34 22.705        0     no  PENNSYLVANIA       Country          Master
## 5 5  32 28.880        0     no  PENNSYLVANIA       Country             PhD
## 6 7  47 33.440        1     no  PENNSYLVANIA         Urban        Bachelor
##   yearly_physical   exercise married hypertension gender cost    state_name
## 1              No     Active Married            0 female 1746   CONNECTICUT
## 2              No Not-Active Married            0   male  602  RHODE ISLAND
## 3              No     Active Married            0   male  576 MASSACHUSETTS
## 4              No Not-Active Married            1   male 5562  PENNSYLVANIA
## 5              No Not-Active Married            0   male  836  PENNSYLVANIA
## 6              No Not-Active Married            0 female 3842  PENNSYLVANIA
##   expensive
## 1     FALSE
## 2     FALSE
## 3     FALSE
## 4      TRUE
## 5     FALSE
## 6     FALSE
```

```
str(proj_df)
```

```
## ’data.frame':    7582 obs. of  16 variables:
##  $ X              : num  1 2 3 4 5 7 9 10 11 12 ...
##  $ age            : num  18 19 27 34 32 47 36 59 24 61 ...
##  $ bmi            : num  27.9 33.8 33 22.7 28.9 ...
##  $ children       : num  0 1 3 0 0 1 2 0 0 0 ...
##  $ smoker         : chr  "yes" "no" "no" "no" ...
##  $ location       : chr  "CONNECTICUT" "RHODE ISLAND" "MASSACHUSETTS" "PENNSYLVANIA" ...
##  $ location_type  : chr  "Urban" "Urban" "Urban" "Country" ...
##  $ education_level: chr  "Bachelor" "Bachelor" "Master" "Master" ...
##  $ yearly_physical: chr  "No" "No" "No" "No" ...
##  $ exercise       : chr  "Active" "Not-Active" "Active" "Not-Active" ...
##  $ married        : chr  "Married" "Married" "Married" "Married" ...
##  $ hypertension   : num  0 0 0 1 0 0 0 1 0 0 ...
##  $ gender         : chr  "female" "male" "male" "male" ...
##  $ cost           : num  1746 602 576 5562 836 ...
##  $ state_name     : chr  "CONNECTICUT" "RHODE ISLAND" "MASSACHUSETTS" "PENNSYLVANIA" ...
##  $ expensive      : Factor w/ 2 levels "FALSE","TRUE": 1 1 1 2 1 1 1 2 1 1 ...
```

```
mean(Expensive$bmi)
```

```
## [1] 32.83403
```

```
mean(Expensive$age)
```

```
## [1] 45.3847
```

```
mean(Expensive$children)
```

```
## [1] 1.238522
```

```
mean(InExpensive$bmi)
```

```
## [1] 30.11793
```

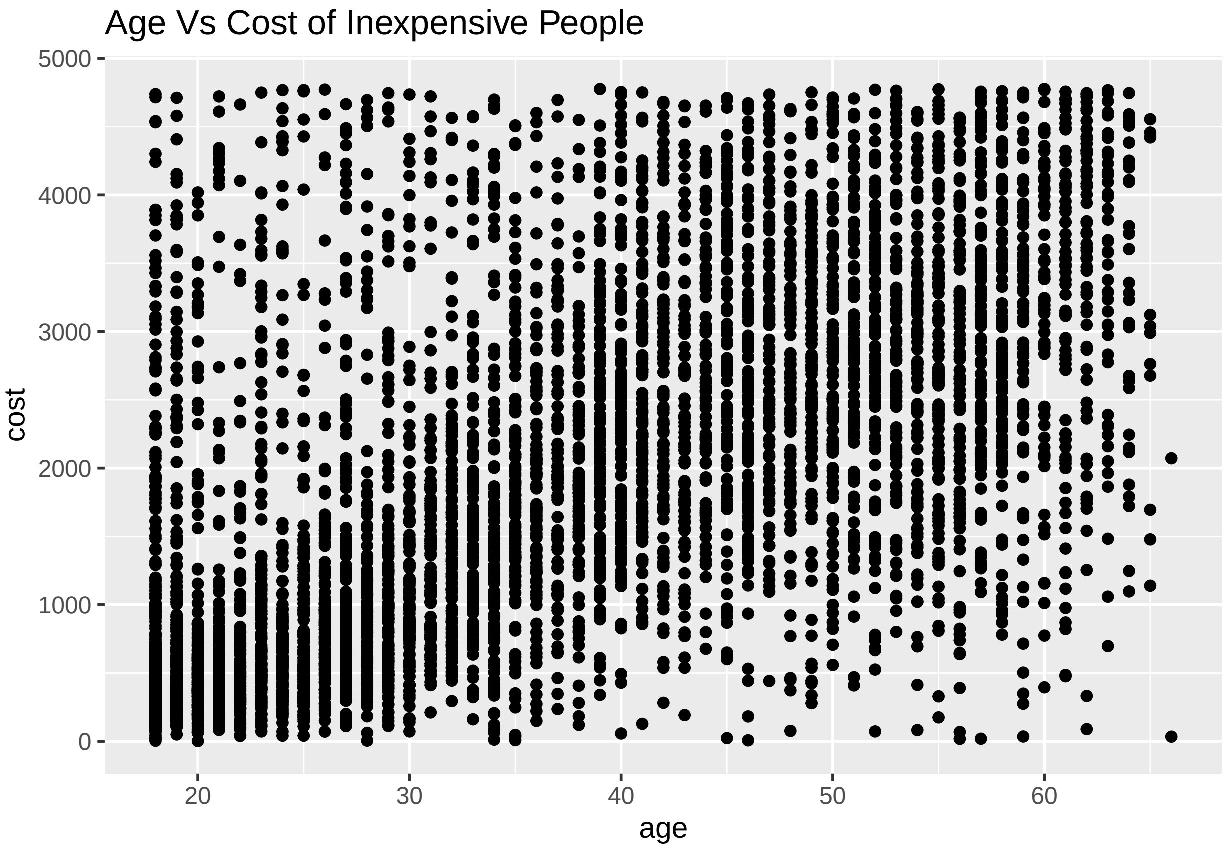
```
mean(InExpensive$age)
```

```
## [1] 36.72006
```

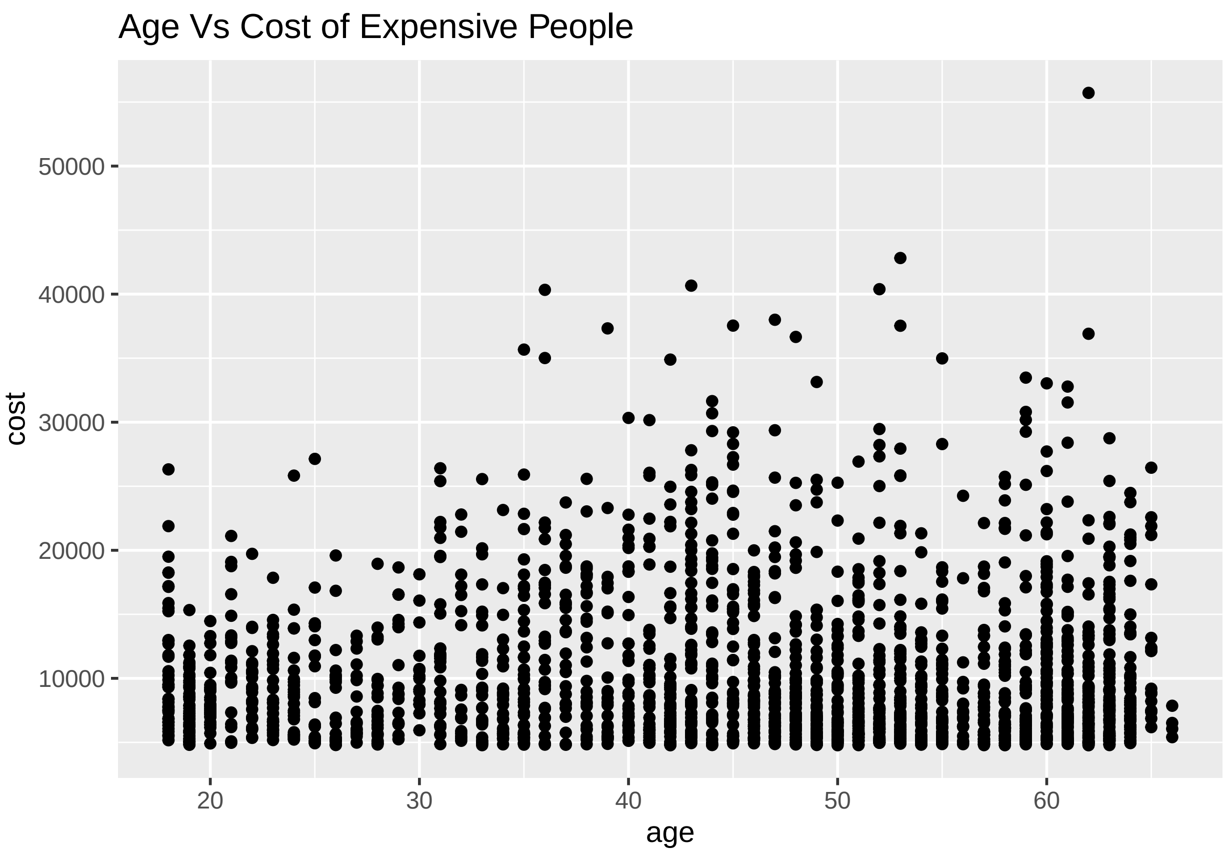
```
mean(InExpensive$children)
```

```
## [1] 1.066467
```

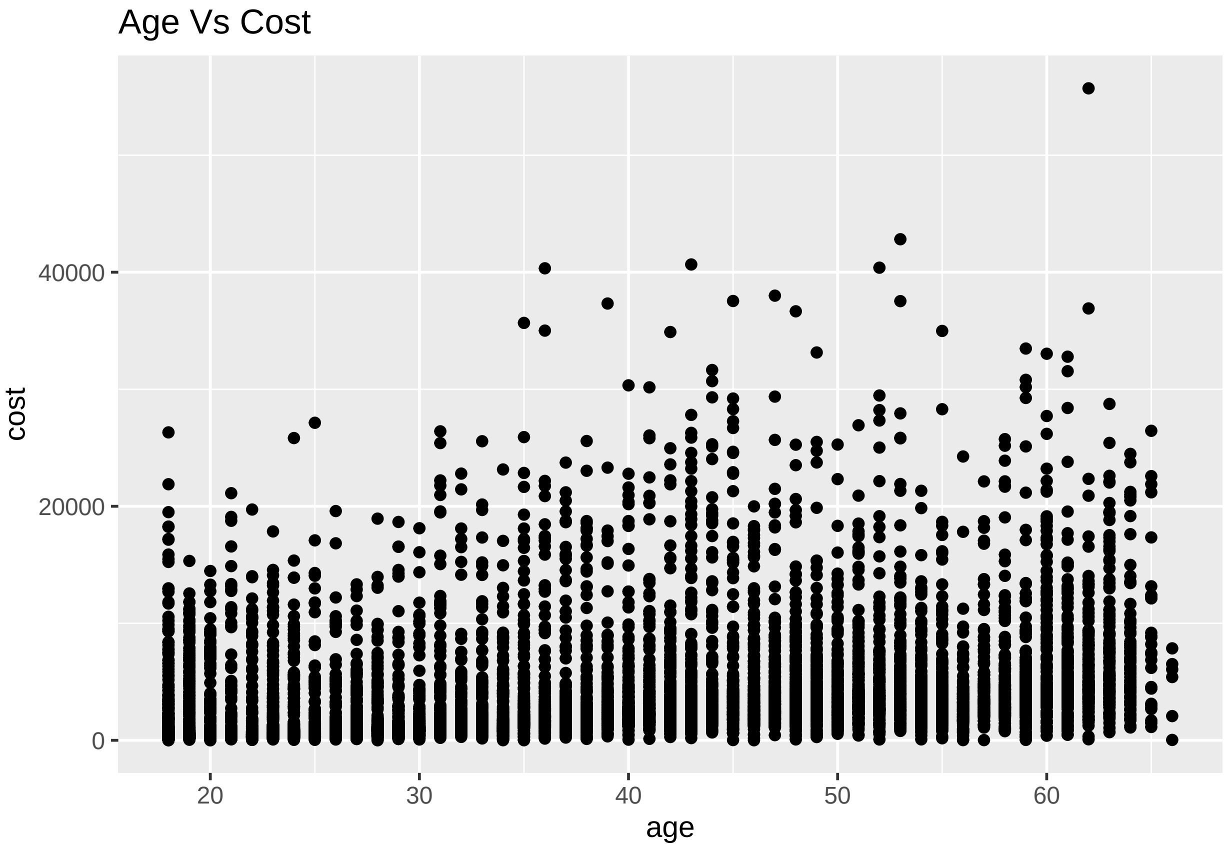
```
ggplot(InExpensive, aes(x=age,y=cost))+geom_point() + ggtitle("Age Vs Cost of Inexpensive People")
```



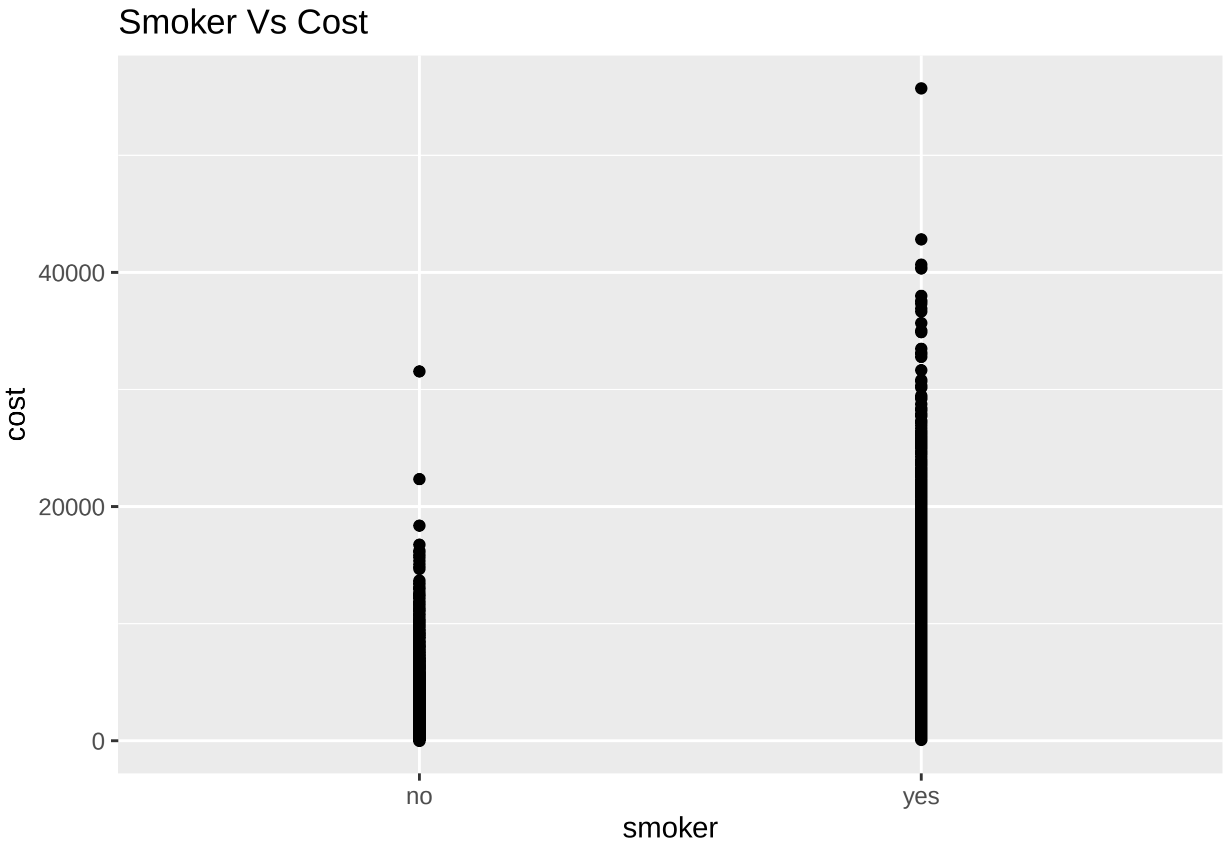
```
ggplot(Expensive, aes(x=age,y=cost))+geom_point() + ggtitle("Age Vs Cost of Expensive People")
```



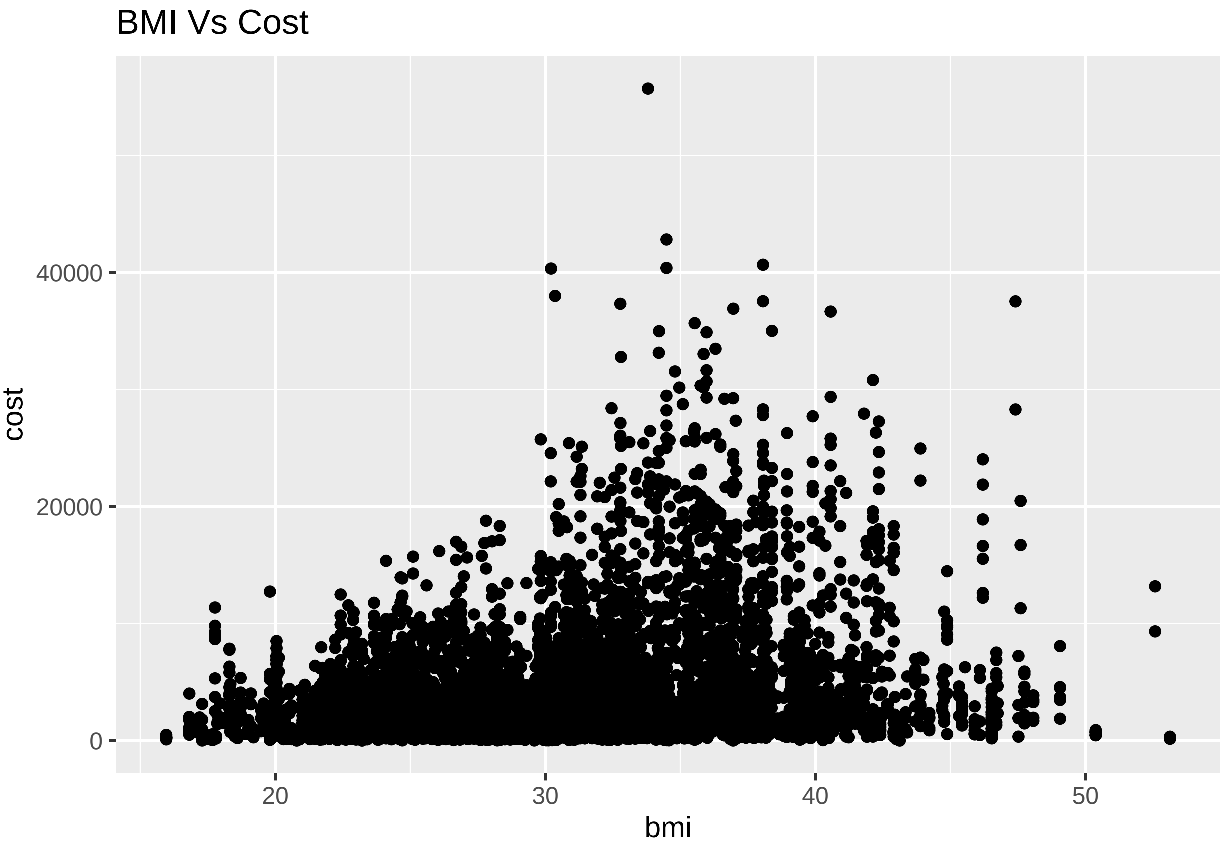
```
ggplot(proj_df, aes(x=age,y=cost))+geom_point() + ggtitle("Age Vs Cost")
```



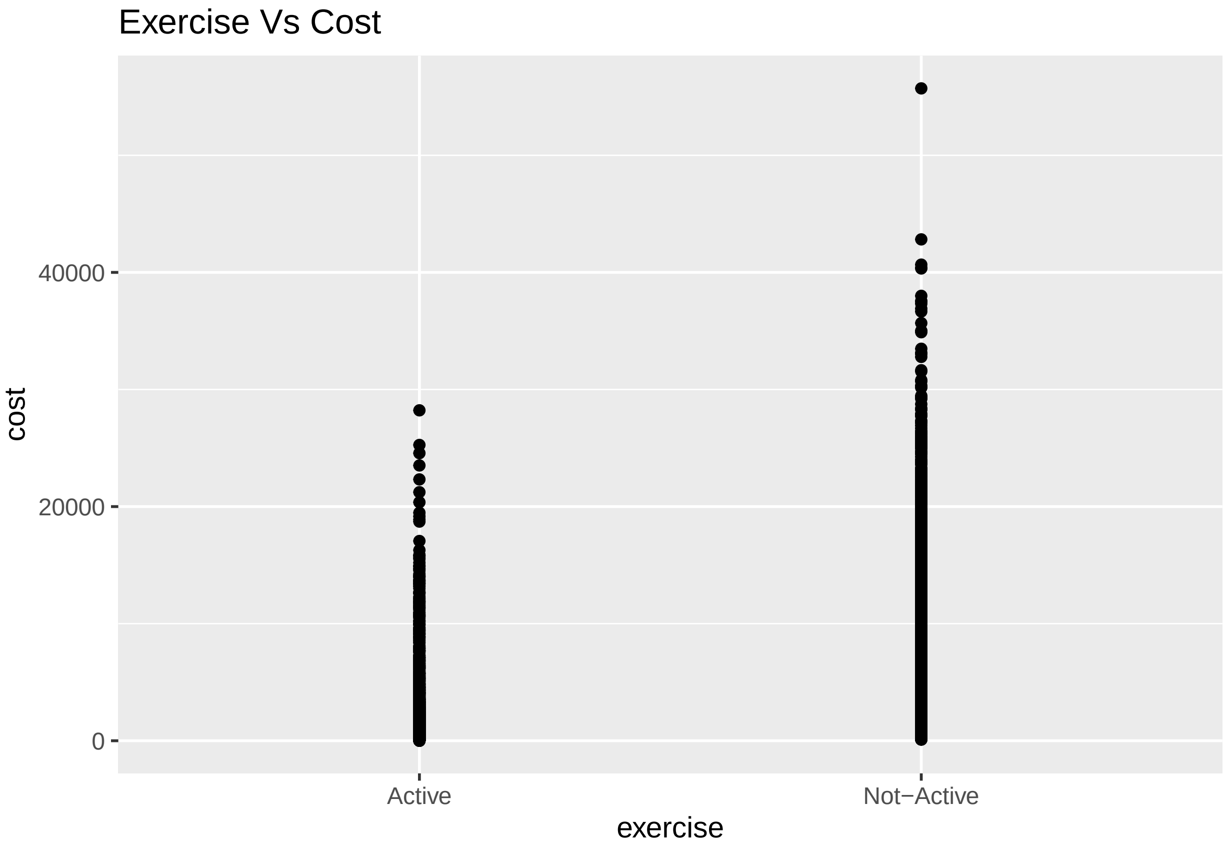
```
ggplot(proj_df, aes(x=smoker,y=cost))+geom_point() + ggtitle("Smoker Vs Cost")
```



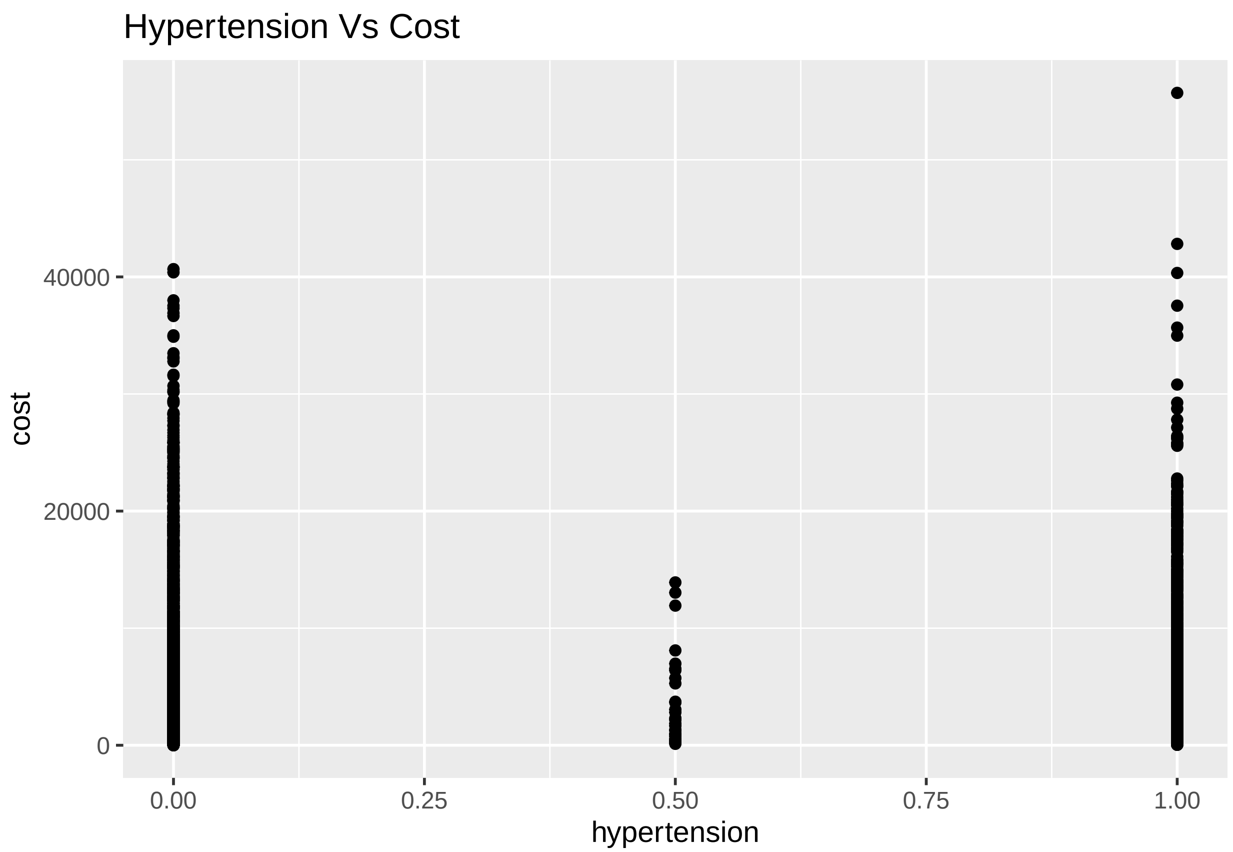
```
ggplot(proj_df, aes(x=bmi,y=cost))+geom_point() + ggtitle("BMI Vs Cost")
```



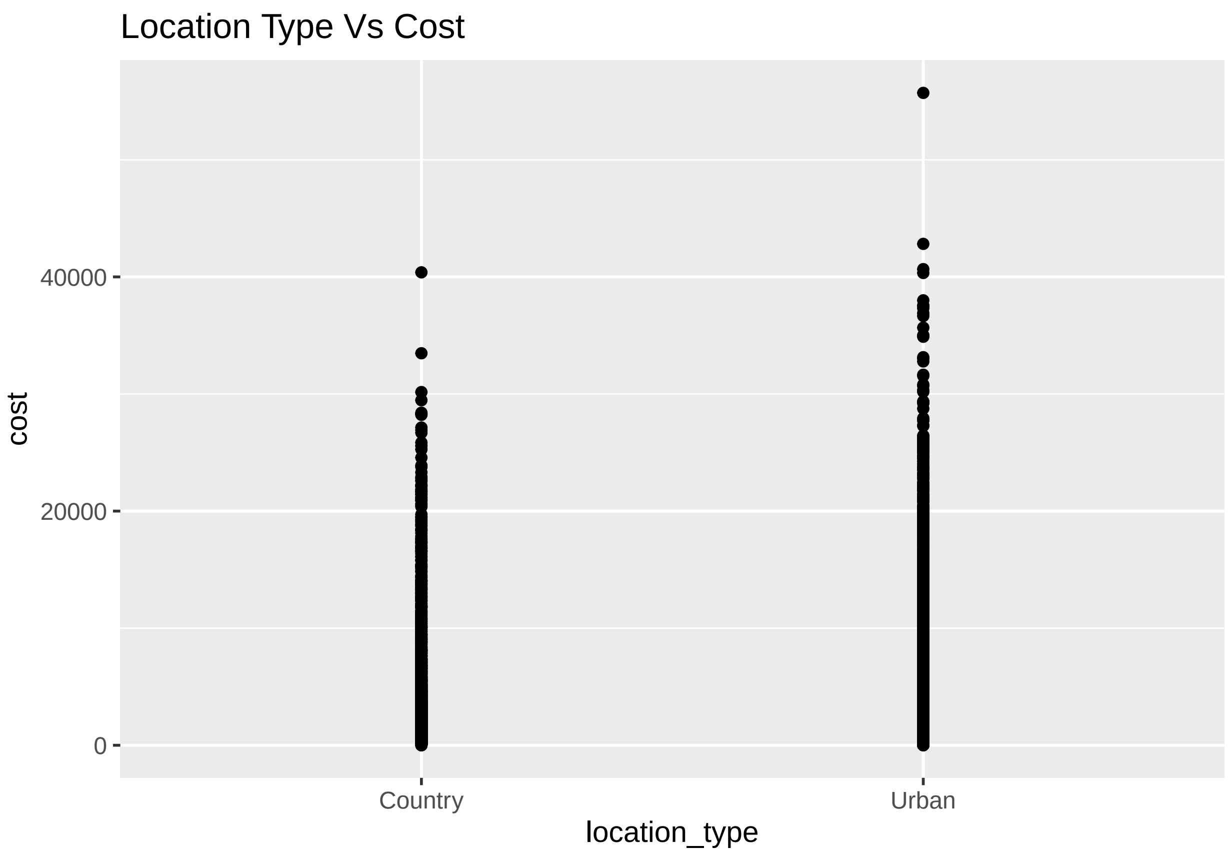
```
ggplot(proj_df, aes(x=exercise,y=cost))+geom_point() + ggtitle("Exercise Vs Cost")
```



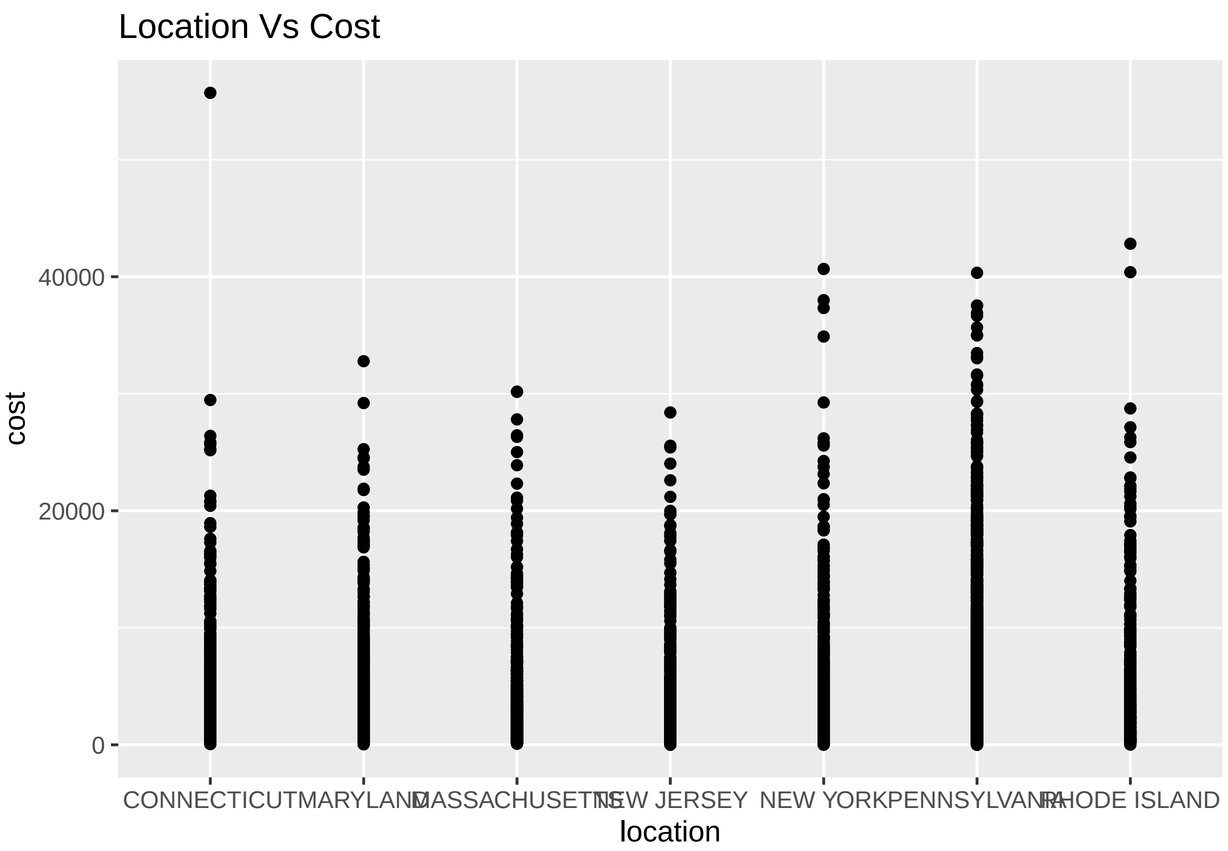
```r
ggplot(proj_df, aes(x=hypertension,y=cost))+geom_point() + ggtitle("Hypertension Vs Cost")
```



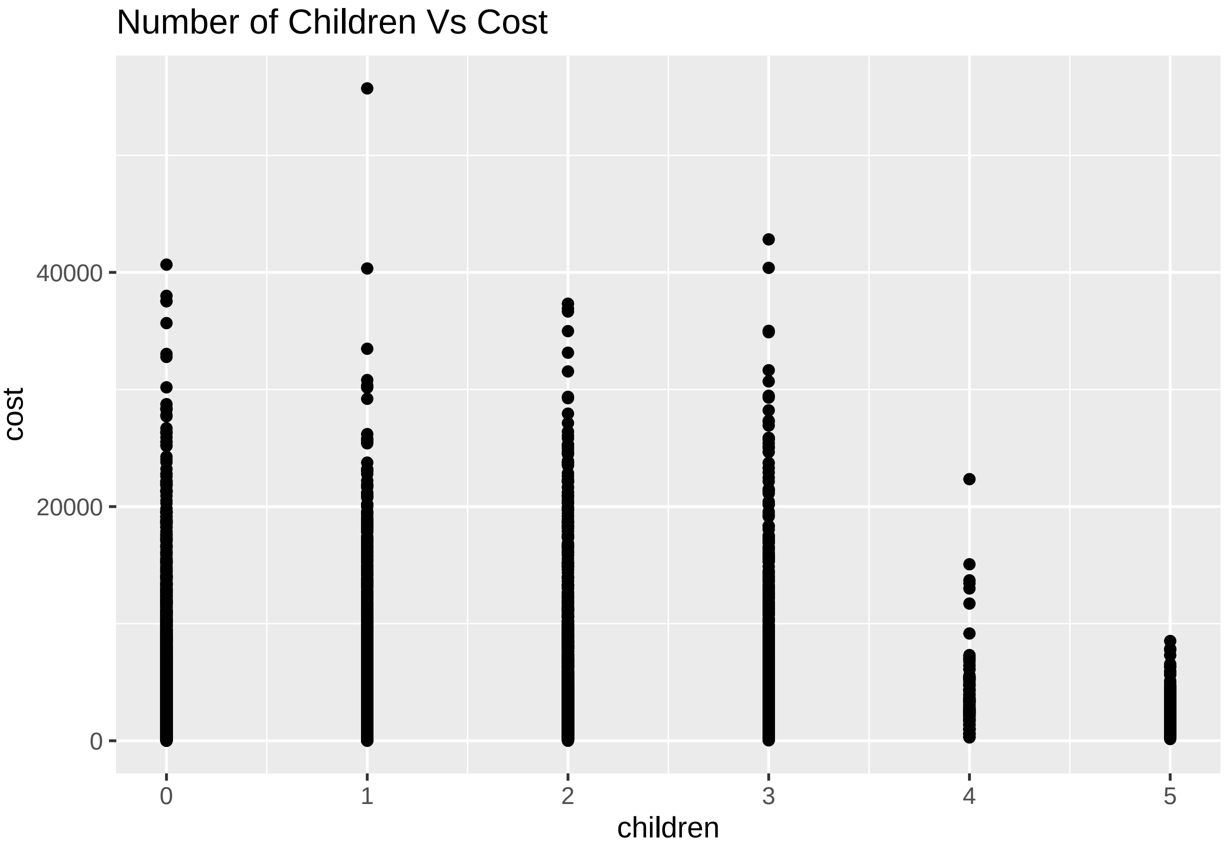
```
ggplot(proj_df, aes(x=location_type,y=cost))+geom_point() + ggtitle("Location Type Vs Cost")
```



```
ggplot(proj_df, aes(x=location,y=cost))+geom_point() + ggtitle("Location Vs Cost")
```

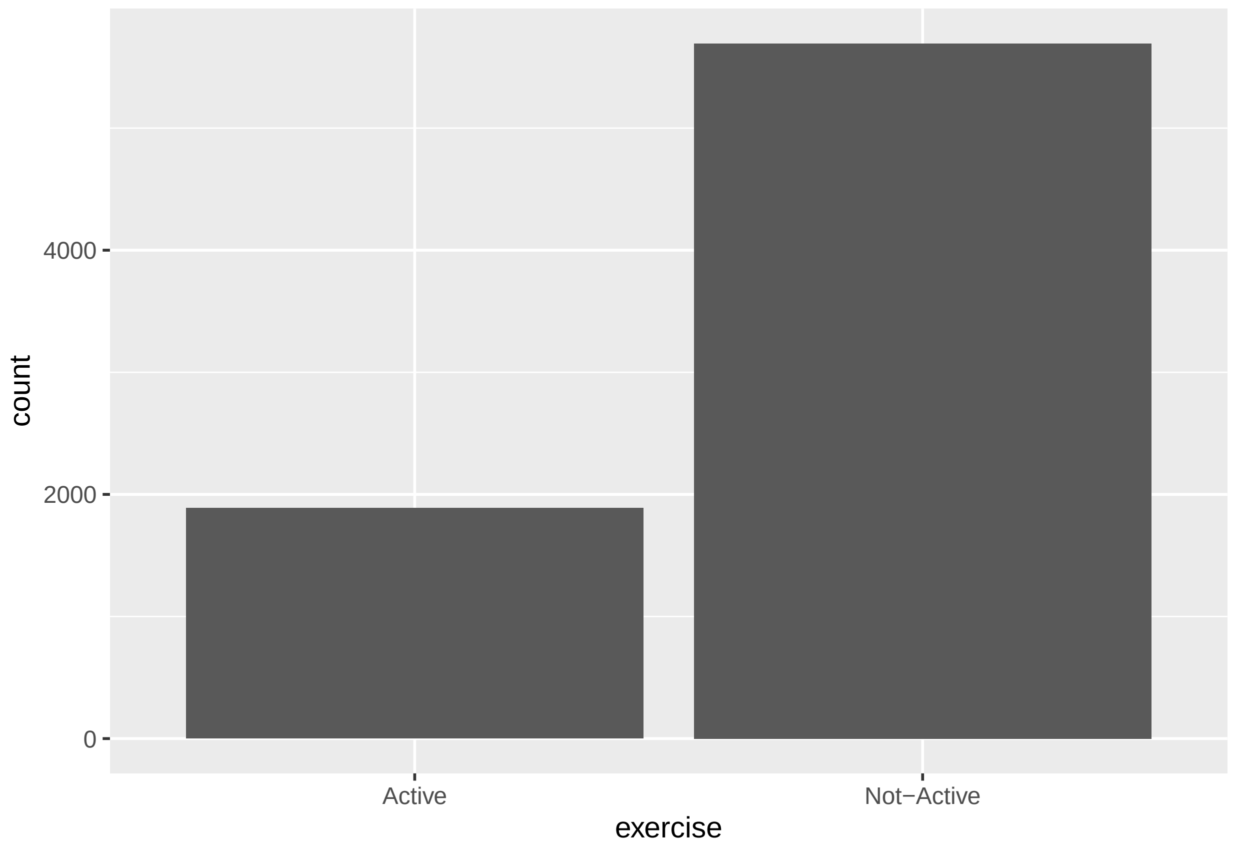


```
ggplot(proj_df, aes(x=children,y=cost))+geom_point() + ggtitle("Number of Children Vs Cost")
```

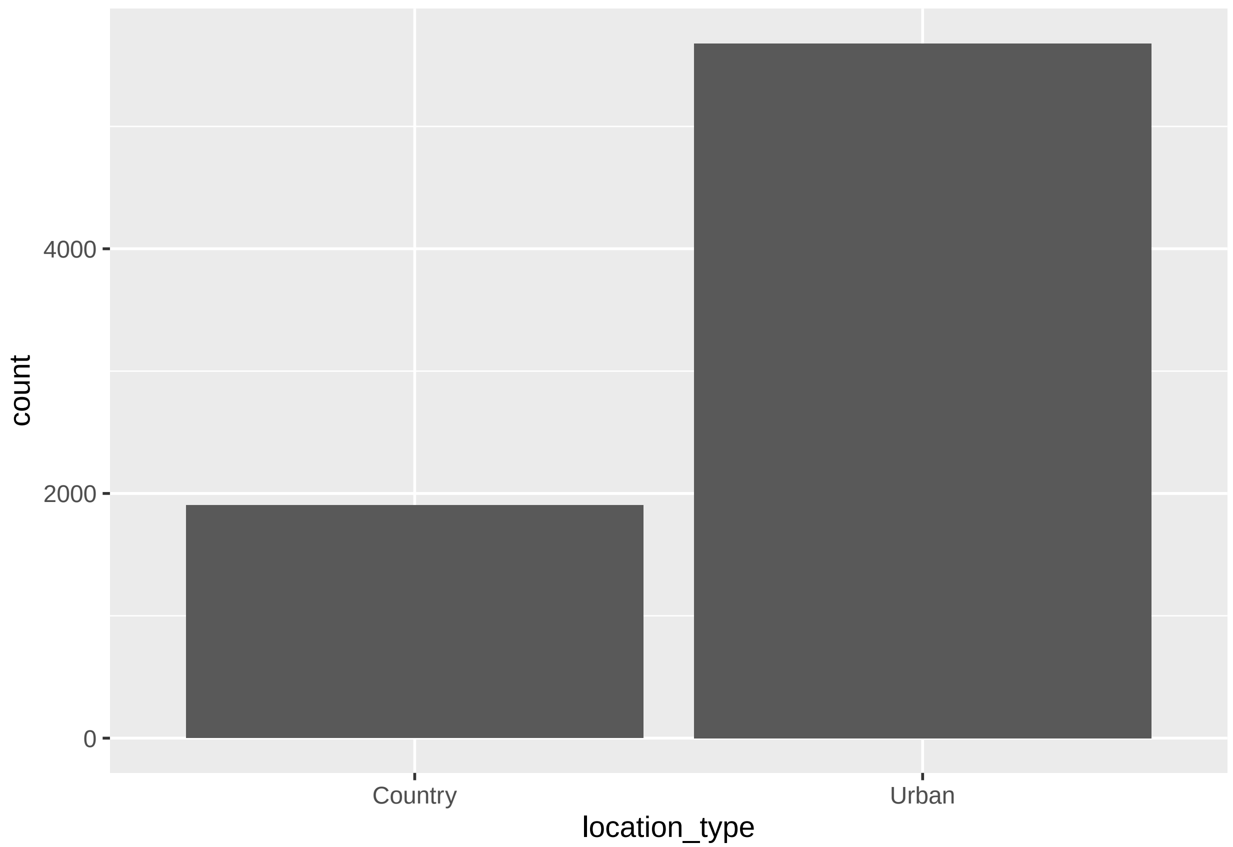


```
#samp_age <- sample(proj_df$age, 500)
#samp_cost <- sample(proj_df$cost, 500)
#data_samp <- data.frame(samp_age,samp_cost)
#View(data_samp)
#ggplot(data_samp, aes(x=samp_cost,y=samp_age))+geom_point()
#ggplot(data, aes(x=age, y=cost, color=smoker))+geom_point()
```

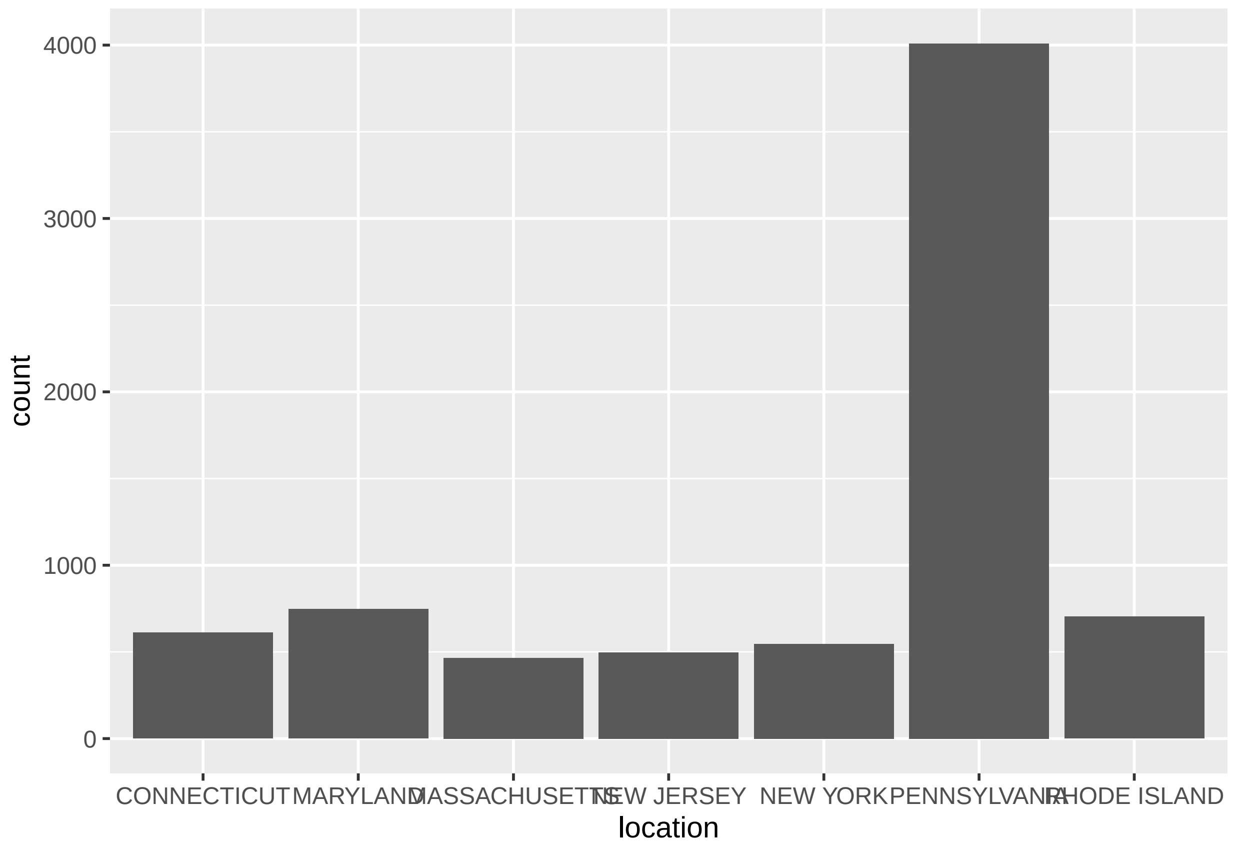
```
ggplot(proj_df) + aes(x=exercise) + geom_bar()
```



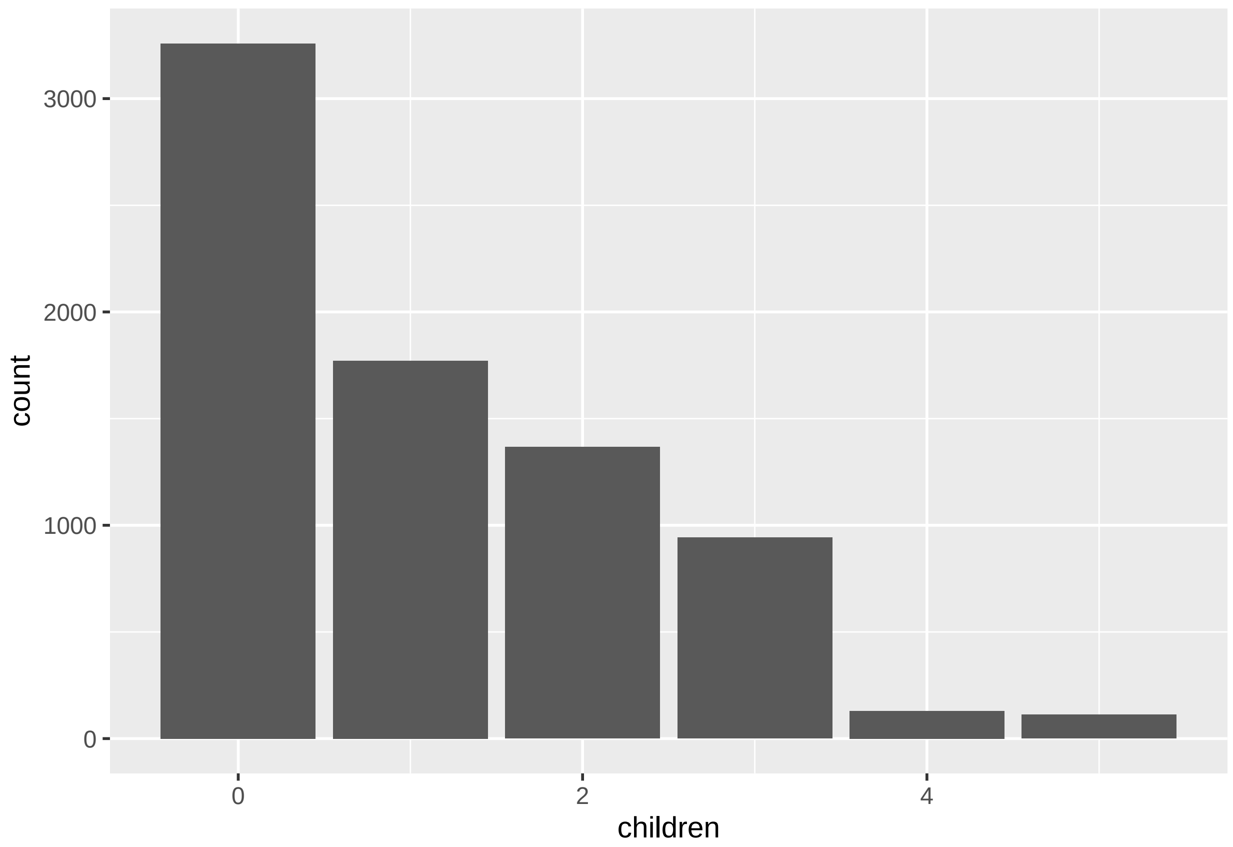
```
ggplot(proj_df) + aes(x=location_type) + geom_bar()
```



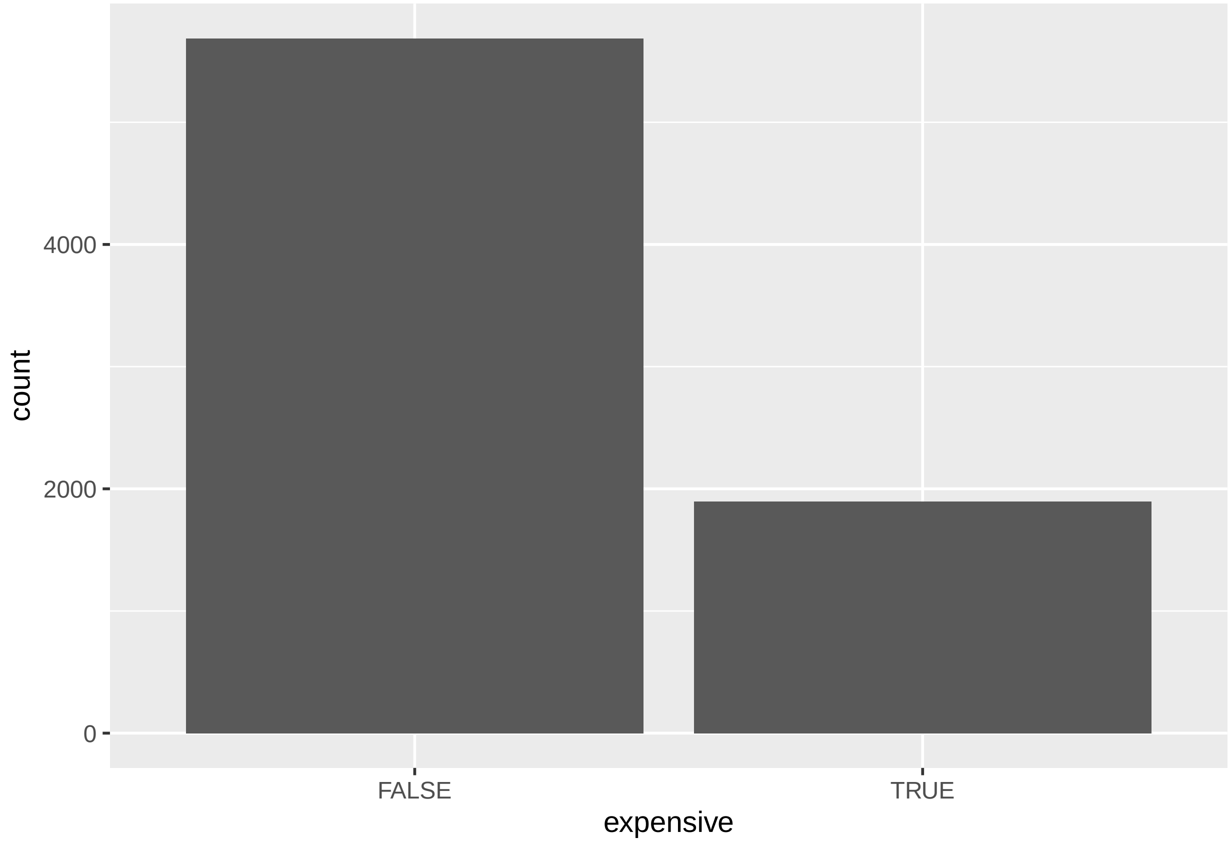
```
ggplot(proj_df) + aes(x=location) + geom_bar()
```



```
ggplot(proj_df) + aes(x=children) + geom_bar()
```



```
ggplot(proj_df) + aes(x=expensive) + geom_bar()
```



```
us <- map_data("state")
#View(us)
us$state_name <- tolower(us$region)
proj_df$state_name <- tolower(proj_df$state_name)
mapping <- merge(us,proj_df,by="state_name")
#View(mapping)
```

```
# map <- ggplot(us, aes(map_id="state"))
# map <- map + aes(x=long, y=lat, group=group) + geom_polygon(fill = "white", color = "black")
# map <- map + expand_limits(x=us$long, y=us$lat)
# map <- map + coord_map("mercator") + ggtitle("Cost as per Location")
# map <- map + geom_point(data=mapping,aes(x=long,y=lat,colour=cost),inherit.aes =F)
# map
```

```
# map <- ggplot(us, aes(map_id="state"))
# map <- map + aes(x=long, y=lat, group=group) + geom_polygon(fill = "white", color = "black")
# map <- map + expand_limits(x=us$long, y=us$lat)
# map <- map + coord_map("mercator") + ggtitle("Expensive data as per Location")
# map <- map + geom_point(data=mapping,aes(x=long,y=lat,colour=expensive),inherit.aes =F)
# map
```

```
# hist(proj_df$age)
# hist(proj_df$bmi)
# hist(proj_df$children)
# hist(proj_df$hypertension)
# hist(proj_df$cost)
```

```
# ggplot(proj_df)+aes(x=age,y=cost,)+geom_boxplot()+ ggtitle("Box Plot of Age Vs Cost")
# ggplot(proj_df)+aes(x=bmi,y=cost)+geom_boxplot()+ ggtitle("Box Plot of BMI Vs Cost")
# ggplot(proj_df)+aes(x=smoker,y=cost)+geom_boxplot()+ ggtitle("Box Plot of Smoker Vs Cost")
# ggplot(proj_df)+aes(x=yearly_physical,y=cost)+geom_boxplot()+ ggtitle("Box Plot of Yearly Physical Vs
# ggplot(proj_df)+aes(x=exercise,y=cost)+geom_boxplot()+ ggtitle("Box Plot of Exercise Vs Cost")
# ggplot(proj_df)+aes(x=hypertension,y=cost)+geom_boxplot()+ ggtitle("Box Plot of Hypertension Vs Cost"
```

1. Multiple regression model

```
# mrLmOut <- lm(expensive ~ age+bmi+hypertension+smoker+exercise,proj_df)
# summary(mrLmOut)
```

Conversion to factors

```
# proj_fact <- data.frame(
#   #X= as.factor(proj_df$X),
#   age= (proj_df$age),
#   bmi = (proj_df$bmi),
#   #children = as.factor(proj_df$children),
#   smoker = (proj_df$smoker),
#   #location = as.factor(proj_df$location),
#   #location_type = as.factor(proj_df$location_type),
#   #education_level = as.factor(proj_df$education_level),
#   yearly_physical = (proj_df$yearly_physical),
#   exercise = (proj_df$exercise),
#   #married = as.factor(proj_df$married),
#   hypertension = (proj_df$hypertension),
#   #gender = (proj_df$gender),
#   #cost= (proj_df$cost),
#   expensive = as.factor(proj_df$expensive)
# )
```

SVM MODELS

```
TrnList <- createDataPartition(y=proj_df$expensive, p=.60,list=FALSE)
TrnSet <- proj_df[TrnList,]
TstSet <- proj_df[-TrnList,]
#proj_df$expensive <- as.factor(proj_df$expensive)
#View(TrnSet)
```

```
SVMmod <- ksvm(data = TrnSet, expensive~ age+bmi+children+smoker+hypertension+exercise+yearly_physical,
summary(SVMmod)
```

```
## Length  Class   Mode
##      1   ksvm     S4
```

```
svmPredict <- predict(SVMmod, newdata = TstSet, type = "response" )
#confusionMatrix(svmPredict,as.factor(TstSet$expensive))
```

Apriori Algorithm

```
#data_apr <- proj_fact
#data_apr <- as(data_apr,'transactions')
```

```
# proj_rules <- apriori(data_apr,
#  parameter=list(supp=0.030, conf=0.7),
#  control=list(verbose=F),
#  appearance=list(default="lhs",rhs=("expensive=1")))
#
# summary(proj_rules)
# #inspect(proj_rules)
```

Tree Model

```
proj_rpart <- rpart(expensive ~ age+bmi+children+smoker+hypertension+exercise+yearly_physical, data = Tr
rpart_Pred <- predict(proj_rpart, newdata= TstSet, type= "class")

confusionMatrix(rpart_Pred, TstSet$expensive)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction FALSE TRUE
##      FALSE  2203  311
##      TRUE     71  447
##
##                Accuracy : 0.874
##                  95% CI : (0.8617, 0.8856)
##     No Information Rate : 0.75
##     P-Value [Acc > NIR] : < 2.2e-16
##
##                   Kappa : 0.6244
##
##  Mcnemar's Test P-Value : < 2.2e-16
##
##             Sensitivity : 0.9688
##             Specificity : 0.5897
##          Pos Pred Value : 0.8763
##          Neg Pred Value : 0.8629
##              Prevalence : 0.7500
##          Detection Rate : 0.7266
##    Detection Prevalence : 0.8292
##       Balanced Accuracy : 0.7792
##
##        'Positive' Class : FALSE
##
```

```
#rpart.plot(proj_rpart)
```

Association Rule

```
#asso_Data <- proj_fact[,-7]
#asso_Data[,1:14] <- lapply(asso_Data[,1:7],factor)
#str(asso_Data)
```

```
#our_Model <- SVMmod
#save(our_Model,file = "our_Model.rda")
```

```
our_Model3 <- proj_rpart
saveRDS(our_Model3,file="/Users/vedantpatil/Documents/IDS Project/our_Model3.rds")
readRDS(file="/Users/vedantpatil/Documents/IDS Project/our_Model3.rds")
```

```
## n= 4550
##
## node), split, n, loss, yval, (yprob)
##       * denotes terminal node
##
##  1) root 4550 1137 FALSE (0.75010989 0.24989011)
##    2) smoker=no 3656  484 FALSE (0.86761488 0.13238512)
##      4) age< 45.5 2308  130 FALSE (0.94367418 0.05632582) *
##      5) age>=45.5 1348  354 FALSE (0.73738872 0.26261128)
##       10) exercise=Active 329   25 FALSE (0.92401216 0.07598784) *
##       11) exercise=Not-Active 1019  329 FALSE (0.67713445 0.32286555)
##         22) bmi< 31.4525 513   97 FALSE (0.81091618 0.18908382) *
##         23) bmi>=31.4525 506  232 FALSE (0.54150198 0.45849802)
##           46) age< 58.5 377  138 FALSE (0.63395225 0.36604775) *
##           47) age>=58.5 129   35 TRUE (0.27131783 0.72868217) *
##    3) smoker=yes 894  241 TRUE (0.26957494 0.73042506)
##      6) bmi< 29.875 393  178 FALSE (0.54707379 0.45292621)
##       12) age< 36.5 203   35 FALSE (0.82758621 0.17241379) *
##       13) age>=36.5 190   47 TRUE (0.24736842 0.75263158)
##         26) exercise=Active 49   14 FALSE (0.71428571 0.28571429) *
##         27) exercise=Not-Active 141   12 TRUE (0.08510638 0.91489362) *
##      7) bmi>=29.875 501   26 TRUE (0.05189621 0.94810379) *
```

```
library(shiny)
library(shinydashboard)
```

```
##
## Attaching package: 'shinydashboard'
```

```
## The following object is masked from 'package:graphics':
##
##     box
```

```
library(shiny)
library(caret)
```

```r
library(kernlab)
library(e1071)
library(tidyverse)
ui <- fluidPage (
  h1("IDS Project Group 4"),
  hr(),
  br(),
  h4(p(em("This App gives predictions based on the Rpart model"))),
  hr(),
  #Read the data
  fileInput("upload", label="UPLOAD SAMPLE TEST FILE", accept = c(".csv")),
  #Read the actual (solution) data
  fileInput("upload_Solution", label="UPLOAD SOLUTION FILE", accept = c(".csv")),
  #get a number (how much of the dataframe to show)
  numericInput("n", "Number of Rows", value = 5, min = 1, step = 1),
  #a place to output a table (i.e., a dataframe)
  tableOutput("headForDF"),
  #output the results (for now, just simple text)
  verbatimTextOutput("txt_results", placeholder = TRUE)
)

server <- function(input, output, session) {
  #load a model, do prediction and compute the confusion matrix
  use_model_to_predict <- function(df, df_solution){
    #load the pre-built model, we named it ‘out_model.rda’)
    my_model <- readRDS("/Users/vedantpatil/Documents/IDS Project/our_Model3.rds")

    print('enter')
    prd <- predict(my_model, df, type = "class")
    #show how the model performed
    print(prd)
    #glimpse(df)
    #df_solution$isexpensive<- as.factor(df_solution$isexpensive)
    confusionMatrix(prd, as.factor(df_solution$expensive))
  }
  #require an input file, then read a CSV file
  getTestData <- reactive({
    req(input$upload)
    read_csv(input$upload$name)
  })
  #require an the actual values for the prediction (i.e. solution file)
  getSolutionData <- reactive({
    req(input$upload_Solution)
    read_csv(input$upload_Solution$name)
  })
  output$txt_results <- renderPrint({
    #load the data
    dataset <- getTestData()
    dataset_solution <- getSolutionData()
    #load and use the model on the new data
    use_model_to_predict(dataset, dataset_solution)
  })
  #show a few lines of the dataframe
  output$headForDF <- renderTable({
    df <- getTestData()
    head(df, input$n)
  })
}
shinyApp(ui, server)
```