initial_result_code

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Introduction

Every ethnic group has a different diet and lifestyle. When people moved to North America, they brought their eating habits, level of education, and life style with them. The large size and highly diverse population resulted in different types of diseases that effected different age and ethnic groups. “Diagnosis has important implications for patient care. When a diagnosis is accurate and made in a timely manner, a patient has the best opportunity for positive health outcome because clinical decision making well be tailored to a correct understanding of the patient’s health problem.” [1] The research question is to define what factors are relevant to predicting the disease the patient might have. Also, who might be susceptible to which type of disease. After exploring the data, there is a possibility that a patient might have multiple diseases. Therefore, each instance can be assigned with multiple categories, as such, this type of problem needs to use multi-label classification.

Install R packages

```
#install.packages("rpart")
#install.packages("caret")
#install.packages("e1071")
#install.packages("randomForest")
#install.packages("corrplot")
```

Prepare for analyses

```
set.seed(1234)
library(lubridate)
```

```
## Warning: package 'lubridate' was built under R version 3.5.3
```

```
##
## Attaching package: 'lubridate'
```

```
## The following object is masked from 'package:base':
##
##     date
```

```
library(ggplot2)
```

```
## Warning: package 'ggplot2' was built under R version 3.5.3
```

```
library(randomForest)
```

```
## Warning: package 'randomForest' was built under R version 3.5.3
```

```
## randomForest 4.6-14
```

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

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

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

```r
library(dplyr)
```

```
## Warning: package 'dplyr' was built under R version 3.5.3
```

```
##
## Attaching package: 'dplyr'
```

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

```
## The following objects are masked from 'package:lubridate':
##
##     intersect, setdiff, union
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```r
library(rpart)
```

```
## Warning: package 'rpart' was built under R version 3.5.3
```

```r
library(caret)
```

```
## Warning: package 'caret' was built under R version 3.5.3
```

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

```r
library(e1071)
```

```
## Warning: package 'e1071' was built under R version 3.5.3
```

```r
library(corrplot)
```

```
## Warning: package 'corrplot' was built under R version 3.5.3
## corrplot 0.84 loaded
```

Includes functions to clean datasets

Read datasets from csv file

```
build_clean_dataset <- function() {
  datasetloc = "C:/Users/abdel/Desktop/Ryerson
University/capstone/capstone/R/Health_Care_History.csv"
  if (file.exists(datasetloc)) {
    alldata <- read.csv(file=datasetloc, header = T)
  }
  return(alldata)
}
```

Convert the date to age and group them into four groups (0-25, 26-40, 41-50, 50-65, 65+)

```
age <- function(dob, age.day = today(), units = "years", floor = TRUE) {
  calc.age = interval(dob, age.day) / duration(num = 1, units = units)
  if (floor) return(as.integer(floor(calc.age)))

  return(calc.age)
}

get_age_group <- function(a) {
  ifelse(a<25,25, ifelse(a<40, 40, ifelse(a<50,50,65)))
}
```

Group the countries of the patients based on ethnic groups

```
east_europe <- c('Ukraine','Russia','Poland','Czech Republic','Hungary')
west_europe <-
c('Austria','Belgium','France','Germany','Italy','Netherlands','Portugal','Spain','Switzerland')

north_europe <- c('Sweden', 'Finland', 'Denmark')
british <- c('England','Scotland','Ireland')

get_ethnic_group <- function(country) {
  ifelse((country %in% east_europe), 'east_europe',
         ifelse((country %in% west_europe) ,'west_europe',
                ifelse((country %in% north_europe), 'north_europe',
                       ifelse((country %in% british), 'british',
                              country))))
}
```

Read the dataset and remove patient ids from the analysis

```
patients <- build_clean_dataset()
```

```
#remove the patient ids from the dataset
patients <- patients[,-1]
str(patients)
```

```
## 'data.frame':    2000 obs. of  13 variables:
##  $ gender           : Factor w/ 2 levels "female","male": 1 1 2 2 1 1 1 1
1 2 ...
##  $ dob              : Factor w/ 1877 levels "1923-10-10","1924-03-28",..:
505 1502 1811 545 327 1120 628 1378 631 1176 ...
##  $ zipcode          : int  89136 94105 89127 44101 89136 94105 60612
43221 89127 43210 ...
##  $ employment_status : Factor w/ 4 levels "employed","retired",..: 2 1 1 2
2 4 2 1 2 1 ...
##  $ education        : Factor w/ 6 levels "bachelors","highschool",..: 1 5
4 1 4 2 5 1 4 2 ...
##  $ marital_status   : Factor w/ 2 levels "married","single": 1 1 1 1 1 1
1 1 2 1 ...
##  $ children         : int  1 4 2 2 3 2 0 2 2 7 ...
##  $ ancestry         : Factor w/ 20 levels "Austria","Belgium",..: 14 18 8
4 1 1 9 10 1 20 ...
##  $ avg_commute      : num  13.4 15.2 23.6 19.6 36.5 ...
##  $ daily_internet_use: num  2.53 6.77 3.63 5 7.75 3.34 6.75 3.01 4.12 3.15
...
##  $ available_vehicles: int  2 2 1 3 1 0 2 3 1 1 ...
##  $ military_service  : Factor w/ 2 levels "no","yes": 1 1 1 1 1 1 1 1 1 1
...
##  $ disease          : Factor w/ 13 levels "Alzheimer disease",..: 8 4 11
10 13 1 9 2 1 7 ...
```

Fix the education column values by fixing the misspelled words

```
patients$education <- ifelse(patients$education == 'highscool', as.character('highschool'),
as.character(patients$education))
patients$education <- ifelse(as.factor(patients$education) == 'phD/MD',
as.character('phd/md'), as.character(patients$education))
patients$education <- as.factor(patients$education)
```

Group the ancestry countries to ethnic groups

```
patients$ancestry <- as.factor(get_ethnic_group(patients$ancestry))
```

Convert the date of birth into age and group them into 25 40 50 65

```
patients$age <- age(patients$dob)
#patients$age <- get_age_group(age(patients$dob))
```

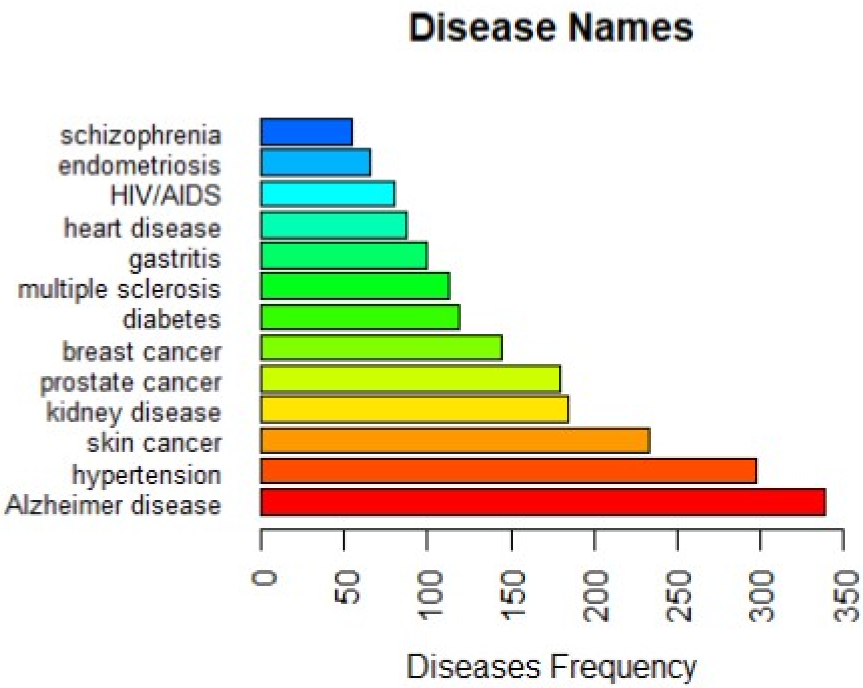
For the analysis purposes, move each disease to separate column with binary values, where 0: patient does not has the disease and 1: patient has the disease

```r
get_binary_value <- function(value, compare_to) {
 ifelse(value==compare_to,1,0)
}
patients$prostate_cancer <- get_binary_value(patients$disease,'prostate cancer')
patients$skin_cancer <- get_binary_value(patients$disease,'skin cancer')
patients$breast_cancer <- get_binary_value(patients$disease,'breast cancer')
patients$hiv_aids <- get_binary_value(patients$disease,'HIV/AIDS')
patients$diabetes <- get_binary_value(patients$disease,'diabetes')
patients$heart_disease <- get_binary_value(patients$disease,'heart disease')
patients$hypertension <- get_binary_value(patients$disease,'hypertension')
patients$endometriosis <- get_binary_value(patients$disease,'endometriosis')
patients$multiple_sclerosis <- get_binary_value(patients$disease,'multiple sclerosis')
patients$schizophrenia <- get_binary_value(patients$disease,'schizophrenia')
patients$kidney_disease <- get_binary_value(patients$disease,'kidney disease')
patients$gastritis <- get_binary_value(patients$disease,'gastritis')
patients$alzheimer <- get_binary_value(patients$disease,'Alzheimer disease')
str(patients)
```

```
## 'data.frame':    2000 obs. of  27 variables:
##  $ gender            : Factor w/ 2 levels "female","male": 1 1 2 2 1 1 1 1
1 2 ...
##  $ dob               : Factor w/ 1877 levels "1923-10-10","1924-03-28",..:
505 1502 1811 545 327 1120 628 1378 631 1176 ...
##  $ zipcode           : int  89136 94105 89127 44101 89136 94105 60612
43221 89127 43210 ...
##  $ employment_status : Factor w/ 4 levels "employed","retired",..: 2 1 1 2
2 4 2 1 2 1 ...
##  $ education         : Factor w/ 4 levels "bachelors","highschool",..: 1 4
3 1 3 2 4 1 3 2 ...
##  $ marital_status    : Factor w/ 2 levels "married","single": 1 1 1 1 1 1
1 1 2 1 ...
##  $ children          : int  1 4 2 2 3 2 0 2 2 7 ...
##  $ ancestry          : Factor w/ 4 levels "british","east_europe",..: 4 3
4 3 4 4 2 1 4 2 ...
##  $ avg_commute       : num  13.4 15.2 23.6 19.6 36.5 ...
##  $ daily_internet_use: num  2.53 6.77 3.63 5 7.75 3.34 6.75 3.01 4.12 3.15
...
##  $ available_vehicles: int  2 2 1 3 1 0 2 3 1 1 ...
##  $ military_service  : Factor w/ 2 levels "no","yes": 1 1 1 1 1 1 1 1 1 1
...
##  $ disease           : Factor w/ 13 levels "Alzheimer disease",..: 8 4 11
10 13 1 9 2 1 7 ...
##  $ age               : int  75 53 38 74 80 63 73 56 73 61 ...
##  $ prostate_cancer   : num  0 0 1 0 0 0 0 0 0 0 ...
##  $ skin_cancer       : num  0 0 0 0 1 0 0 0 0 0 ...
##  $ breast_cancer     : num  0 0 0 0 0 0 0 1 0 0 ...
##  $ hiv_aids          : num  0 0 0 0 0 0 0 0 0 1 ...
##  $ diabetes          : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ heart_disease     : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ hypertension      : num  1 0 0 0 0 0 0 0 0 0 ...
##  $ endometriosis     : num  0 1 0 0 0 0 0 0 0 0 ...
##  $ multiple_sclerosis: num  0 0 0 1 0 0 0 0 0 0 ...
##  $ schizophrenia     : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ kidney_disease    : num  0 0 0 0 0 0 1 0 0 0 ...
##  $ gastritis         : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ alzheimer         : num  0 0 0 0 0 1 0 0 1 0 ...
```

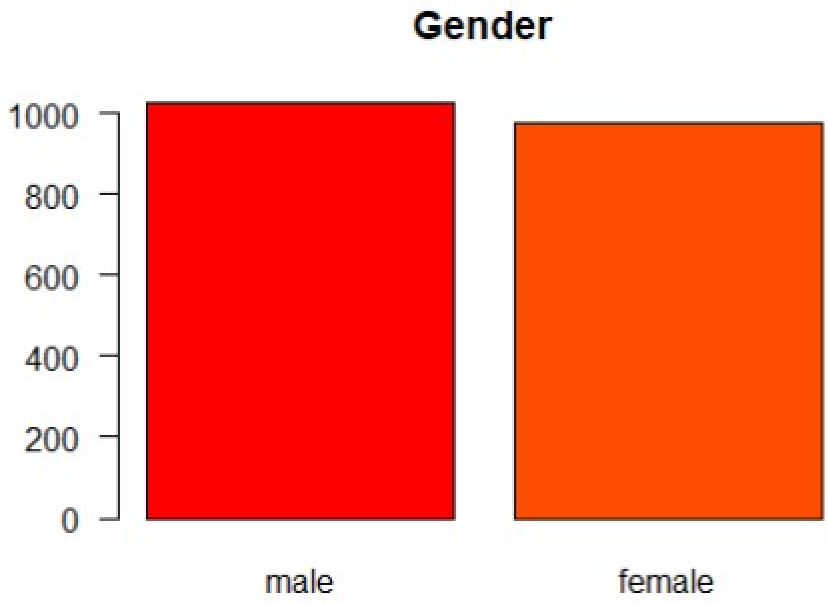
Draw a bar plot to count the total number of diseases in the dataset

```
par(las=2) # make label text perpendicular to axis
par(mar=c(5,8,4,2)) # increase y-axis margin.

disease_counts <- table(patients$disease)
barplot(sort(disease_counts, decreasing = TRUE), main="Disease Names",
    xlab="Diseases Frequency",
    col=rainbow(20),
    horiz=TRUE,
    cex.names=0.8,
    xlim = c(0, 350))
```



Observation : Male are more sick than Female

```
gender_counts <- table(patients$gender)
barplot(sort(gender_counts, decreasing = TRUE), main="Gender",
    col=rainbow(20), las=1)
```

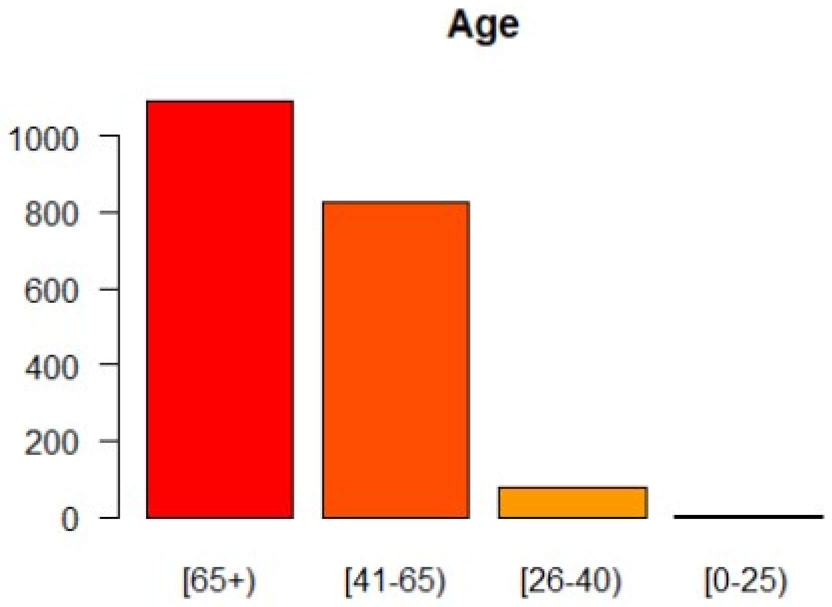


Observation : age group that are more sick

```
age_breaks <- c(0,25,40,65,100)
tags <- c("[0-25)","[26-40)", "[41-65)", "[65+)")
age_group_tags <- cut(patients$age,
            breaks=age_breaks,
            include.lowest=TRUE,
            right=FALSE,
            labels=tags)
summary(age_group_tags)
```

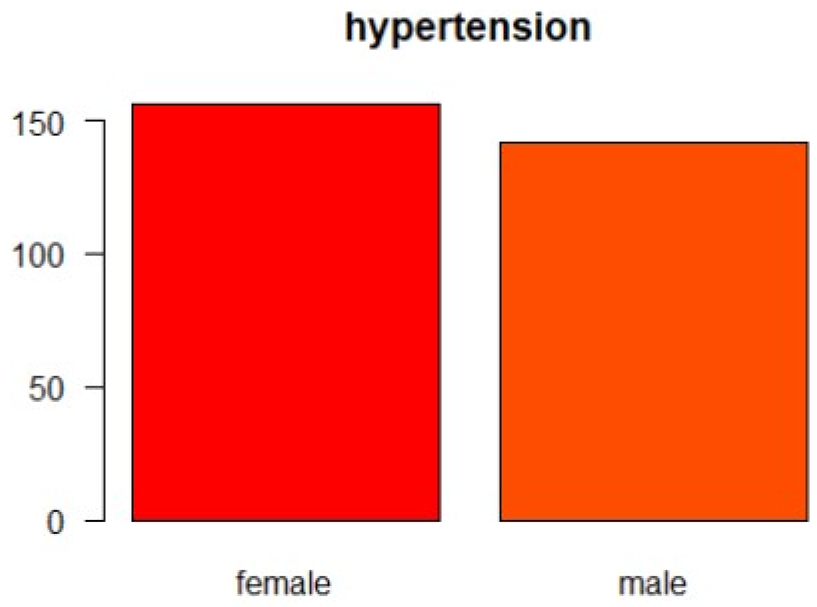
```
##  [0-25) [26-40) [41-65)   [65+)
##       4      78     827    1091
```

```
#age_counts <- table(patients$age)
age_counts <- table(age_group_tags)
barplot(sort(age_counts, decreasing = TRUE), main="Age",
    col=rainbow(20), las=1)
```

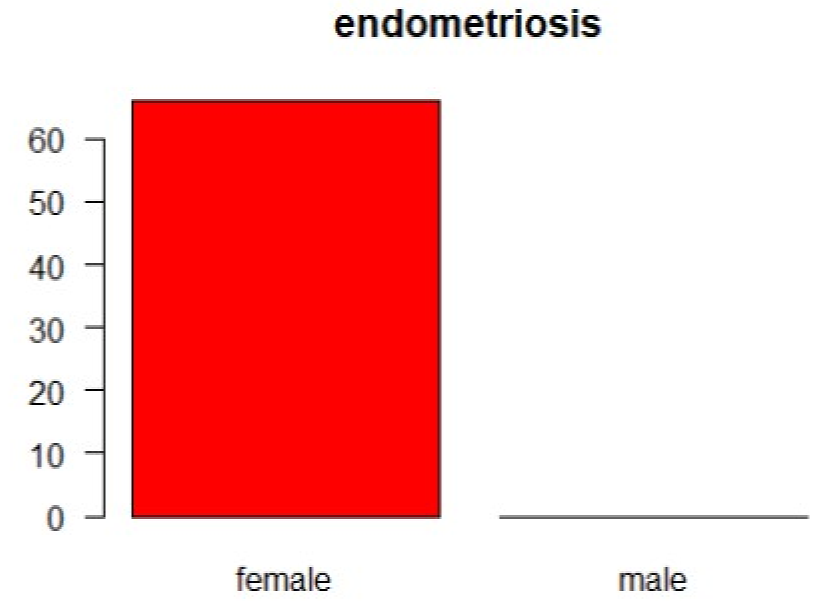


Observation : Disease and Gender distrubution

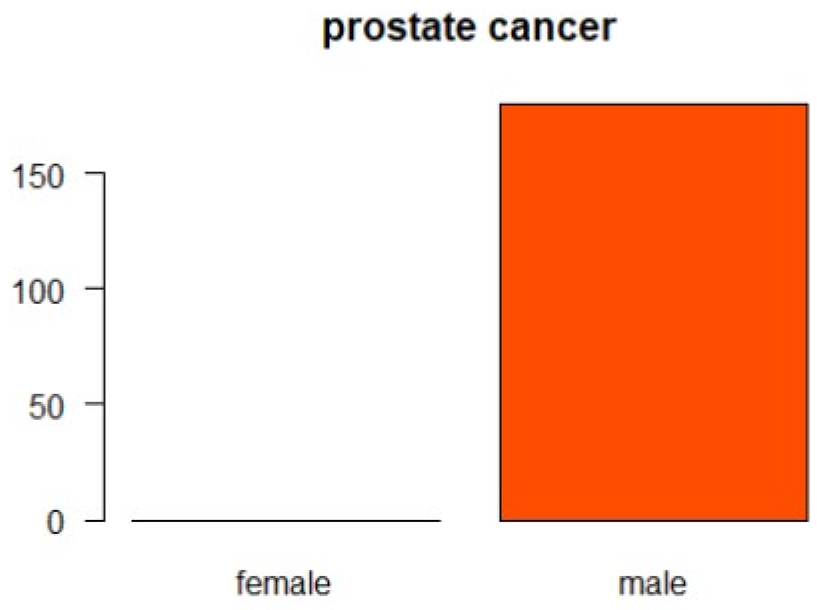
```
disease_name = c(as.character(unique(patients$disease)))

for (d in disease_name) {
 gender_disease_counts <- subset(patients, patients$disease == d)
 gender_disease_counts <- table(gender_disease_counts$gender)
 barplot(gender_disease_counts, main=d, col=rainbow(20), las=1)
}
```

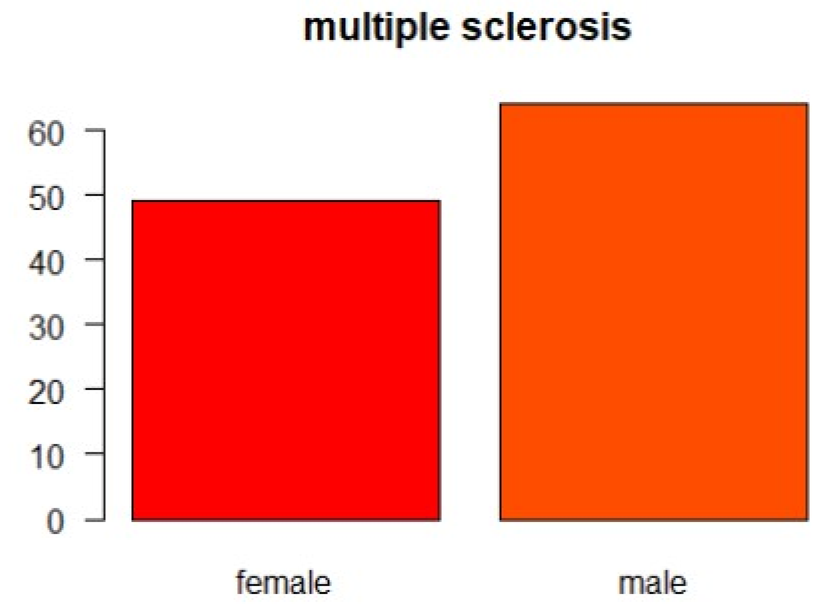


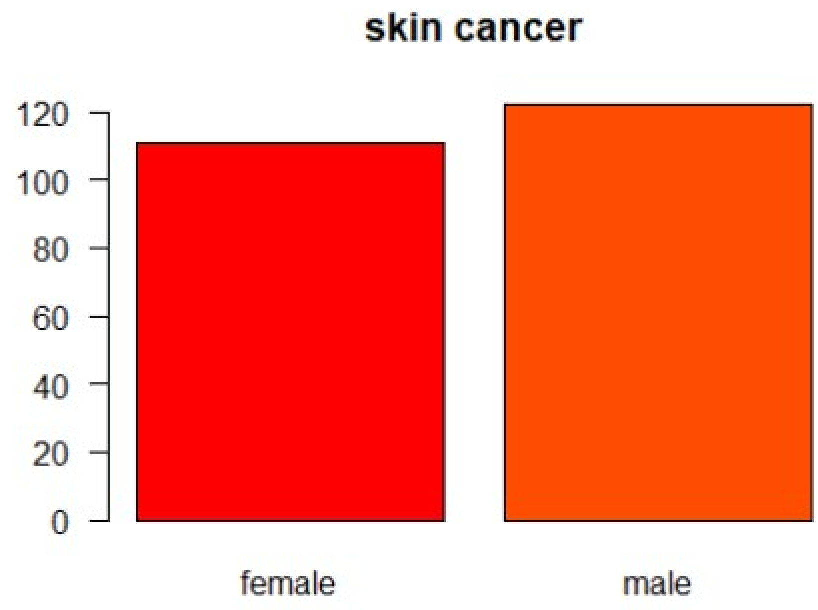
hypertension



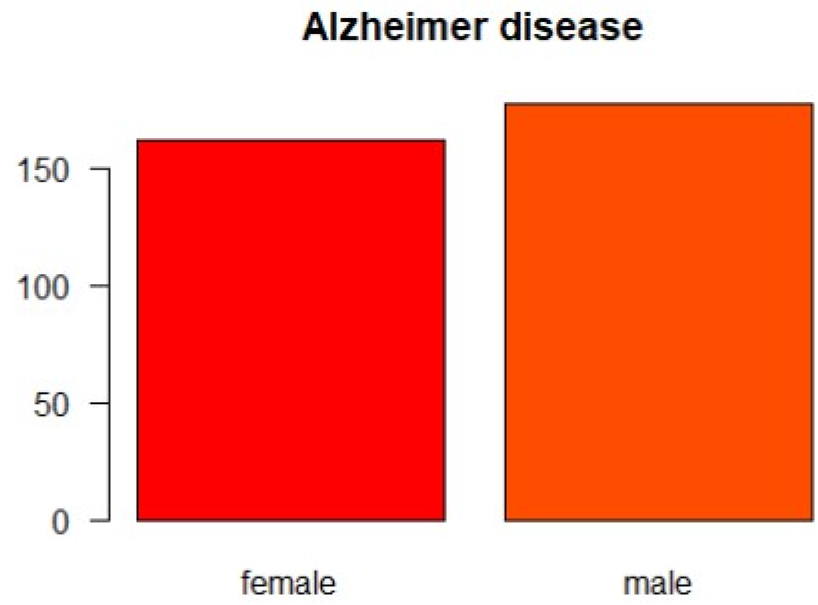
endometriosis


prostate cancer

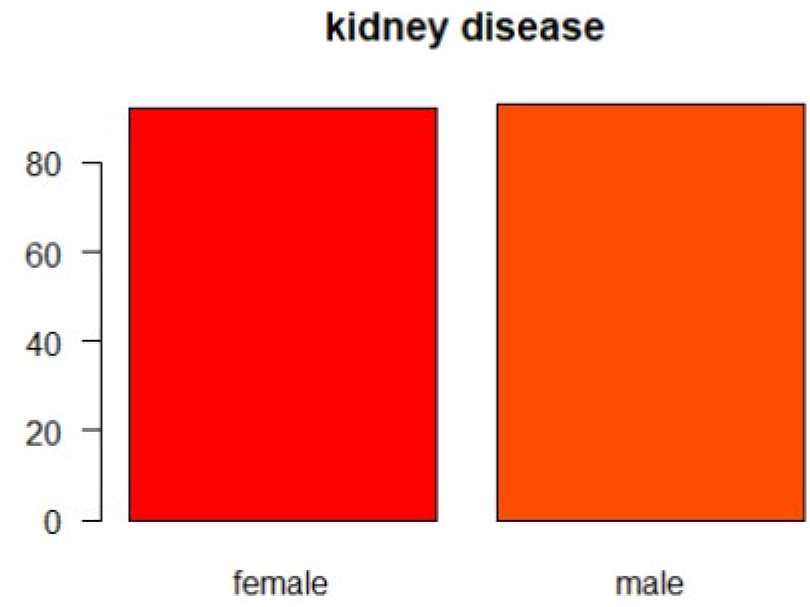

multiple sclerosis

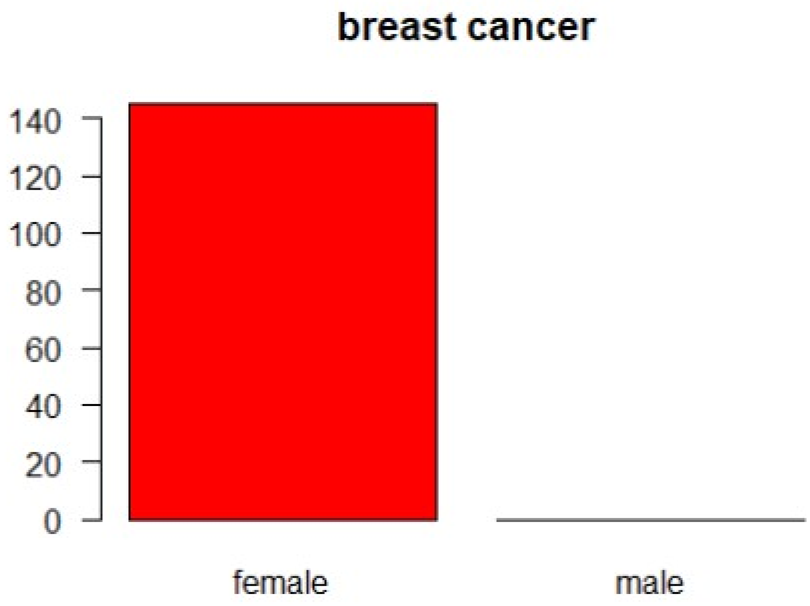


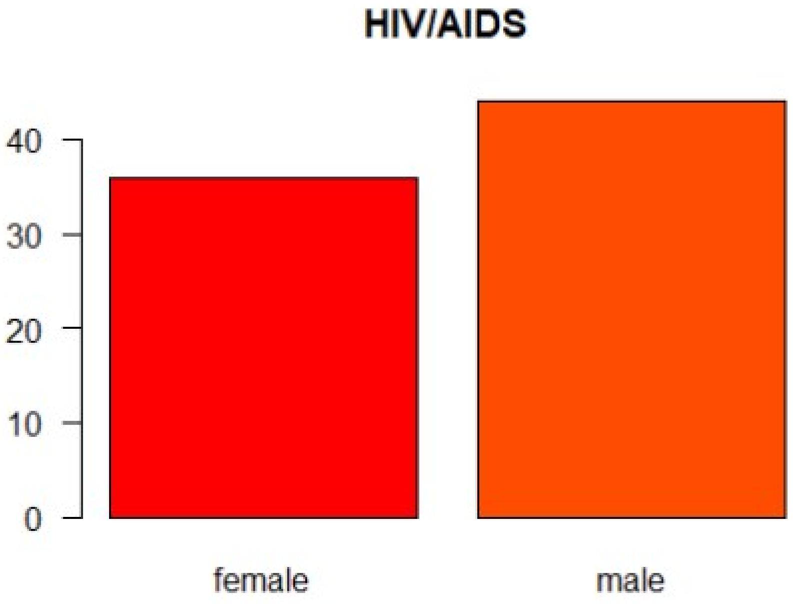
skin cancer

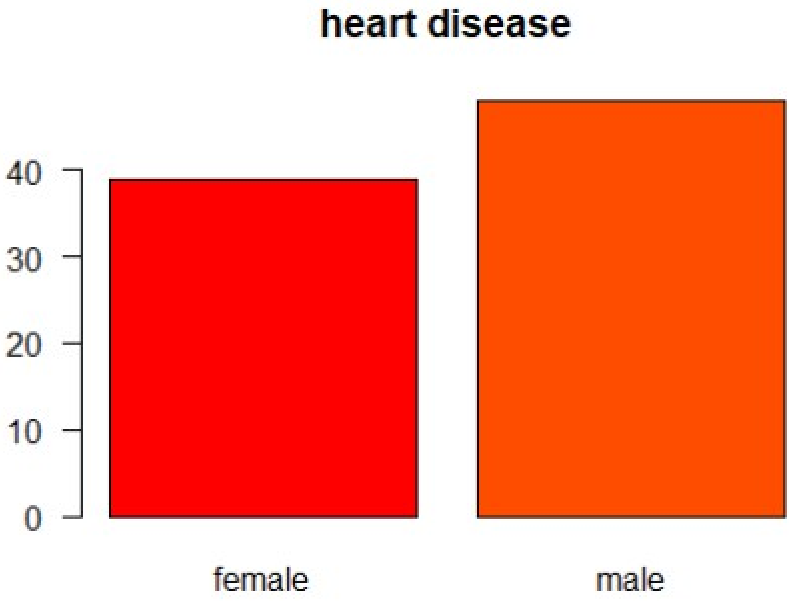


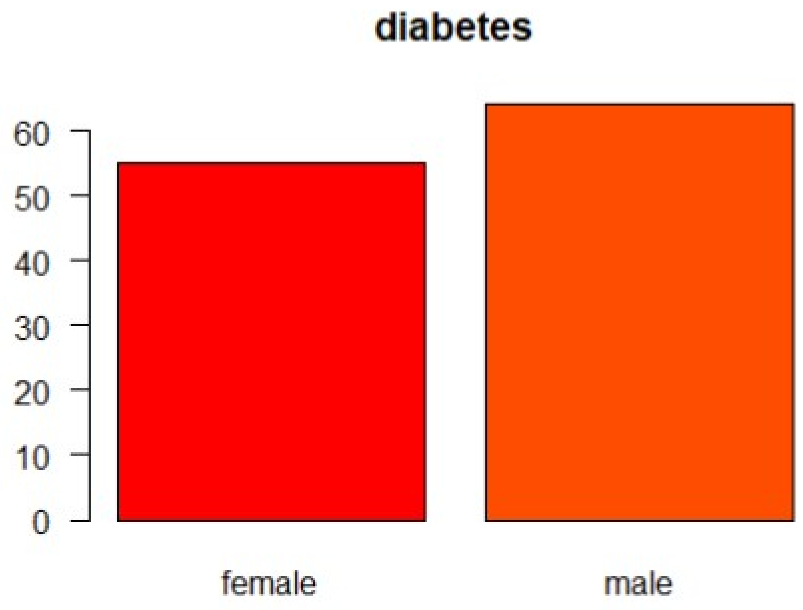
Alzheimer disease

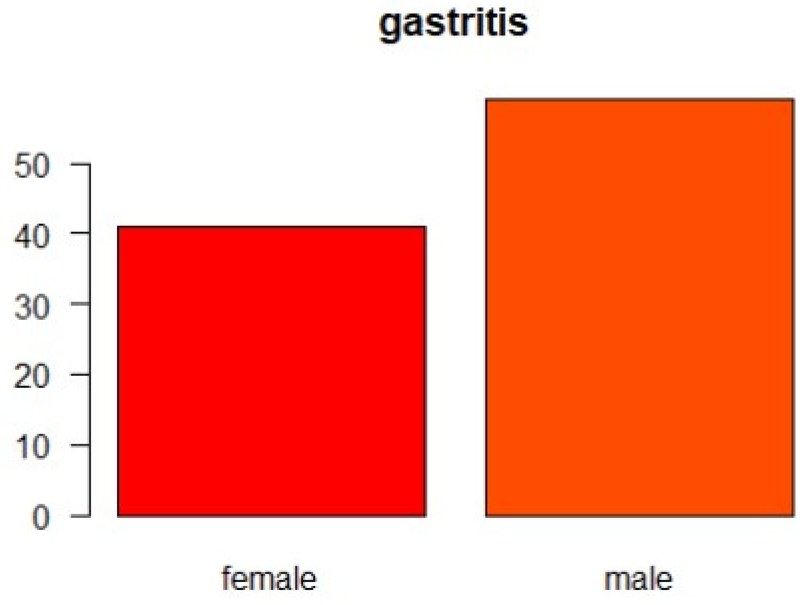

kidney disease
80
60
40
20
0
female
male

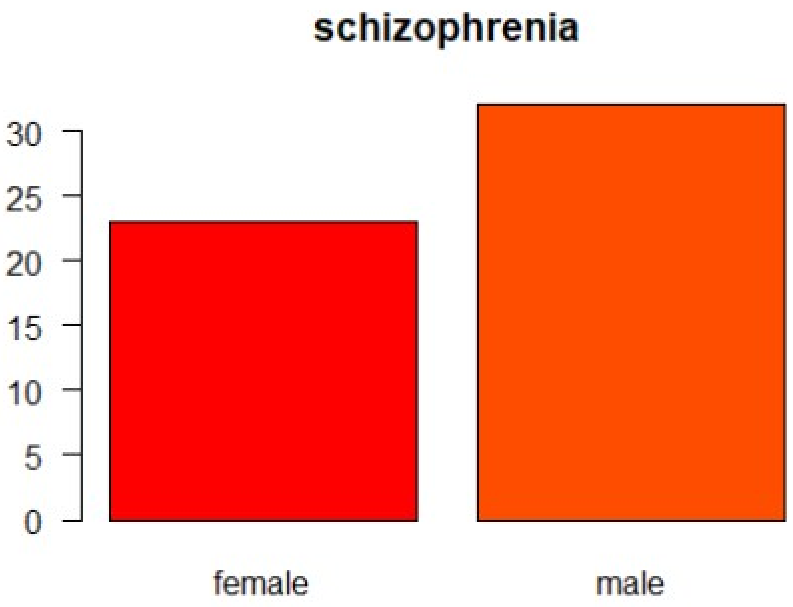

breast cancer
140
120
100
80
60
40
20
0
female
male


HIV/AIDS
40
30
20
10
0
female
male


heart disease
40
30
20
10
0
female
male

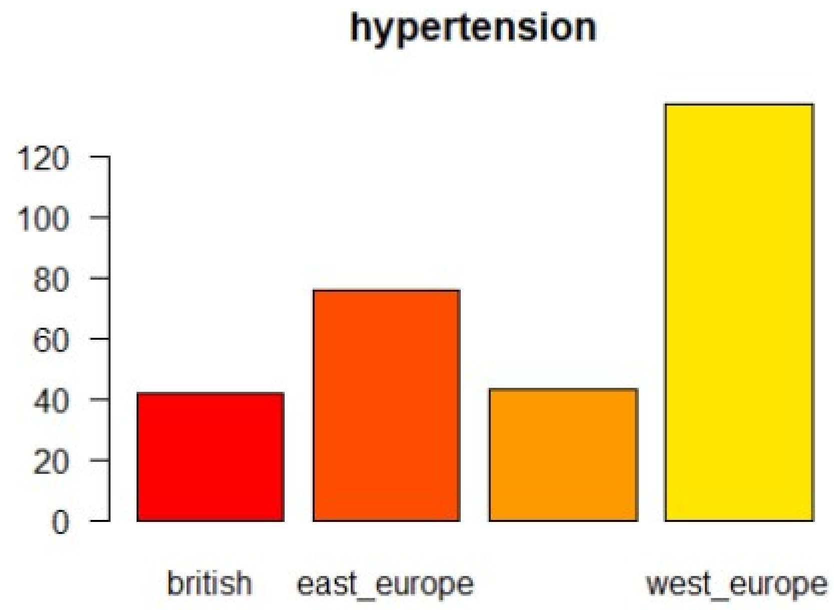

diabetes
0
10
20
30
40
50
60
female
male

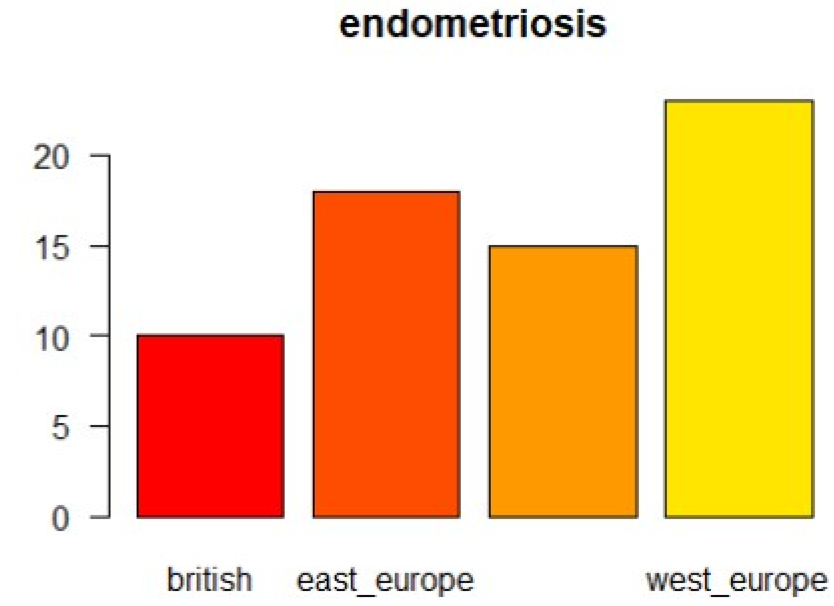

gastritis
0
10
20
30
40
50
female
male

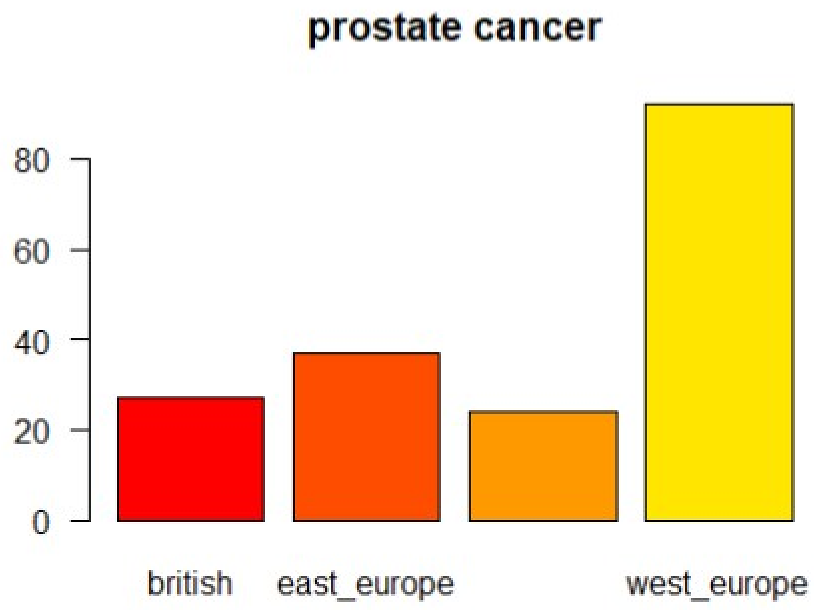


Observation : Disease and ancestry distrubution

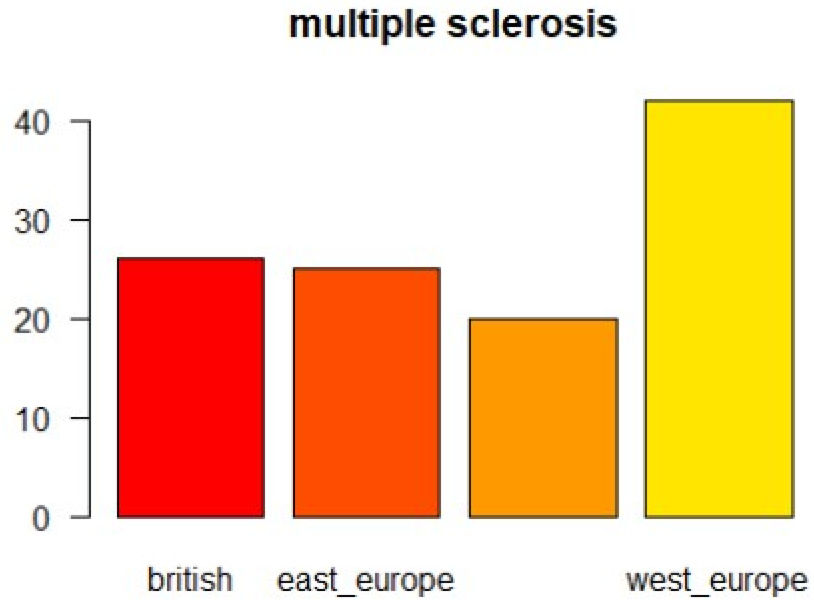
```
for (d in disease_name) {
  ancestry_disease_counts <- subset(patients, patients$disease == d)
  ancestry_disease_counts <- table(ancestry_disease_counts$ancestry)
  barplot(ancestry_disease_counts, main=d, col=rainbow(20), las=1)
}
```


hypertension
120
100
80
60
40
20
0
british
east_europe
west_europe

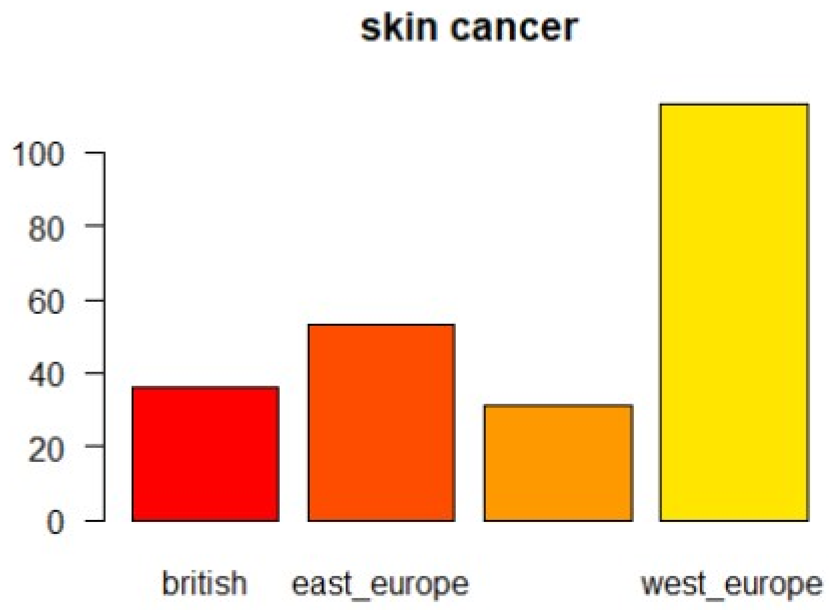

endometriosis
20
15
10
5
0
british
east_europe
west_europe

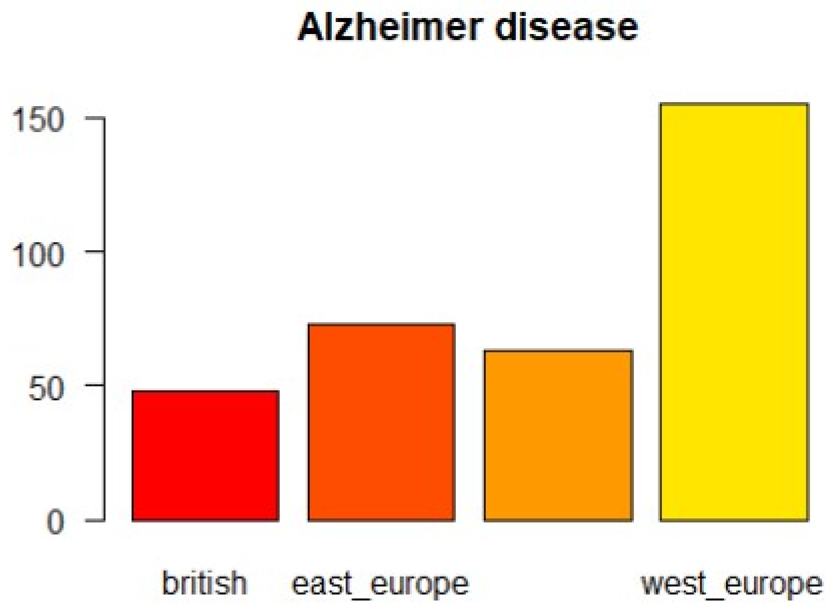


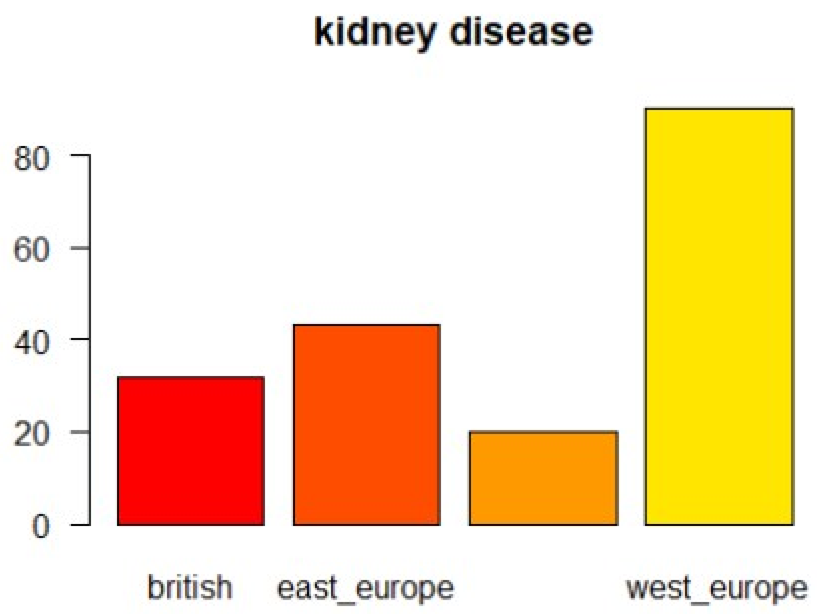
prostate cancer

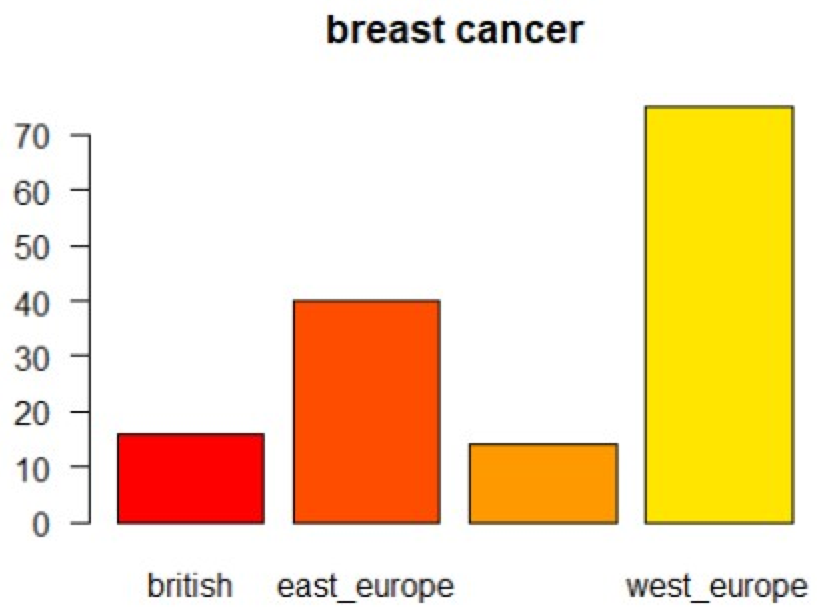


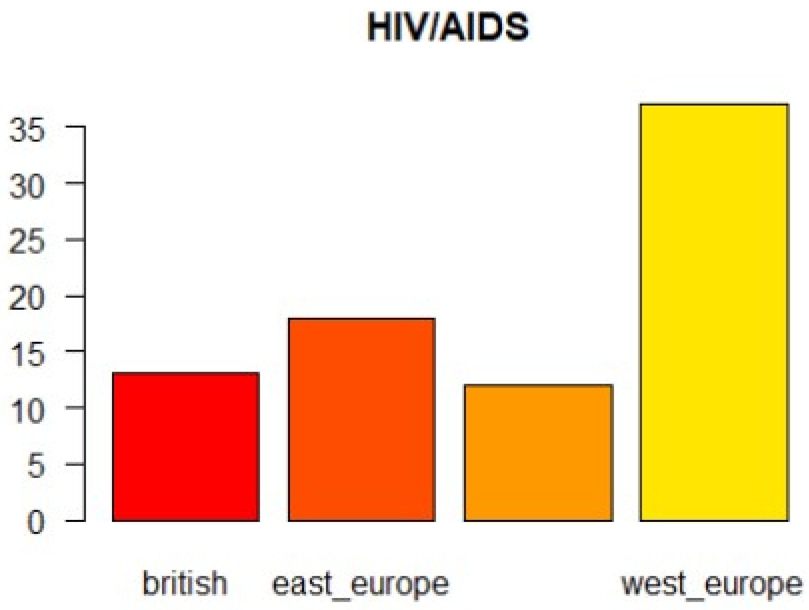
multiple sclerosis


skin cancer
0
20
40
60
80
100
british
east_europe
west_europe

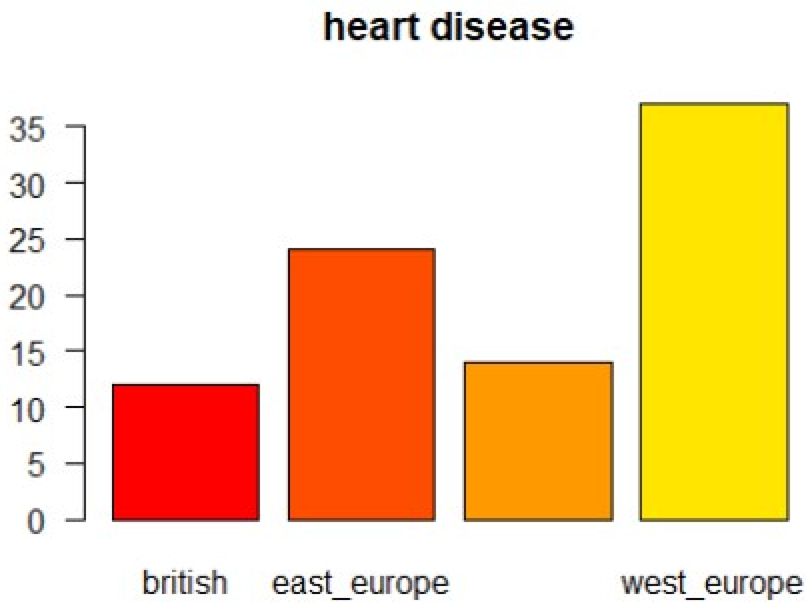

Alzheimer disease
0
50
100
150
british
east_europe
west_europe


kidney disease
0
20
40
60
80
british
east_europe
west_europe


breast cancer
0
10
20
30
40
50
60
70
british
east_europe
west_europe

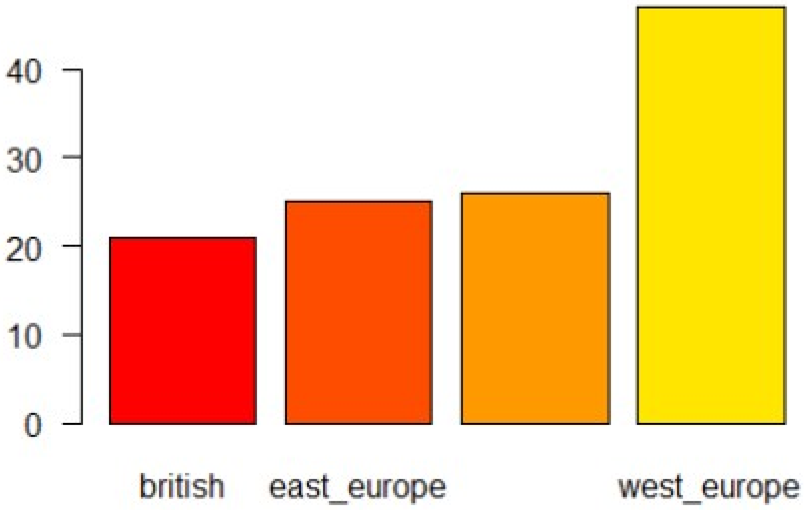


HIV/AIDS

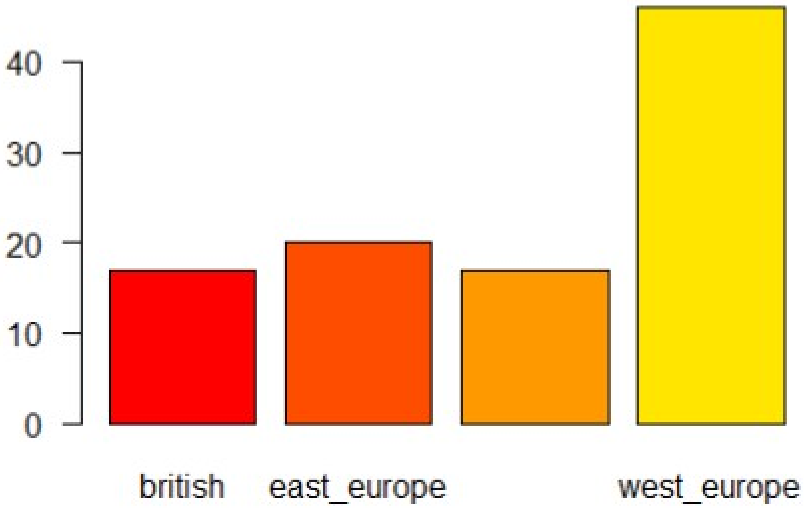


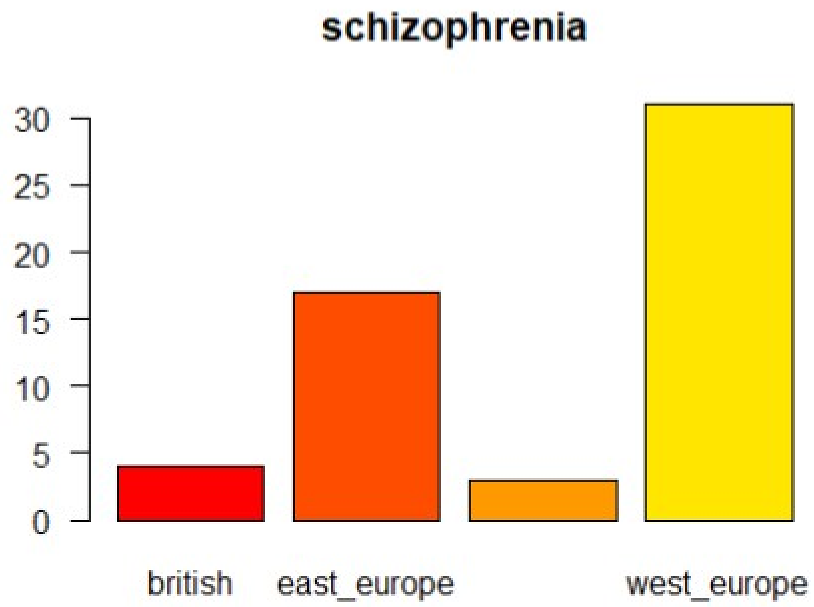
heart disease

diabetes



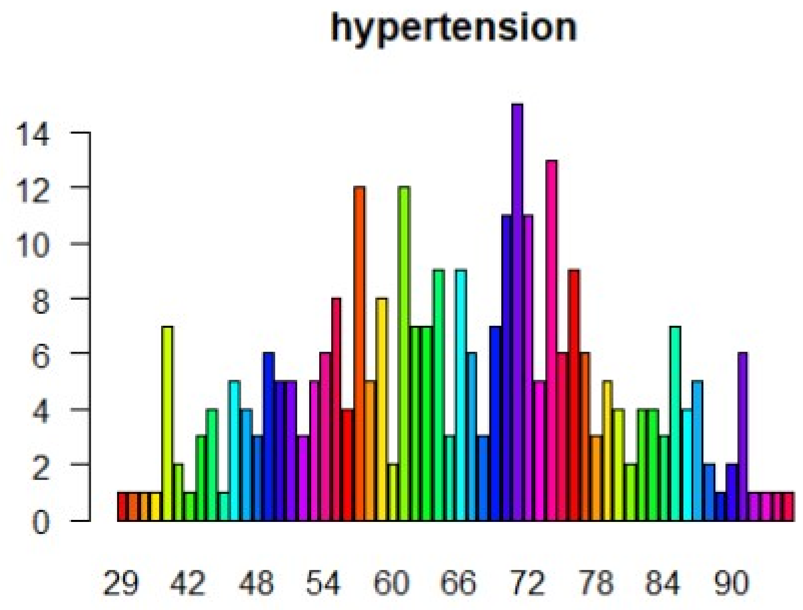
gastritis

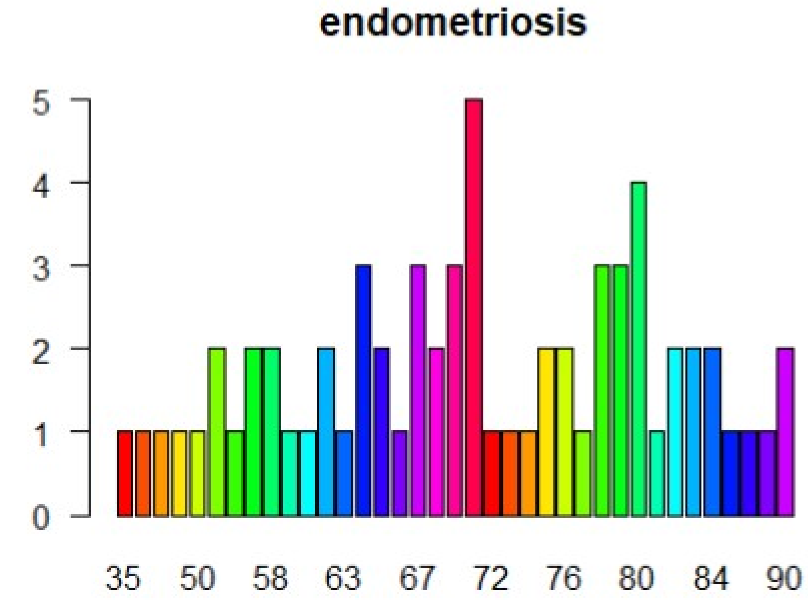


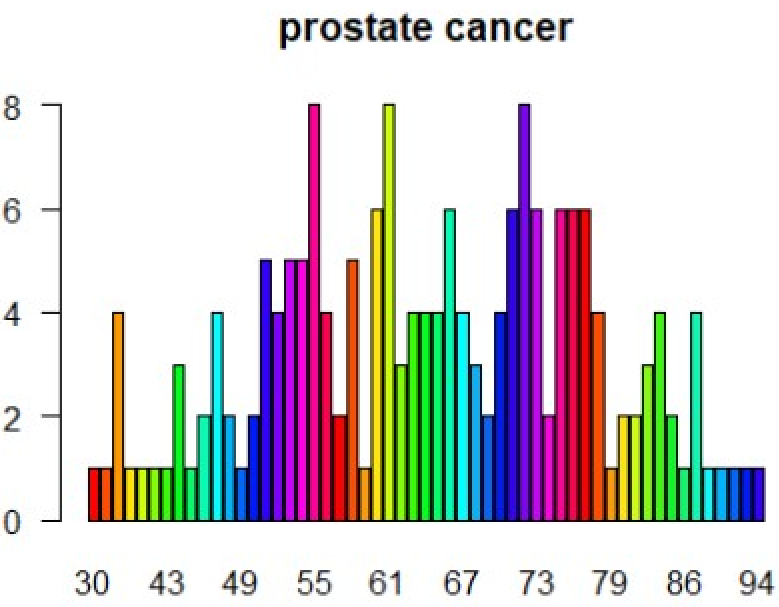


Observation : Disease and age distrubution

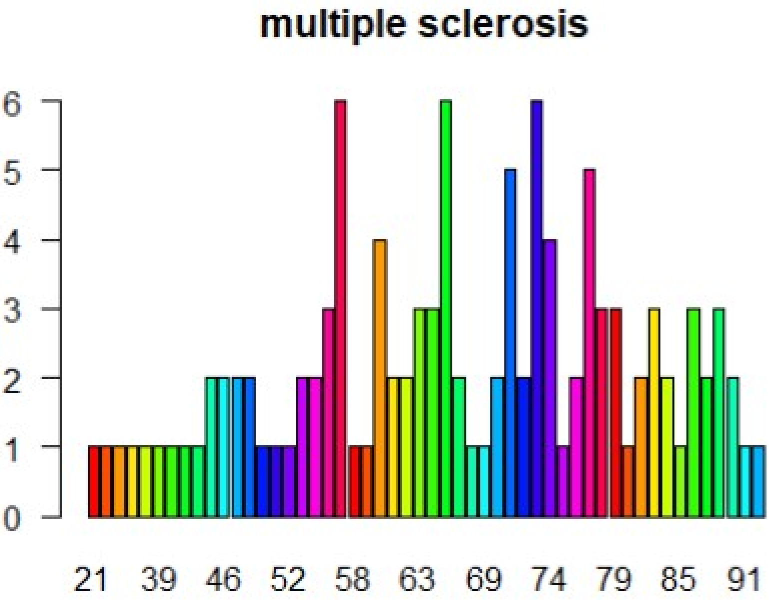
```
for (d in disease_name) {
  age_disease_counts <- subset(patients, patients$disease == d)
  #age_disease_counts <- table(age_disease_counts$age_group_tags)
  age_disease_counts <- table(age_disease_counts$age)
  barplot(age_disease_counts, main=d, col=rainbow(20), las=1)
}
```


hypertension
14
12
10
8
6
4
2
0
29
42
48
54
60
66
72
78
84
90

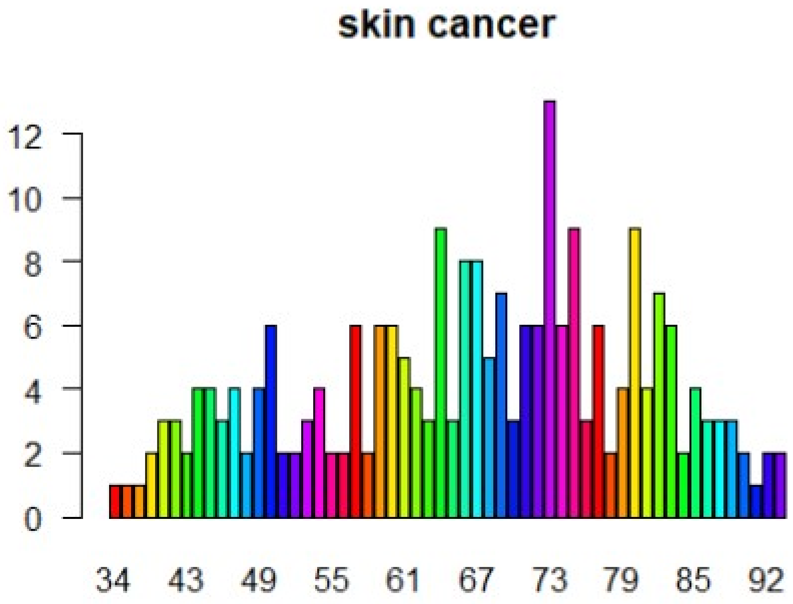

endometriosis
5
4
3
2
1
0
35
50
58
63
67
72
76
80
84
90

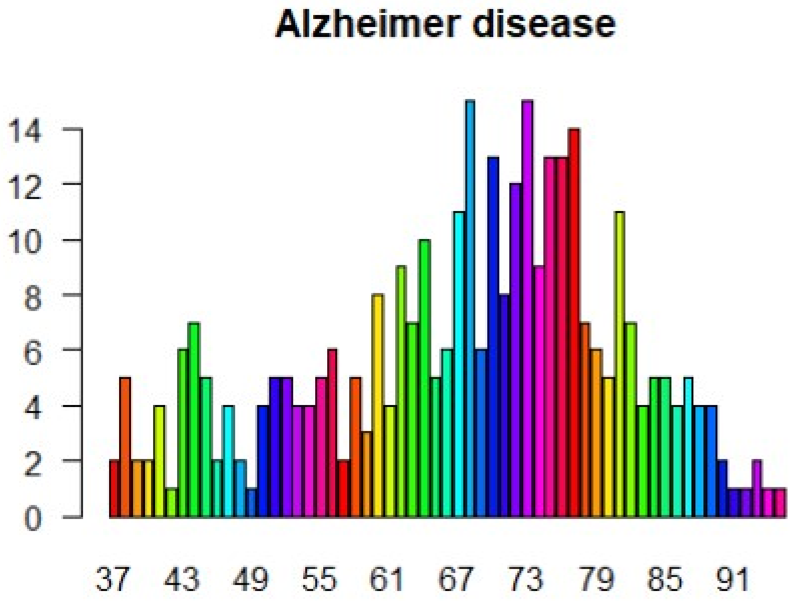


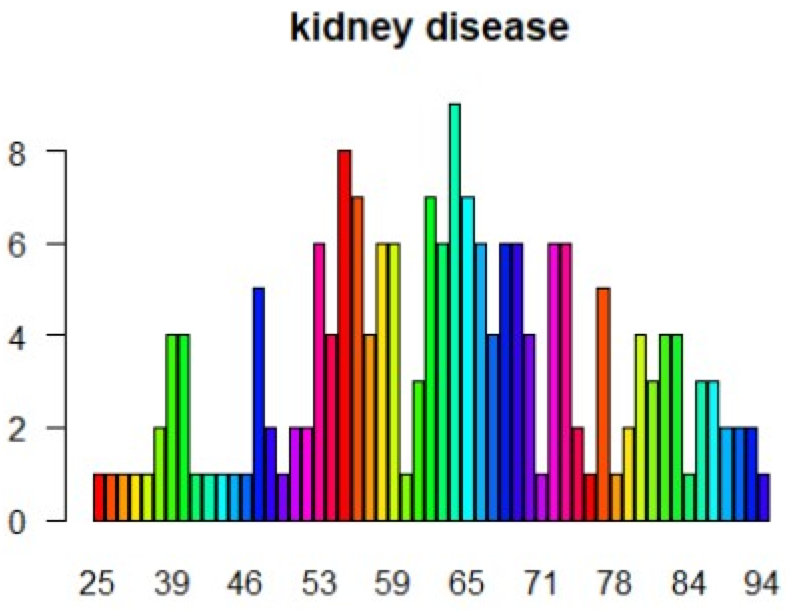
prostate cancer

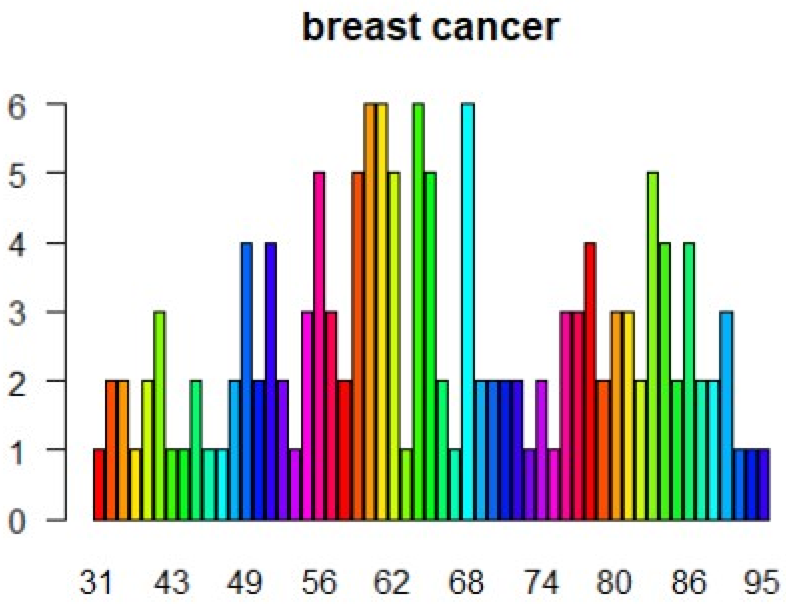


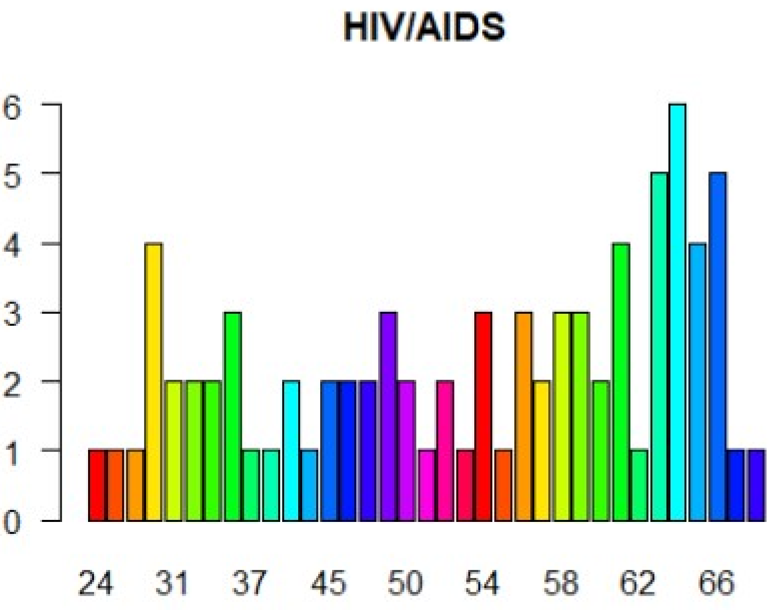
multiple sclerosis

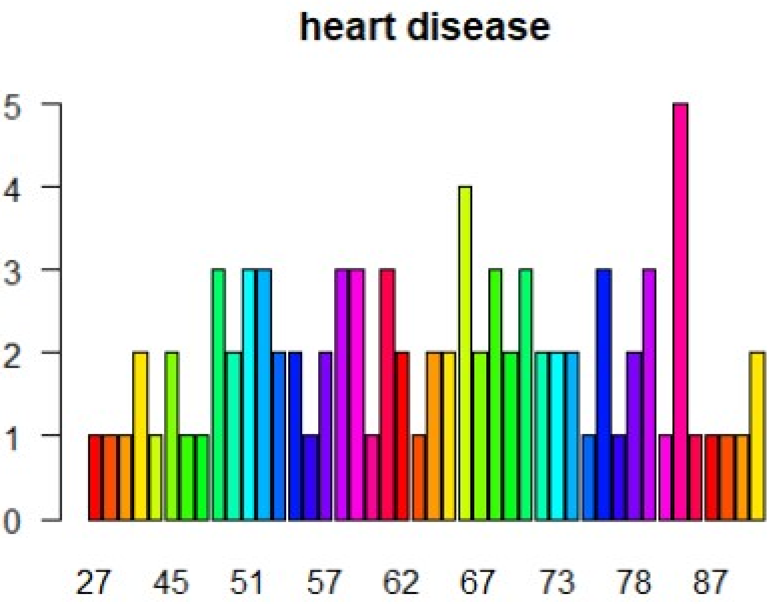

skin cancer
12
10
8
6
4
2
0
34
43
49
55
61
67
73
79
85
92

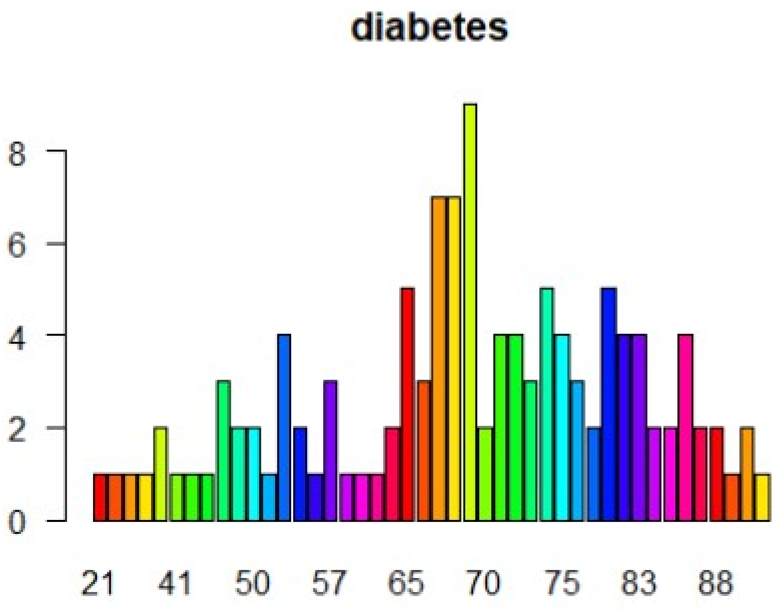

Alzheimer disease
14
12
10
8
6
4
2
0
37
43
49
55
61
67
73
79
85
91

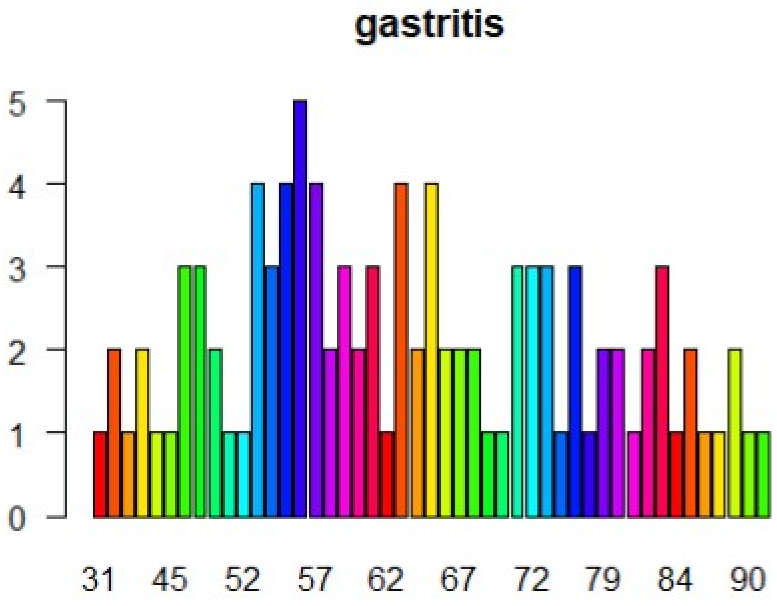

kidney disease
0
2
4
6
8
25
39
46
53
59
65
71
78
84
94

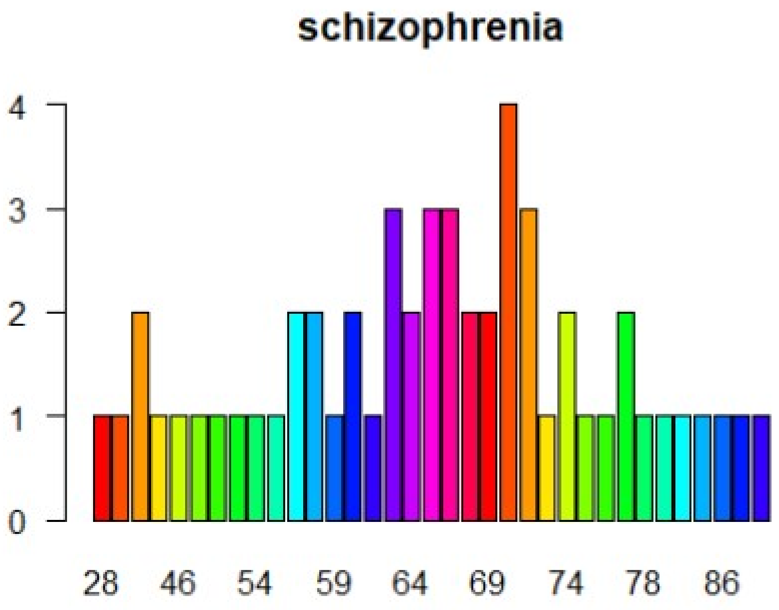

breast cancer
0
1
2
3
4
5
6
31
43
49
56
62
68
74
80
86
95


HIV/AIDS


heart disease

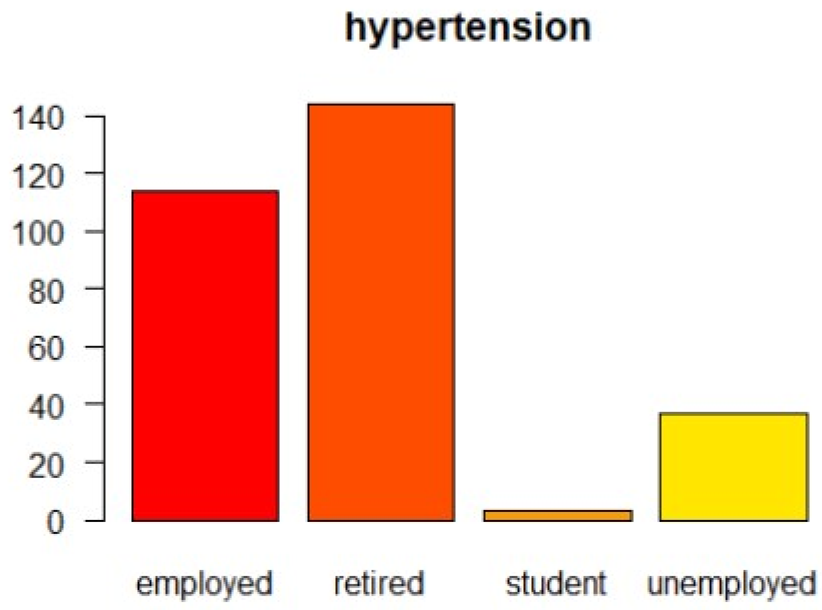

diabetes
0
2
4
6
8
21
41
50
57
65
70
75
83
88

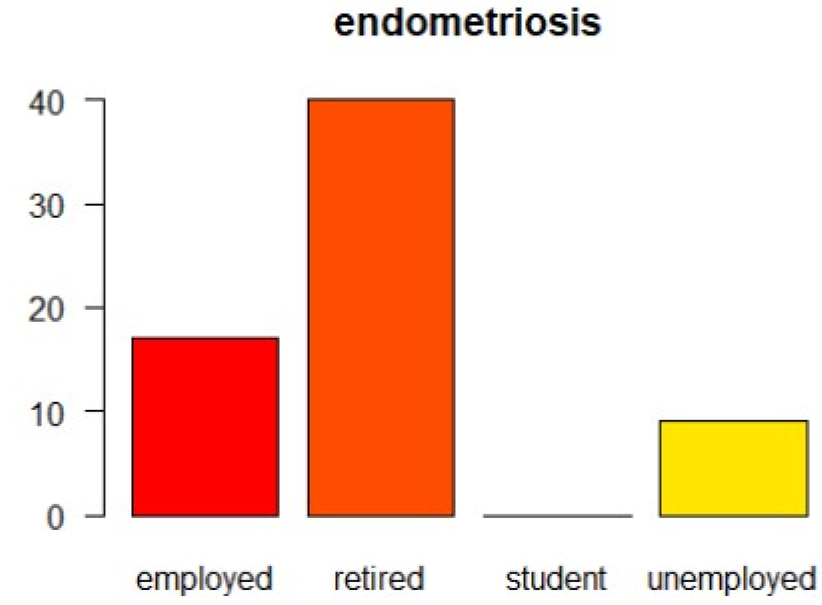

gastritis
0
1
2
3
4
5
31
45
52
57
62
67
72
79
84
90

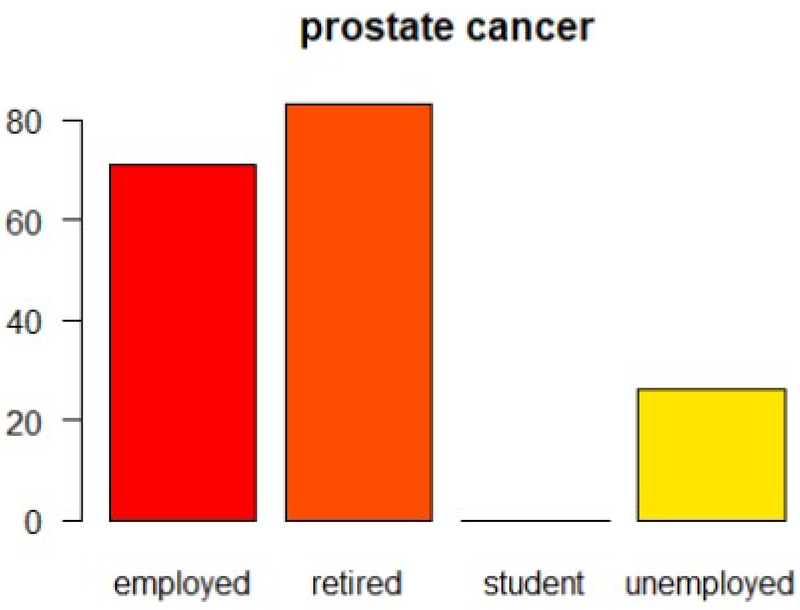


Observation : Disease and employment status distrubution

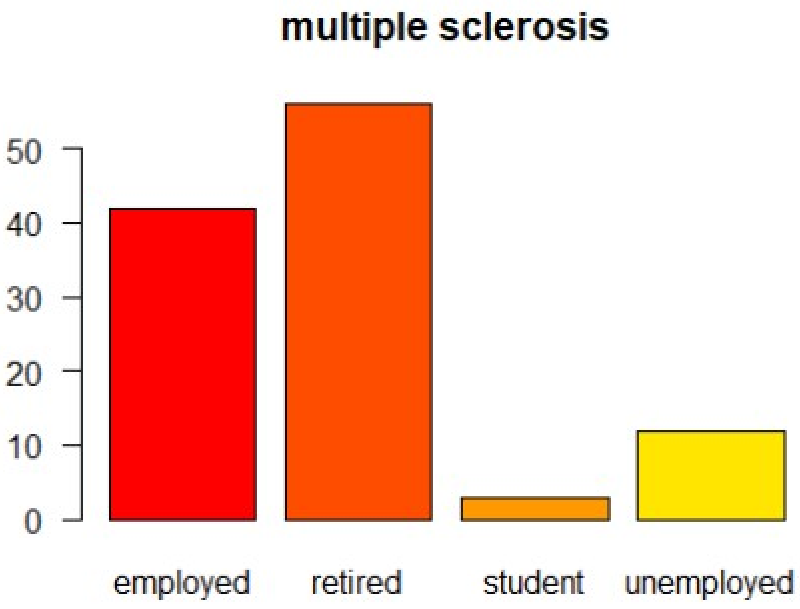
```
for (d in disease_name) {
  emp_disease_counts <- subset(patients, patients$disease == d)
  emp_disease_counts <- table(emp_disease_counts$employment_status)
  barplot(emp_disease_counts, main=d, col=rainbow(20), las=1)
}
```


hypertension
140
120
100
80
60
40
20
0
employed
retired
student
unemployed

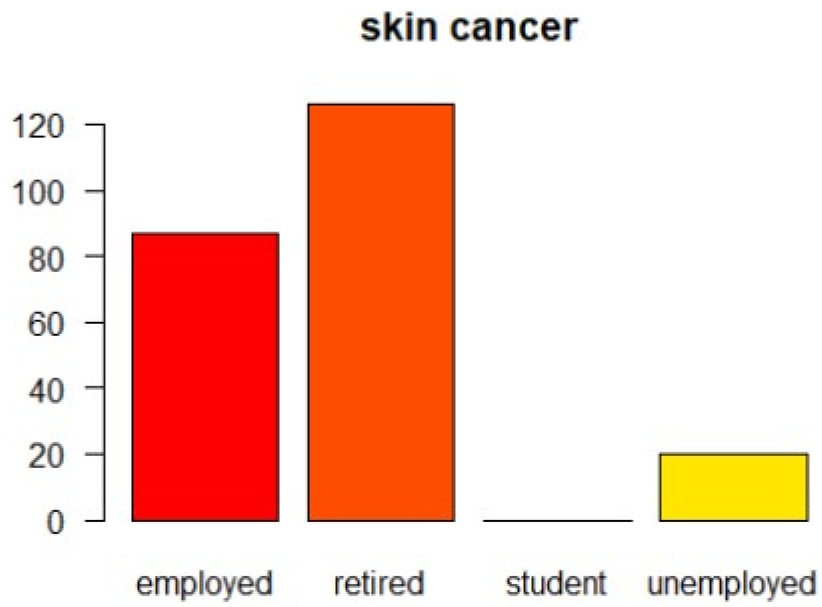

endometriosis
40
30
20
10
0
employed
retired
student
unemployed



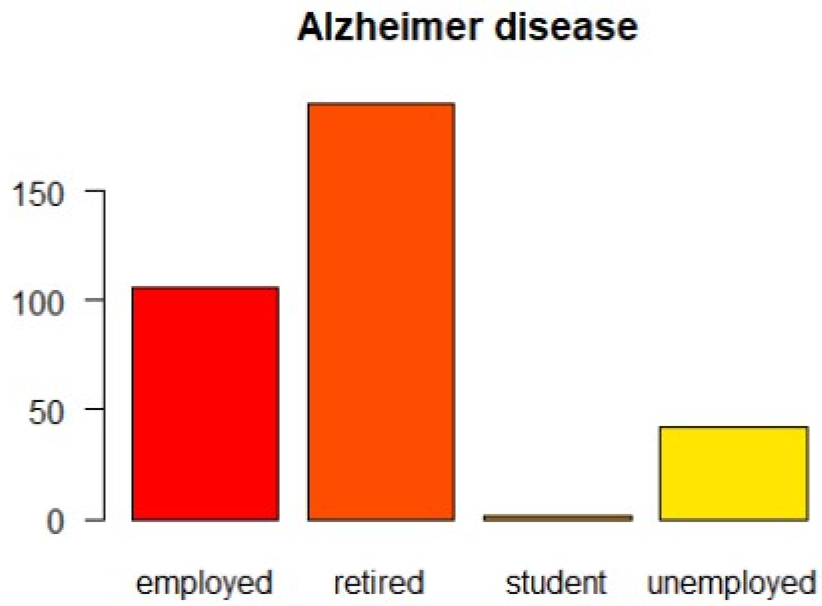
prostate cancer



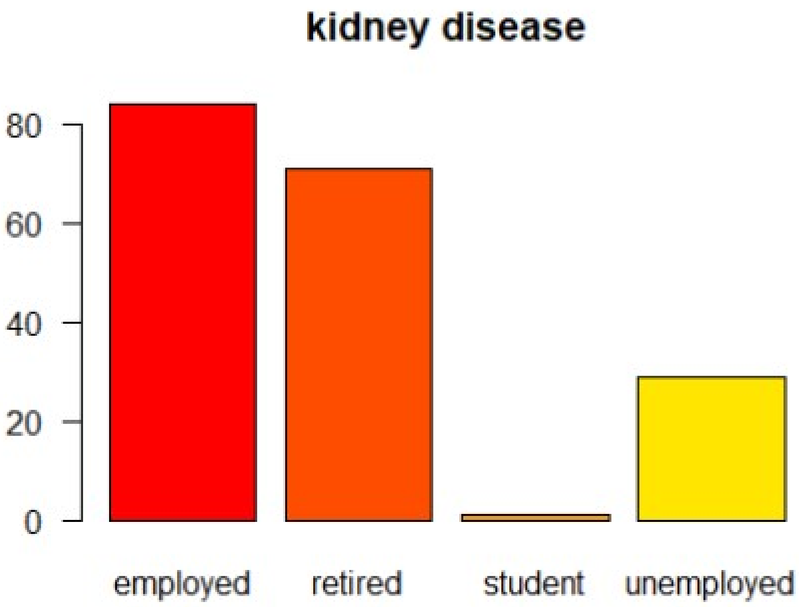
multiple sclerosis



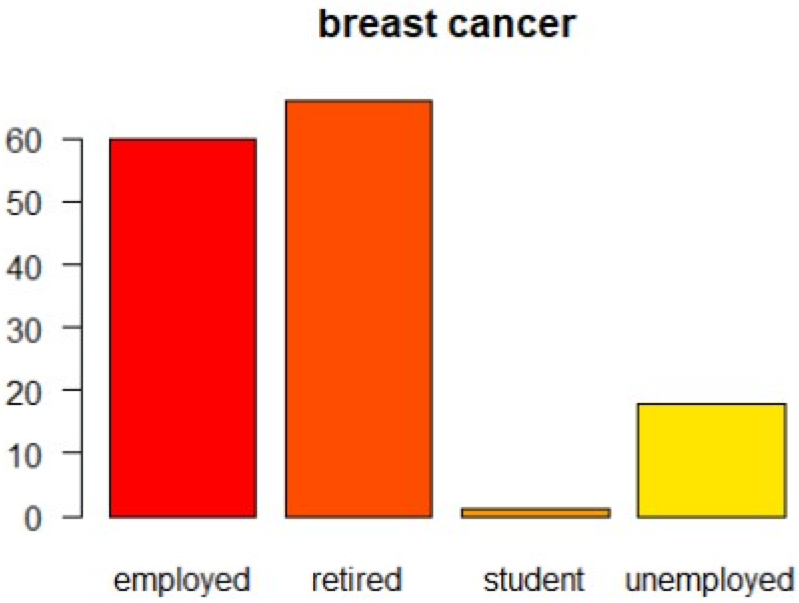
skin cancer



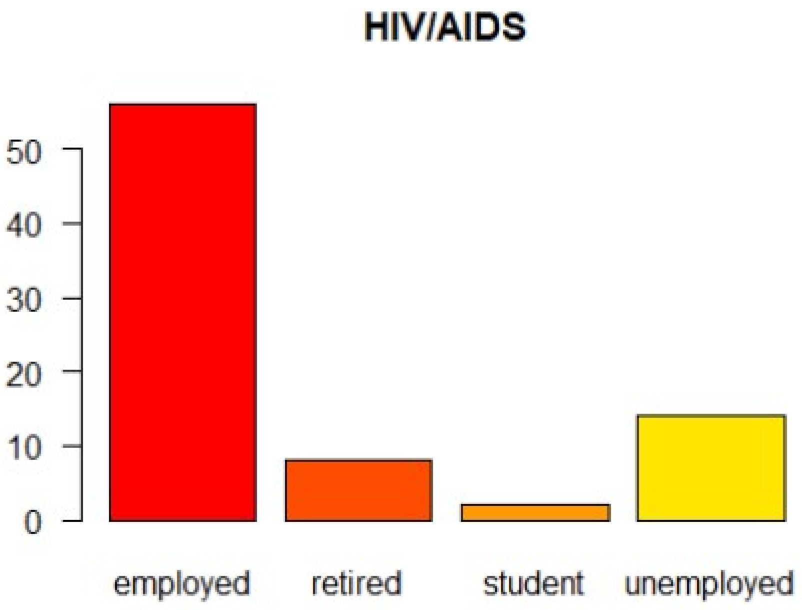
Alzheimer disease

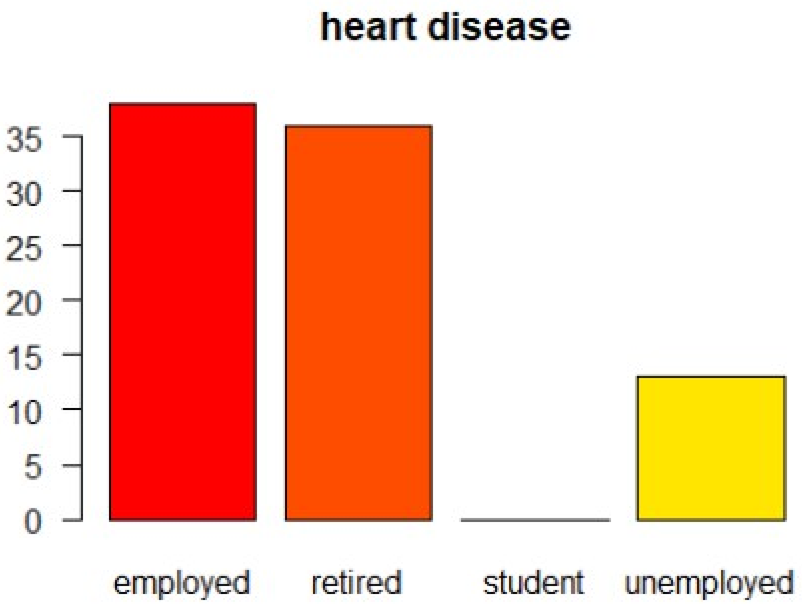


kidney disease

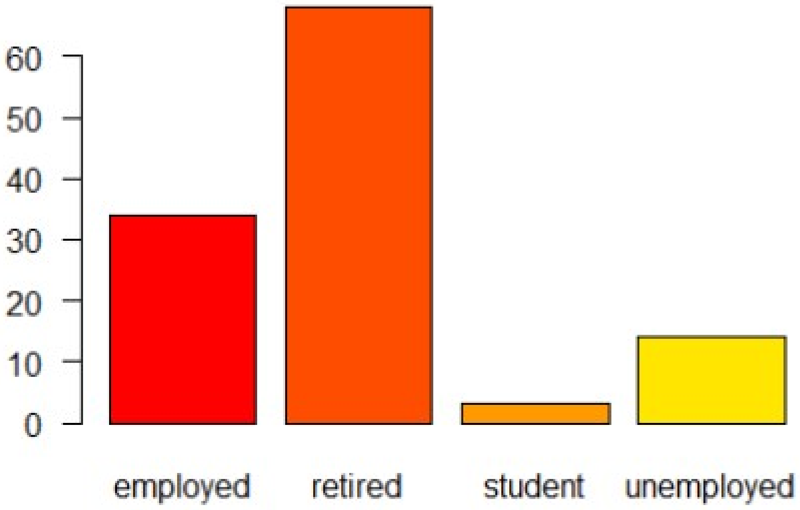


breast cancer

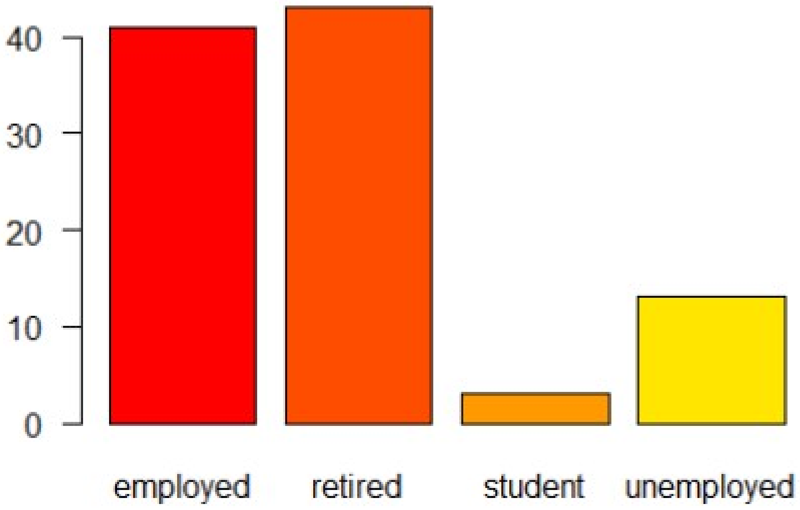

HIV/AIDS
0
10
20
30
40
50
employed
retired
student
unemployed

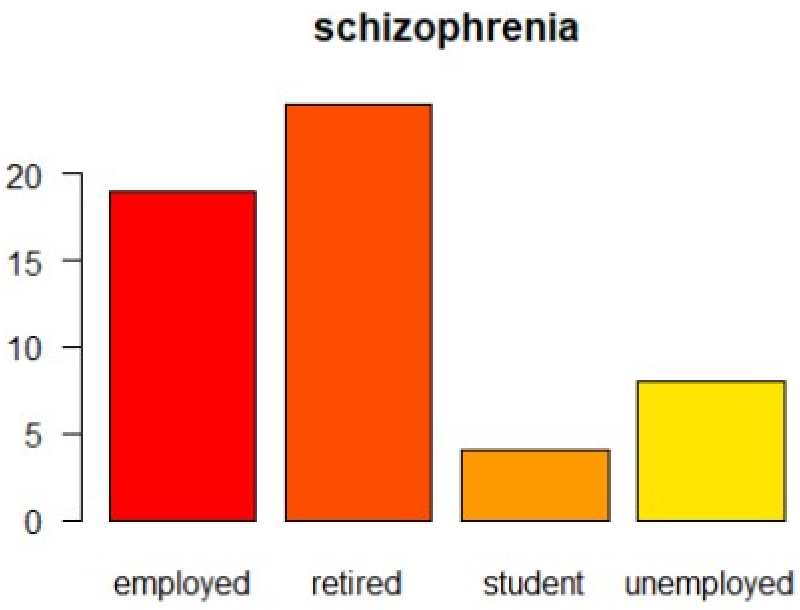

heart disease
0
5
10
15
20
25
30
35
employed
retired
student
unemployed

diabetes



gastritis





Results

The data from the clened dataset were explored using basic R functions to determine reasonable candidate features for the model. The cleaned dataset contains 13 potential classes. However, only 5 were used to reduce computation.

Partitioning

The data were partitioned into a test and training set using a 70/30 split.

```
set.seed(100)
train <- sample(nrow(patients), 0.7*nrow(patients), replace = FALSE)
TrainSet <- patients[train,]
ValidSet <- patients[-train,]
summary(TrainSet)
```

```
##     gender            dob          zipcode       employment_status
##  female:688   1946-02-22:   3   Min.   :10001   employed  :525  
##  male  :712   1960-08-01:   3   1st Qu.:43221   retired   :678  
##               1934-01-28:   2   Median :60612   student   : 15  
##               1934-06-19:   2   Mean   :62719   unemployed:182  
##               1936-11-01:   2   3rd Qu.:90008                   
##               1939-04-18:   2   Max.   :94110                   
##               (Other)   :1386                                   
##       education    marital_status    children             ancestry
##  bachelors :762   married:1036   Min.   :0.000   british     :204  
##  highschool:326   single : 364   1st Qu.:1.000   east_europe :324  
##  masters   :185                  Median :2.000   north_europe:210
##  phd/md    :127                  Mean   :2.294   west_europe :662
##                                  3rd Qu.:3.000
##                                  Max.   :7.000
##
##   avg_commute    daily_internet_use available_vehicles military_service
##  Min.   :-2.47   Min.   :1.010      Min.   :0.000      no :1272
##  1st Qu.:23.43   1st Qu.:4.048      1st Qu.:1.000      yes: 128
##  Median :30.32   Median :5.055      Median :2.000
##  Mean   :30.37   Mean   :5.039      Mean   :1.738
##  3rd Qu.:37.16   3rd Qu.:6.000      3rd Qu.:3.000
##  Max.   :63.73   Max.   :8.820      Max.   :4.000
##
##               disease         age        prostate_cancer
##  Alzheimer disease:241   Min.   :21.00   Min.   :0.00000
##  hypertension     :209   1st Qu.:56.00   1st Qu.:0.00000
##  skin cancer      :150   Median :67.00   Median :0.00000
##  prostate cancer  :127   Mean   :65.76   Mean   :0.09071
##  kidney disease   :126   3rd Qu.:76.00   3rd Qu.:0.00000
##  breast cancer    :106   Max.   :96.00   Max.   :1.00000
##  (Other)          :441
##   skin_cancer     breast_cancer       hiv_aids          diabetes
##  Min.   :0.0000   Min.   :0.00000   Min.   :0.00000   Min.   :0.00000
##  1st Qu.:0.0000   1st Qu.:0.00000   1st Qu.:0.00000   1st Qu.:0.00000
##  Median :0.0000   Median :0.00000   Median :0.00000   Median :0.00000
##  Mean   :0.1071   Mean   :0.07571   Mean   :0.04357   Mean   :0.06357
##  3rd Qu.:0.0000   3rd Qu.:0.00000   3rd Qu.:0.00000   3rd Qu.:0.00000
##  Max.   :1.0000   Max.   :1.00000   Max.   :1.00000   Max.   :1.00000
##
##  heart_disease      hypertension    endometriosis     multiple_sclerosis
##  Min.   :0.00000   Min.   :0.0000   Min.   :0.00000   Min.   :0.00000
##  1st Qu.:0.00000   1st Qu.:0.0000   1st Qu.:0.00000   1st Qu.:0.00000
##  Median :0.00000   Median :0.0000   Median :0.00000   Median :0.00000
##  Mean   :0.04214   Mean   :0.1493   Mean   :0.03071   Mean   :0.05929
##  3rd Qu.:0.00000   3rd Qu.:0.0000   3rd Qu.:0.00000   3rd Qu.:0.00000
##  Max.   :1.00000   Max.   :1.0000   Max.   :1.00000   Max.   :1.00000
##
##  schizophrenia     kidney_disease   gastritis      alzheimer
##  Min.   :0.00000   Min.   :0.00   Min.   :0.00   Min.   :0.0000
##  1st Qu.:0.00000   1st Qu.:0.00   1st Qu.:0.00   1st Qu.:0.0000
##  Median :0.00000   Median :0.00   Median :0.00   Median :0.0000
##  Mean   :0.02571   Mean   :0.09   Mean   :0.05   Mean   :0.1721
##  3rd Qu.:0.00000   3rd Qu.:0.00   3rd Qu.:0.00   3rd Qu.:0.0000
##  Max.   :1.00000   Max.   :1.00   Max.   :1.00   Max.   :1.0000
##
```

```
summary(ValidSet)
```

```
##     gender          dob         zipcode      employment_status
##  female:287   1959-09-22:  3   Min.   :10001   employed  :244
##  male  :313   1932-04-10:  2   1st Qu.:43221   retired   :277
##               1935-07-27:  2   Median :60612   student   :  6
##               1946-01-07:  2   Mean   :64948   unemployed: 73
##               1954-12-31:  2   3rd Qu.:90015
##               1961-12-21:  2   Max.   :94110
##               (Other)   :587
##       education   marital_status    children           ancestry
##  bachelors :314   married:460    Min.   :0.000   british     :100
##  highschool:137   single :140    1st Qu.:1.000   east_europe :145
##  masters   : 95                  Median :2.000   north_europe: 92
##  phd/md    : 54                  Mean   :2.203   west_europe :263
##                                  3rd Qu.:3.000
##                                  Max.   :7.000
##
##   avg_commute    daily_internet_use available_vehicles military_service
##  Min.   :-0.74   Min.   :1.400      Min.   :0.000      no :545
##  1st Qu.:23.59   1st Qu.:3.940      1st Qu.:1.000      yes: 55
##  Median :30.30   Median :4.905      Median :2.000
##  Mean   :30.39   Mean   :4.887      Mean   :1.765
##  3rd Qu.:36.98   3rd Qu.:5.832      3rd Qu.:3.000
##  Max.   :56.27   Max.   :8.340      Max.   :4.000
##
##               disease         age         prostate_cancer
##  Alzheimer disease: 98   Min.   :21.00   Min.   :0.00000
##  hypertension     : 89   1st Qu.:54.00   1st Qu.:0.00000
##  skin cancer      : 83   Median :65.00   Median :0.00000
##  kidney disease   : 59   Mean   :64.19   Mean   :0.08833
##  prostate cancer  : 53   3rd Qu.:75.00   3rd Qu.:0.00000
##  breast cancer    : 39   Max.   :94.00   Max.   :1.00000
##  (Other)          :179
##   skin_cancer     breast_cancer      hiv_aids          diabetes
##  Min.   :0.0000   Min.   :0.000   Min.   :0.00000   Min.   :0.00
##  1st Qu.:0.0000   1st Qu.:0.000   1st Qu.:0.00000   1st Qu.:0.00
##  Median :0.0000   Median :0.000   Median :0.00000   Median :0.00
##  Mean   :0.1383   Mean   :0.065   Mean   :0.03167   Mean   :0.05
##  3rd Qu.:0.0000   3rd Qu.:0.000   3rd Qu.:0.00000   3rd Qu.:0.00
##  Max.   :1.0000   Max.   :1.000   Max.   :1.00000   Max.   :1.00
##
##  heart_disease      hypertension    endometriosis     multiple_sclerosis
##  Min.   :0.00000   Min.   :0.0000   Min.   :0.00000   Min.   :0.00
##  1st Qu.:0.00000   1st Qu.:0.0000   1st Qu.:0.00000   1st Qu.:0.00
##  Median :0.00000   Median :0.0000   Median :0.00000   Median :0.00
##  Mean   :0.04667   Mean   :0.1483   Mean   :0.03833   Mean   :0.05
##  3rd Qu.:0.00000   3rd Qu.:0.0000   3rd Qu.:0.00000   3rd Qu.:0.00
##  Max.   :1.00000   Max.   :1.0000   Max.   :1.00000   Max.   :1.00
##
##  schizophrenia     kidney_disease      gastritis      alzheimer
##  Min.   :0.00000   Min.   :0.00000   Min.   :0.00   Min.   :0.0000
##  1st Qu.:0.00000   1st Qu.:0.00000   1st Qu.:0.00   1st Qu.:0.0000
##  Median :0.00000   Median :0.00000   Median :0.00   Median :0.0000
##  Mean   :0.03167   Mean   :0.09833   Mean   :0.05   Mean   :0.1633
##  3rd Qu.:0.00000   3rd Qu.:0.00000   3rd Qu.:0.00   3rd Qu.:0.0000
##  Max.   :1.00000   Max.   :1.00000   Max.   :1.00   Max.   :1.0000
##
```

Analysing the hypertension disease

The dataset will predict the hypertension disease with selected attributes that contributes to the analysis

```
hyper_TrainSet <- select(TrainSet, gender, age, employment_status, education,
marital_status, ancestry, hypertension)
hyper_ValidSet <- select(ValidSet, gender, age, employment_status, education,
marital_status, ancestry, hypertension)
hyper_TrainSet$hypertension <- as.factor(hyper_TrainSet$hypertension)
```

Logistic Regression Model

The model was fit using a binomial logistic regression with the glm function in R, with family = binomial on the training data.

```
fit <- glm(hypertension~.,data=hyper_TrainSet,family=binomial())
summary(fit) # display results
```

```
##
## Call:
## glm(formula = hypertension ~ ., family = binomial(), data =
hyper_TrainSet)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -0.7219  -0.5948  -0.5559  -0.5057   2.2905
##
## Coefficients:
##                              Estimate Std. Error z value Pr(>|z|)
## (Intercept)                 -1.598064   0.517515  -3.088  0.00202 **
## gendermale                  -0.161921   0.150647  -1.075  0.28245
## age                          0.003875   0.008270   0.469  0.63938
## employment_statusretired    -0.256010   0.238934  -1.071  0.28396
## employment_statusstudent    -0.746796   1.071625  -0.697  0.48588
## employment_statusunemployed  0.180992   0.266726   0.679  0.49741
## educationhighschool         -0.222720   0.206987  -1.076  0.28192
## educationmasters            -0.168767   0.238080  -0.709  0.47841
## educationphd/md             -0.245495   0.298308  -0.823  0.41053
## marital_statussingle        -0.093976   0.182966  -0.514  0.60752
## ancestryeast_europe         -0.064898   0.245987  -0.264  0.79191
## ancestrynorth_europe        -0.235585   0.279753  -0.842  0.39972
## ancestrywest_europe         -0.106049   0.220397  -0.481  0.63040
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 1180.1  on 1399  degrees of freedom
## Residual deviance: 1172.9  on 1387  degrees of freedom
## AIC: 1198.9
##
## Number of Fisher Scoring iterations: 5
```

```
confint(fit) # 95% CI for the coefficients
```

```
## Waiting for profiling to be done...
```

```
##                                   2.5 %      97.5 %
## (Intercept)                 -2.63062208 -0.60001322
## gendermale                  -0.45806884  0.13311766
## age                         -0.01213159  0.02031294
## employment_statusretired    -0.72705408  0.21039324
## employment_statusstudent    -3.67947133  0.96593490
## employment_statusunemployed -0.34968605  0.69837542
## educationhighschool         -0.63726228  0.17554844
## educationmasters            -0.65415958  0.28270854
## educationphd/md             -0.86581671  0.31121822
## marital_statussingle        -0.46024152  0.25818123
## ancestryeast_europe         -0.54320612  0.42389803
## ancestrynorth_europe        -0.78905865  0.31176835
## ancestrywest_europe         -0.52887951  0.33751264
```

```
exp(coef(fit)) # exponentiated coefficients
```

```
##                 (Intercept)                  gendermale
##                   0.2022878                   0.8505084
##                         age    employment_statusretired
##                   1.0038825                   0.7741340
##    employment_statusstudent employment_statusunemployed
##                   0.4738823                   1.1984052
##        educationhighschool            educationmasters
##                  0.8003391                   0.8447060
##            educationphd/md       marital_statussingle
##                  0.7823171                   0.9103049
##        ancestryeast_europe       ancestrynorth_europe
##                  0.9371634                   0.7901085
##        ancestrywest_europe
##                  0.8993810
```

```
exp(confint(fit)) # 95% CI for exponentiated coefficients
```

```
## Waiting for profiling to be done...
```

```
##                                 2.5 %    97.5 %
## (Intercept)                0.07203364 0.5488044
## gendermale                 0.63250393 1.1423844
## age                        0.98794171 1.0205207
## employment_statusretired   0.48333075 1.2341633
## employment_statusstudent   0.02523631 2.6272427
## employment_statusunemployed 0.70490936 2.0104839
## educationhighschool        0.52873798 1.1918997
## educationmasters           0.51987880 1.3267184
## educationphd/md            0.42070782 1.3650871
## marital_statussingle       0.63113119 1.2945734
## ancestryeast_europe        0.58088289 1.5279058
## ancestrynorth_europe       0.45427222 1.3658383
## ancestrywest_europe        0.58926486 1.4014573
```

```
#predict(fit, type="response") # predicted values
#residuals(fit, type="deviance") # residuals
```

Performace

Probabilites for the response varable based on the test data were assigned using the predict functin.

```
#probs <- predict(fit, test, type = "response")
#pred <- predict(fit, newdata = ValidSet)
#pred
```

Confusion Matrix

```
#confusionMatrix(pred, ValidSet$hypertension)
```

Randomforest model

Apply randomforest model

```
# Fine tuning parameters of Random Forest model
```

```
model2 <- randomForest(hypertension ~ ., data = hyper_TrainSet,  importance = TRUE)
model2
```

```
##
## Call:
##  randomForest(formula = hypertension ~ ., data = hyper_TrainSet,
importance = TRUE)
##                Type of random forest: classification
##                      Number of trees: 500
## No. of variables tried at each split: 2
##
##         OOB estimate of  error rate: 14.93%
## Confusion matrix:
##      0 1  class.error
## 0 1190 1 0.0008396306
## 1  208 1 0.9952153110
```

```
# Predicting on train set
predTrain <- predict(model2, hyper_TrainSet, type = "class")

# Checking classification accuracy
table(predTrain, hyper_TrainSet$hypertension)
```

```
##
## predTrain    0    1
##         0 1191  193
##         1    0   16
```

```
#model2 <- na.omit(model2)

# Predicting on Validation set
predValid <- predict(model2, hyper_ValidSet, type = "class")

# Checking classification accuracy
mean(predValid == hyper_ValidSet$hypertension)
```

```
## [1] 0.8516667
```

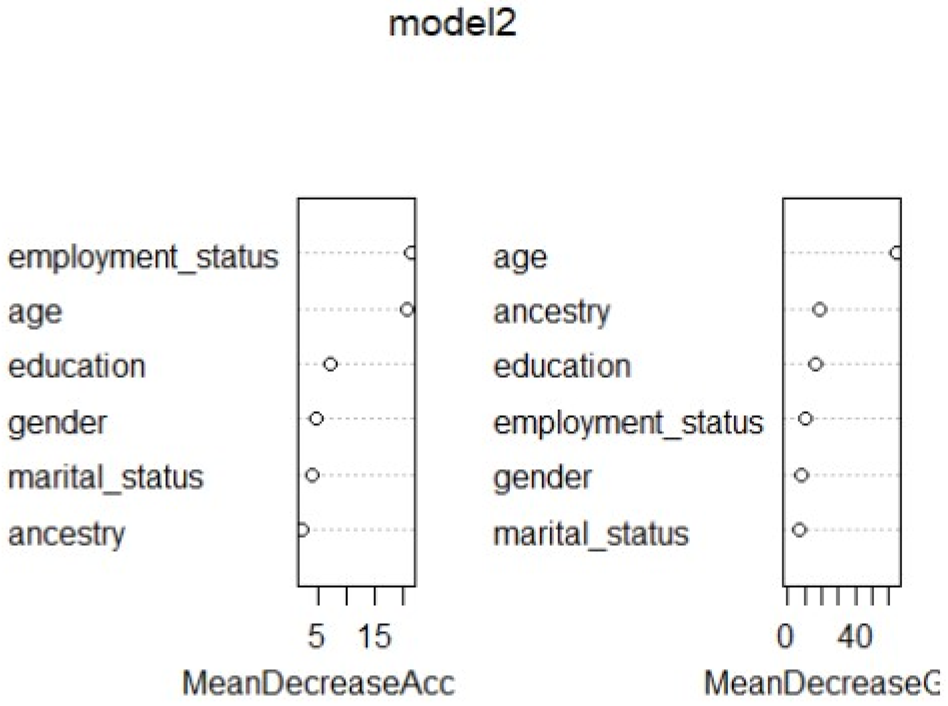
```
table(predValid,hyper_ValidSet$hypertension)
```

```
##
## predValid   0   1
##         0 511  89
##         1   0   0
```

```
# To check important variables
importance(model2)
```

```
##                            0           1 MeanDecreaseAccuracy
## gender             2.993876   4.0978549             4.415259
## age               21.552305 -14.6831814            20.817189
## employment_status 21.759440 -14.7451270            21.549575
## education          7.903064  -1.4755122             6.995147
## marital_status     5.229751  -3.0194415             3.768667
## ancestry           2.518510  -0.7734031             2.128883
##                   MeanDecreaseGini
## gender                    7.570786
## age                      64.612706
## employment_status        10.175206
## education                15.749273
## marital_status            7.063689
## ancestry                 18.210400
```

```
varImpPlot(model2)
```



Naive Bayes Model

```
NBclassfier = naiveBayes(hypertension~., data=hyper_TrainSet)
print(NBclassfier)
```

```
##
## Naive Bayes Classifier for Discrete Predictors
##
## Call:
## naiveBayes.default(x = X, y = Y, laplace = laplace)
```

```
##
## A-priori probabilities:
## Y
##         0         1
## 0.8507143 0.1492857
##
## Conditional probabilities:
##    gender
## Y      female      male
##   0 0.4853065 0.5146935
##   1 0.5263158 0.4736842
##
##    age
## Y       [,1]     [,2]
##   0 65.82032 14.02212
##   1 65.43541 13.12685
##
##    employment_status
## Y      employed     retired     student  unemployed
##   0 0.370277078 0.491183879 0.011754828 0.126784215
##   1 0.401913876 0.444976077 0.004784689 0.148325359
##
##    education
## Y    bachelors highschool    masters     phd/md
##   0 0.53736356 0.23425693 0.13434089 0.09403862
##   1 0.58373206 0.22488038 0.11961722 0.07177033
##
##    marital_status
## Y     married    single
##   0 0.7380353 0.2619647
##   1 0.7511962 0.2488038
##
##    ancestry
## Y     british east_europe north_europe west_europe
##   0 0.1435768   0.2300588    0.1528128   0.4735516
##   1 0.1578947   0.2392344    0.1339713   0.4688995
```