Analysis and Study of UCI Heart Disease dataset

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Part 1:- Getting the feature dataset from the actual data

Dataset details

Attribute information

- age
- sex
- chest pain type (4 values) -> cp
- resting blood pressure -> trestbps
- serum cholestoral in mg/dl-> chol
- fasting blood sugar > 120 mg/dl -> fbs
- resting electrocardiographic results (values 0,1,2) -> restecg
- maximum heart rate achieved -> thalach
- exercise induced angina -> exang
- oldpeak = ST depression induced by exercise relative to rest -> oldpeak
- the slope of the peak exercise ST segment -> slope
- number of major vessels (0-3) colored by flourosopy -> ca
- thal: 3 = normal; 6 = fixed defect; 7 = reversable defect

Program for exploratory analysis and preprocessing

Function to Normalize the data

```
normalize <- function(x) {
  return ((x - min(x)) / (max(x) - min(x)))
}
```

Import dataset and view it as a dataframe

```
heart <- read.csv("~/HeartDisease/heart.csv")
head(heart)
```

```
##   age sex cp trestbps chol fbs restecg thalach exang oldpeak slope ca thal
```

```
## 1  63   1  3       145  233   1       0      150      0      2.3      0  0    1
## 2  37   1  2       130  250   0       1      187      0      3.5      0  0    2
## 3  41   0  1       130  204   0       0      172      0      1.4      2  0    2
## 4  56   1  1       120  236   0       1      178      0      0.8      2  0    2
## 5  57   0  0       120  354   0       1      163      1      0.6      2  0    2
## 6  57   1  0       140  192   0       1      148      0      0.4      1  0    1
##   target
## 1      1
## 2      1
## 3      1
## 4      1
## 5      1
## 6      1
```

Normalize the age and separate it in various groups to show which age group is more prone to heart disease

It uses the normalize function defined above and then categorize the data into **four** groups.
After normalization the valuesaranges from **0-1**
It is grouped as follows
- **0.00 to 0.25** as **Group 1** giving it value **0.1**
- **0.25 to 0.50** as **Group 2** giving it value **0.4**
- **0.50 to 0.75** as **Group 3** giving it value **0.6**
- **0.75 to 1.00** as **Group 4** giving it value **0.9**

```
library(dplyr)
```

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

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

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

```
dfNorm <- as.data.frame(lapply(heart["age"], normalize))
heart["age"] <- dfNorm
heart["age"] <- as.data.frame(lapply(heart["age"], function(x){replace(x,between(x, 0.0, 0.25), 0.1)}))
heart["age"] <- as.data.frame(lapply(heart["age"], function(x){replace(x,between(x, 0.25, 0.6), 0.4)}))
heart["age"] <- as.data.frame(lapply(heart["age"], function(x){replace(x,between(x, 0.5, 0.75), 0.6)}))
heart["age"] <- as.data.frame(lapply(heart["age"], function(x){replace(x,between(x, 0.75, 1), 0.9)}))
```

Normalize the Rest Blood Pressure and separate it in various groups to show what blood pressure group is more prone to heart disease

It uses the normalize function defined above and then categorize the data into **three** groups.
After normalization the valuesaranges from **0-1**
It is grouped as follows
- **0.00 to 0.33** as **Group 1** giving it value **0.2**
- **0.33 to 0.67** as **Group 2** giving it value **0.6**
- **0.67 to 1.00** as **Group 3** giving it value **1.0**

```
dfNorm <- as.data.frame(lapply(heart["trestbps"], normalize))
heart["trestbps"] <- dfNorm
```

```
heart["trestbps"] <- as.data.frame(lapply(heart["trestbps"], function(x){replace(x, between(x, 0.0, 0.33
heart["trestbps"] <- as.data.frame(lapply(heart["trestbps"], function(x){replace(x, between(x, 0.33, 0.6
heart["trestbps"] <- as.data.frame(lapply(heart["trestbps"], function(x){replace(x, between(x, 0.67, 1)
```

Normalize the Cholestrole level and separate it in various groups to show what cholestrole level is more prone to heart disease

It uses the normalize function defined above and then categorize the data into **five** groups.
After normalization the valuesaranges from **0-1**
It is grouped as follows
- **0.00 to 0.20** as **Group 1** giving it value **0.1**
- **0.20 to 0.40** as **Group 2** giving it value **0.3**
- **0.40 to 0.60** as **Group 3** giving it value **0.5**
- **0.60 to 0.80** as **Group 4** giving it value **0.7**
- **0.80 to 1.00** as **Group 5** giving it value **0.9**

```
dfNorm <- as.data.frame(lapply(heart["chol"], normalize))
heart["chol"] <- dfNorm
heart["chol"] <- as.data.frame(lapply(heart["chol"], function(x){replace(x, between(x, 0.0, 0.2), 0.1)})
heart["chol"] <- as.data.frame(lapply(heart["chol"], function(x){replace(x, between(x, 0.2, 0.4), 0.3)})
heart["chol"] <- as.data.frame(lapply(heart["chol"], function(x){replace(x, between(x, 0.4, 0.6), 0.5)})
heart["chol"] <- as.data.frame(lapply(heart["chol"], function(x){replace(x, between(x, 0.6, 0.8), 0.7)})
heart["chol"] <- as.data.frame(lapply(heart["chol"], function(x){replace(x, between(x, 0.8, 1), 0.9)}))
```

Normalize the chest pain and separate it in various groups to show what percentage of chest pain is more prone to heart disease

It uses the normalize function defined above and then categorize the data into **four** groups.
After normalization the valuesaranges from **0-1**
It is grouped as follows
- **0.00 to 0.25** as **Group 1** giving it value **0.1**
- **0.25 to 0.50** as **Group 2** giving it value **0.4**
- **0.50 to 0.75** as **Group 3** giving it value **0.6**
- **0.75 to 1.00** as **Group 4** giving it value **0.9**

```
dfNorm <- as.data.frame(lapply(heart["cp"], normalize))
heart["cp"] <- dfNorm
heart["cp"] <- as.data.frame(lapply(heart["cp"], function(x){replace(x, between(x, 0.0, 0.25), 0.1)}))
heart["cp"] <- as.data.frame(lapply(heart["cp"], function(x){replace(x, between(x, 0.25, 0.5), 0.4)}))
heart["cp"] <- as.data.frame(lapply(heart["cp"], function(x){replace(x, between(x, 0.5, 0.75), 0.6)}))
heart["cp"] <- as.data.frame(lapply(heart["cp"], function(x){replace(x, between(x, 0.75, 1), 0.9)}))
```

Normailze the maximum heart rate of the patient

```
dfNorm <- as.data.frame(lapply(heart["thalach"], normalize))
heart["thalach"] <- dfNorm
```

Normalize the thal and separate it in various groups to show what thal is more prone to heart disease

It uses the normalize function defined above and then categorize the data into **three** groups.
Thal: 3 = normal; 6 = fixed defect; 7 = reversable defect
After normalization the valuesaranges from **0-1**
It is grouped as follows

- **0.00 to 0.33** as **Group 1** giving it value **0.2**
- **0.33 to 0.67** as **Group 2** giving it value **0.6**
- **0.67 to 1.00** as **Group 3** giving it value **0.9**

```
dfNorm <- as.data.frame(lapply(heart["thal"], normalize))
heart["thal"] <- dfNorm
heart["thal"] <- as.data.frame(lapply(heart["thal"], function(x){replace(x, between(x, 0.0, 0.33), 0.2)
heart["thal"] <- as.data.frame(lapply(heart["thal"], function(x){replace(x, between(x, 0.33, 0.67), 0.6
heart["thal"] <- as.data.frame(lapply(heart["thal"], function(x){replace(x, between(x, 0.67, 1), 0.9)})
```

Normailze the peak exercise ST segment of the patient

```
dfNorm <- as.data.frame(lapply(heart["slope"], normalize))
heart["slope"] <- dfNorm
```

Normailze the major vessels (0-3) colored by flourosopy

```
dfNorm <- as.data.frame(lapply(heart["ca"], normalize))
heart["ca"] <- dfNorm
```

Value modification for feeding into Neural Network

Values of **Sex**, **Fasting blood suger**, **Resting electrocardiographic results** and **Exercise induced angina** are replaced so that it can be fed to the neural network.
- *1* is replaced with *0.9*
- *0* is replaced with *0.1*

```
heart["sex"] <- as.data.frame(lapply(heart["sex"], function(x){replace(x, x == 0, 0.1)}))
heart["sex"] <- as.data.frame(lapply(heart["sex"], function(x){replace(x, x == 1, 0.9)}))

heart["fbs"] <- as.data.frame(lapply(heart["fbs"], function(x){replace(x, x == 0, 0.1)}))
heart["fbs"] <- as.data.frame(lapply(heart["fbs"], function(x){replace(x, x == 1, 0.9)}))

heart["restecg"] <- as.data.frame(lapply(heart["restecg"], function(x){replace(x, x == 0, 0.1)}))
heart["restecg"] <- as.data.frame(lapply(heart["restecg"], function(x){replace(x, x == 1, 0.9)}))

heart["exang"] <- as.data.frame(lapply(heart["exang"], function(x){replace(x, x == 0, 0.1)}))
heart["exang"] <- as.data.frame(lapply(heart["exang"], function(x){replace(x, x == 1, 0.9)}))
```

The dataset after the modifications are made.

```
##   age sex  cp trestbps chol fbs restecg   thalach exang oldpeak slope ca thal
## 1 0.6 0.9 0.9      0.6  0.3 0.9     0.1 0.6030534   0.1     2.3   0.0  0  0.6
## 2 0.1 0.9 0.6      0.6  0.3 0.1     0.9 0.8854962   0.1     3.5   0.0  0  0.6
## 3 0.1 0.1 0.4      0.6  0.1 0.1     0.1 0.7709924   0.1     1.4   1.0  0  0.6
## 4 0.4 0.9 0.4      0.2  0.3 0.1     0.9 0.8167939   0.1     0.8   1.0  0  0.6
## 5 0.4 0.1 0.1      0.2  0.5 0.1     0.9 0.7022901   0.9     0.6   1.0  0  0.6
## 6 0.4 0.9 0.1      0.6  0.1 0.1     0.9 0.5877863   0.1     0.4   0.5  0  0.6
##   target
## 1      1
## 2      1
## 3      1
## 4      1
## 5      1
```

```
## 6      1
```

Splitting of training and testing data

We are using both randomly generated and sequentially choosen 75% of the data as training set and rest 25% as our test set.
train_ind_rand gives the indeces of the samples which are to be used as the training sample in the dataset.
trainrand gives the randomly choosen train dataset.
testrand given the randomly choosen test dataset.
trainseq gives the sequencially choosen train dataset.
testseq gives the sequentially choosen test dataset.

```
smp_size <- floor(0.75 * nrow(heart))
train_ind_rand <- sample(seq_len(nrow(heart)), size = smp_size)

trainrand <- heart[train_ind_rand, ]
testrand <- heart[-train_ind_rand, ]

trainseq <- heart[1:227, ]
testseq <- heart[227:303, ]
```

Writting the dataset into csv files so that it can be used in the Python program for Neural network classification.

- **heart1.csv** contain the modified Heart Disease dataset.
- **trainrand.csv** conains the randomly chosen train dataset.
- **testrand.csv** conains the randomly chosen test dataset.
- **trainseq.csv** conains the sequencially choosen train dataset.
- **testseq.csv** conains the sequentially choosen test dataset.

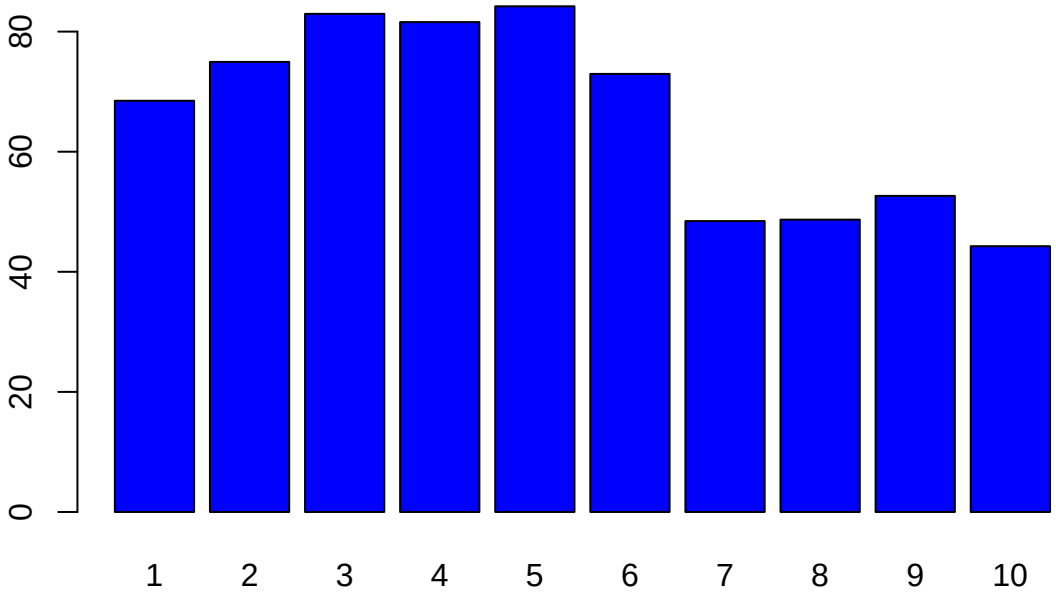
```
write.csv(heart, "~/HeartDisease/heart1.csv", row.names = FALSE)
write.csv(trainrand, "~/HeartDisease/trainrand.csv", row.names = FALSE)
write.csv(testrand, "~/HeartDisease/testrand.csv", row.names = FALSE)
write.csv(trainseq, "~/HeartDisease/trainseq.csv", row.names = FALSE)
write.csv(testseq, "~/HeartDisease/testseq.csv", row.names = FALSE)
```

Part 2:- Analysis of the neural network model

Plot for varying the number of hidden layers

Neural network with various number of hidden layers are tested and the results of the test accuracy are ploted.
Input layer contains **Thirteen** input neurons, each hidden layer has **Tweleve** neurons and the output layer has **One** neuron with **Two** classes.
- Class zero -> The patient is not suffering from heart disease.
- Class one -> The patient is suffering from heart disease.

Plot of test accuracy for different hidden layers



Conclusion from the plot

According to the test runs we can see that model with **Three**, **Four**, **Five** and **Six** hidden layers, having **Tweleve** neuron each perform better than the other choosen models.

Plot for varying the number of neurons

Plots for Accuracy and Mean Square Error

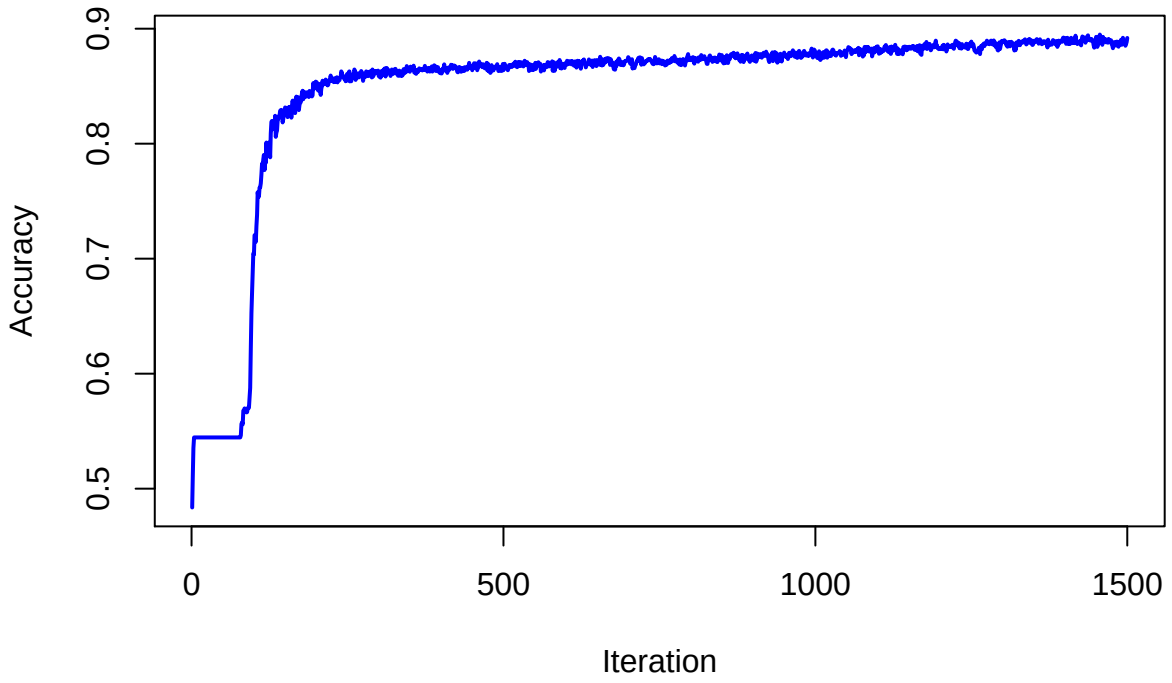
The neural network with the best results is run **Twinty** times and the average mean square error, and accuracy was taken and plot in the following graph.

Cloclusion from the plot

Structure of the model

- Input layer -> 13 input neuron
- First hidden layer -> 12 hidden neuraon
- Second hidden layer -> 12 hidden neuraon
- Third hidden layer -> 10 hidden neuraon
- Fourth hidden layer -> 8 hidden neuraon
- Fifth hidden layer -> 8 hidden neuraon
- Output layer -> 1 neuron, 2 classes

Plot for Accuracy of the model



Plot for Mean Square Error of the model